

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 10:19:04 ; Search time 450.333 Seconds
(without alignments)
8620.743 Million cell updates/sec

Title: US-09-451-739H-4

Perfect score: 857

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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19: /cgn2_6/ptodata/1/pubnpa/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616.4	71.9	2886	13	US-09-874-347-1 Sequence 1, Appli
2	616	71.9	2897	13	US-09-874-347-3 Sequence 3, Appli
3	616	71.9	8487	9	US-09-764-877-3454 Sequence 3454, Ap
4	616	71.9	8487	16	US-10-242-515-3454 Sequence 3454, Ap
5	606.4	70.8	873	10	US-09-968-853A-4 Sequence 4, Appli
6	604	70.5	2061	10	US-09-968-853A-2 Sequence 2, Appli
7	534.4	62.4	633	10	US-09-968-853A-6 Sequence 6, Appli
8	355	41.4	451	9	US-09-738-973-146 Sequence 146, App
9	355	41.4	451	9	US-09-854-133-146 Sequence 146, App
10	355	41.4	451	15	US-10-144-649A-146 Sequence 146, App
11	156.8	18.3	8370	13	US-10-221-714A-437 Sequence 437, App
12	142.6	16.6	840	14	US-10-115-899-6 Sequence 6, Appli
13	142.6	16.6	1078	14	US-10-115-899-7 Sequence 7, Appli
14	142.6	16.6	1080	13	US-10-203-532-7 Sequence 7, Appli

C 15	141	16.5	1890	13	US-10-027-632-261924	Sequence 261924,
C 16	141	16.5	1890	13	US-10-027-632-261925	Sequence 261925,
C 17	141	16.5	1890	16	US-10-027-632-261924	Sequence 261924,
C 18	141	16.5	1890	16	US-10-027-632-261925	Sequence 261925,
C 19	131.4	15.3	8370	13	US-10-221-714A-438	Sequence 438, App
C 20	110.2	12.9	421	10	US-09-918-995-37033	Sequence 37033, A
C 21	96.8	11.3	693	13	US-10-276-774-709	Sequence 709, App
C 22	96.8	11.3	1300	13	US-10-302-172-403	Sequence 403, App
C 23	84	9.8	1611	13	US-10-276-774-951	Sequence 951, App
C 24	77.6	9.1	667	13	US-10-425-114-36447	Sequence 36447, A
C 25	66.6	7.8	1336	16	US-10-264-049-545	Sequence 545, App
C 26	66.6	7.8	1807	13	US-10-203-532-2	Sequence 2, Appli
C 27	66.6	7.8	1864	15	US-10-037-270-435	Sequence 435, App
C 28	66.6	7.8	1864	16	US-10-117-722-435	Sequence 435, App
C 29	63.2	7.4	1254	13	US-10-424-599-73616	Sequence 73616, A
C 30	61.6	7.2	657	13	US-10-424-599-73612	Sequence 73612, A
C 31	61.2	7.1	669	13	US-10-425-114-17679	Sequence 17679, A
C 32	61.2	7.1	1200	13	US-10-424-599-19419	Sequence 19419, A
C 33	60.2	7.0	435	13	US-09-770-423-37	Sequence 37, Appli
C 34	60.2	7.0	813	9	US-09-938-842A-1178	Sequence 1178, Ap
C 35	60.2	7.0	813	11	US-09-938-842A-1178	Sequence 1178, Ap
C 36	59.6	7.0	1926	15	US-10-294-804-3	Sequence 3, Appli
C 37	59.6	7.0	8705	15	US-10-291-230-14	Sequence 14, Appli
C 38	59.6	7.0	8705	15	US-10-231-249-14	Sequence 14, Appli
C 39	59.6	7.0	8705	17	US-10-273-678-16	Sequence 16, Appli
C 40	59.6	7.0	9600	15	US-10-278-751-1	Sequence 1, Appli
C 41	59.6	7.0	10233	15	US-10-050-898-283	Sequence 283, App
C 42	59.6	7.0	10285	15	US-10-050-902-283	Sequence 283, App
C 43	58	6.8	919	13	US-10-425-114-22481	Sequence 22481, A
C 44	57.8	6.7	993	9	US-09-801-368-257	Sequence 257, App
C 45	57.8	6.7	14800	9	US-09-954-456-1601	Sequence 1601, Ap

ALIGNMENTS

RESULT 1

US-09-874-347-1
; Sequence 1, Application US/09874347
; Publication No. US20020039735A1
; GENERAL INFORMATION:
; APPLICANT: RIABOWOL, Karl T.
; APPLICANT: BOLAND, Donna
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO INGI ISOFORMS
; FILE REFERENCE: 028722-296
; CURRENT APPLICATION NUMBER: US/09/874,347
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/208,829
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 09/532,868
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 09/258,372
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 08/751,230
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 08/569,721
; PRIOR FILING DATE: 1995-12-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (433)..(1701)
US-09-874-347-1

Query Match 71.9%; Score 616.4; DB 13; Length 2886;
Best Local Similarity 85.5%; Pred. No. 3.6e-148;
Matches 686; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 56 CGCCCTCGGGCTATCCACCTCTTCTGGGCTCGGCTAGGACGCTTCCCTCTCA 115

811	DB	CTCTCCCGCTCAGCCCGGCCACTTTTCGGCGCGGATTTATAGCACTAGCAGTGATCCCG	970
116	QY	GGCCCCCTTTGTCTCCAAAGCGTTTCCAAACTGAGTACGGGAGACGACACAAAGGGAGGGC	175
871	DB	GGCCTGTGGCTCGGGCGCGGGCTCGAGTTCGACCGCCTCCCGCGACCCGCGGGCCG	930
176	QY	GGTGA CGGATGGCGCAGGCGCGGGACCGCTAGGCTGTGGAGTGTGGTCCGCCCGC	235
931	DB	GCTCGGAGACAGTTTCAGGCGCGATCTTTGCTGACCCGAGGTGGGCGCGCGTGGCGG	990
236	QY	GGAAATCGAGATCTGAAGGAGCTAGACGAGTGTCTAGAGCGTTTCACTGCCGAGACAGAC	295
991	DB	TGGAACAGATCTGAAGGAGCTAGACGAGTGTACGAGCGCTTCACTGGCGAGACAGAC	1050
296	QY	GGGGCGCAAGCGCGGATGTGCACTGTGTCCAGCGCGCTGTATCCGACGCCAGGAG	355
1051	DB	GGGGCGCAGAAGCGCGGATGTGCTCATGTGTGTCAGCGCGCTGTATCCGACGCCAGGAG	1110
356	QY	CTGGGCGACGAGAAGATCCAGATCTGTGAGCCAGATGTTGAGAGCTGTGGAGAACCCACG	415
1111	DB	CTGGGCGACGAGAAGATCCAGATCTGTGAGCCAGATGTTGAGAGCTGTGGAGAACCCACG	1170
416	QY	CGCAGGTGACAGCCACGTGGAGCTTTCGAGGCGCAGCAGAGCTGGGCGACACAGCG	475
1171	DB	CGCAGGTGACAGCCACGTGGAGCTTTCGAGGCGCAGCAGAGCTGGGCGACACAGCG	1230
476	QY	GGCAACAGCGGCAAGGCTGCGCGGACAGCCCAAAGGCGAGGCGGACGCGCAGGCTGAC	535
1231	DB	GGCAACAGCGGCAAGGCTGCGCGGACAGCCCAAAGGCGAGGCGGACGCGCAGGCTGAC	1290
536	QY	AAGCCCAACAGCAGCGCTCACGCGGCGAGCCAAACAGAGAACCGTGAGAACGCGTCC	595
1291	DB	AAGCCCAACAGCAGCGCTCACGCGGCGAGCCAAACAGAGAACCGTGAGAACGCGTCC	1350
596	QY	AGCAACACAGCACACGACGCGGCTCTGGGCGACACCCAAAGGAGAGAGGCCAAGACC	655
1351	DB	AGCAACACAGCACACGACGCGGCTCTGGGCGACACCCAAAGGAGAGAGGCCAAGACC	1410
656	QY	TCCAAGAAAGAGCGCTCCAAAGGCCAAGCGGAGCGAGAGGCGTCCCTGTCGCGACCTC	715
1411	DB	TCCAAGAAAGAGCGCTCCAAAGGCCAAGCGGAGCGAGAGGCGTCCCTGTCGCGACCTC	1470
716	QY	CCCATGACCCCAACGAAACCAAGTACTGTGTGCAACCAAGTCTCTCTATGGGAGATG	775
1471	DB	CCCATGACCCCAACGAAACCAAGTACTGTGTGCAACCAAGTCTCTCTATGGGAGATG	1530
776	QY	ATCGGCTGCGACAACGACGAGTGCCCATCGAGTGGTTTCCACTTCTCGTGCCTGGGGCTC	835
1531	DB	ATCGGCTGCGACAACGACGAGTGCCCATCGAGTGGTTTCCACTTCTCGTGCCTGGGGCTC	1590
836	QY	AATCATAAACCCCAAGGCCAAGT	857
1591	DB	AATCATAAACCCCAAGGCCAAGT	1612

RESULT 2

US-09-874-347-3
 / Sequence 3, Application US/09874347
 / Publication No. US20020039735A1
 / GENERAL INFORMATION:
 / APPLICANT: RIABOWOL, Karl T.
 / APPLICANT: BOLAND, Donna
 / TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO INGI ISOFORMS
 / FILE REFERENCE: 028722-296
 / CURRENT APPLICATION NUMBER: US/09/874,347
 / CURRENT FILING DATE: 2001-06-04
 / PRIOR APPLICATION NUMBER: US 60/208,829
 / PRIOR FILING DATE: 2000-06-02
 / PRIOR APPLICATION NUMBER: US 09/532,868
 / PRIOR FILING DATE: 2000-03-22
 / PRIOR APPLICATION NUMBER: US 09/258,372
 / PRIOR FILING DATE: 1999-02-26

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, , PRIOR APPLICATION NUMBER: US 08/751,230
, ,
, , PRIOR FILING DATE: 1996-11-15
, , PRIOR APPLICATION NUMBER: US 08/569,721
, ,
, , PRIOR FILING DATE: 1995-12-08
, , NUMBER OF SEQ ID NOS: 5
, , SOFTWARE: PatentIn Ver. 2.0
, , SEQ ID NO: 3
, , LENGTH: 2897
, , TYPE: DNA
, , ORGANISM: Homo sapiens
, , FEATURE:
, , NAME/KEY: CDS
, , LOCATION: (873)..(1712)
, , US-09-874,347-3

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Query Match 71.9%; Score 616; DB 13; Length 2897;

Query Match: 12.5%; Score Div: 25.13; Length: 100.00
Best Local Similarity 100.0%; Pred. No. 4.6e-148;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

242	QY	GAGATCTGAAAGAGCTAGACAGAGTGTACGAGCGCTTCAGTTCGGAGACACAGACGGGGCG	301
1008	DB	GAGATCTGAAAGAGCTAGACAGAGTGTACGAGCGCTTCAGTTCGGAGACACAGACGGGGCG	1067
302	QY	CAGAAGCGCGGATGTCGTCACTGTGTGACGCGCGCTGATCCGAGCCAGGAGCTGGGC	361
1068	DB	CAGAAGCGCGGATGTCGTCACTGTGTGACGCGCGCTGATCCGAGCCAGGAGCTGGGC	1127
362	QY	GACGAGAGATCCAGATCGTAGCCAGATGTGTGAGCTGTGTCGAGAACCGCACGCGGCAG	421
1128	DB	GACGAGAGATCCAGATCGTAGCCAGATGTGTGAGCTGTGTCGAGAACCGCACGCGGCAG	1187
422	QY	GTGGACAGCCACGTGTGAGGTGTTTCGAGGGCGCACGAGGAGCTGGCGCACACAGCGGGCAAC	481
1188	DB	GTGGACAGCCACGTGTGAGGTGTTTCGAGGGCGCACGAGGAGCTGGCGCACACAGCGGGCAAC	1247
482	QY	AGCGGCAAGGCTGGCGCGCACAGGCCCAAAGCGAGGCGGCAGCGAGGCTGACAAAGCCC	541
1248	DB	AGCGGCAAGGCTGGCGCGCACAGGCCCAAAGCGAGGCGGCAGCGAGGCTGACAAAGCCC	1307
542	QY	AACAGCAAGGCTTCAGGCGGCGAGCGCAACACACGAGAACCGTGTGAGAACCGCTCCAGCAAC	601
1308	DB	AACAGCAAGGCTTCAGGCGGCGAGCGCAACACACGAGAACCGTGTGAGAACCGCTCCAGCAAC	1367
602	QY	CACGACACGACGACGGCGCCTCGGGCACACCCAAAGGAGAAAGAGCCCAAGACCTCCAAAG	661
1368	DB	CACGACCAACGACGCGCGCTCGGGCACACCCAAAGGAGAAAGAGCCCAAGACCTCCAAAG	1427
662	QY	AGAAGAGGGTCCAAAGGCGAAGGCGGAGCGAGAGGCGTCCCTGCCAGACTCCCCATC	721
1428	DB	AGAAGAGGGTCCAAAGGCGAAGGCGGAGCGAGAGGCGTCCCTGCCAGACTCCCCATC	1487
722	QY	GACCCCAAGCAACCCACGTACTGTCTGTGTGCAACACAGTCTCTATGGGGAGATGATCGGC	781
1488	DB	GACCCCAAGCAACCCACGTACTGTCTGTGTGCAACACAGTCTCTATGGGGAGATGATCGGC	1547
782	QY	TGGGCAACGACGAGGTGCCCAATCGAGTGGTCCACTTCTCGTGGTGGGGCTCAATCAT	841
1548	DB	TGGGCAACGACGAGGTGCCCAATCGAGTGGTCCACTTCTCGTGGTGGGGCTCAATCAT	1607
842	QY	AAACCCCAAGGGCAAGT	857
1608	DB	AAACCCCAAGGGCAAGT	1623

RESULT 3

RESOL-764-877-3454
US Patent 3454 Application US/09764877
Serial No US2003014710A1
Patent No US2003014710A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877

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; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3454
; LENGTH: 8487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3454

Query Match      71.9%; Score 616; DB 9; Length 8487;
Best Local Similarity 100.0%; Pred. No. 5e-148;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 GAGATCTCTGAGGAGCTAGACGAGTCTACGAGCGCTTCAGTCGCGAGACAGCGGGCG 301
DB 6232 GAGATCTCTGAGGAGCTAGACGAGTCTACGAGCGCTTCAGTCGCGAGACAGCGGGCG 6291
QY 302 CAGAAAGCGCGGATCTGCACTGTGTGAGCGCGCTGTATCCGAGCCAGGAGCTGGGC 361
DB 6292 CAGAAAGCGCGGATCTGCACTGTGTGAGCGCGCTGTATCCGAGCCAGGAGCTGGGC 6351
QY 362 GACGAGAGATCCAGATCGTAGCGAGATGTTGGAGCTGTGGAGAACCGCACGCGGAG 421
DB 6352 GACGAGAGATCCAGATCGTAGCGAGATGTTGGAGCTGTGGAGAACCGCACGCGGAG 6411
QY 422 GTGGACAGCCAGCTGAGGAGCTGTTGAGGCGCAGCAGGAGCTGGGCGACACAGCGGCAAC 481
DB 6412 GTGGACAGCCAGCTGAGGAGCTGTTGAGGCGCAGCAGGAGCTGGGCGACACAGCGGCAAC 6471
QY 482 AGCGGAGGCTGGCGGAGCGAGCGCCAAAGCGAGGCGGCGAGCGAGCTGACAGCCC 541
DB 6472 AGCGGAGGCTGGCGGAGCGAGCGCCAAAGCGAGGCGGCGAGCGAGCTGACAGCCC 6531
QY 542 AACAGCAAGCGCTCAAGCGCGGAGCGGCAACAGAGAACCGTGAGAACCGCTCCAGCAAC 601
DB 6532 AACAGCAAGCGCTCAAGCGCGGAGCGGCAACAGAGAACCGTGAGAACCGCTCCAGCAAC 6591
QY 602 CAGGACCGAGCAGCGCGCTTCGGGCGACACCCAAAGAGAGAGAGCGGCAAGCTCCAG 661
DB 6592 CAGGACCGAGCAGCGCGCTTCGGGCGACACCCAAAGAGAGAGAGCGGCAAGCTCCAG 6651
QY 662 AAGAGAGAGCGCTCAAGCGGCAAGCGGAGGAGGCGTCCCTGCGGAGCTCCCGCATC 721
DB 6652 AAGAGAGAGCGCTCAAGCGGCAAGCGGAGGAGGCGTCCCTGCGGAGCTCCCGCATC 6711
QY 722 GACCCCAACGAAACCCAGCTACTGTCTGTGCAACCCAGGCTCTCTATGGGAGATGATCGGC 781
DB 6712 GACCCCAACGAAACCCAGCTACTGTCTGTGCAACCCAGGCTCTCTATGGGAGATGATCGGC 6771
QY 782 TCGGACAAACGAGAGTGGCCCATCGAGTGGTTCCACTTCTCTGCGTGGGCTCAATCAT 841
DB 6772 TCGGACAAACGAGAGTGGCCCATCGAGTGGTTCCACTTCTCTGCGTGGGCTCAATCAT 6831
QY 842 AAACCCCAAGGCAAGT 857
DB 6832 AAACCCCAAGGCAAGT 6847
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RESULT 4
US-10-242-515-3454
; Sequence 3454, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
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; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3454
; LENGTH: 8487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-3454

Query Match      71.9%; Score 616; DB 16; Length 8487;
Best Local Similarity 100.0%; Pred. No. 5e-148;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 GAGATCTCTGAGGAGCTAGACGAGTCTACGAGCGCTTCAGTCGCGAGACAGCGGGCG 301
DB 6232 GAGATCTCTGAGGAGCTAGACGAGTCTACGAGCGCTTCAGTCGCGAGACAGCGGGCG 6291
QY 302 CAGAAAGCGCGGATCTGCACTGTGTGAGCGCGCTGTATCCGAGCCAGGAGCTGGGC 361
DB 6292 CAGAAAGCGCGGATCTGCACTGTGTGAGCGCGCTGTATCCGAGCCAGGAGCTGGGC 6351
QY 362 GACGAGAGATCCAGATCGTAGCGAGATGTTGGAGCTGTGGAGAACCGCACGCGGAG 421
DB 6352 GACGAGAGATCCAGATCGTAGCGAGATGTTGGAGCTGTGGAGAACCGCACGCGGAG 6411
QY 422 GTGGACAGCCAGCTGAGGAGCTGTTGAGGCGCAGCAGGAGCTGGGCGACACAGCGGCAAC 481
DB 6412 GTGGACAGCCAGCTGAGGAGCTGTTGAGGCGCAGCAGGAGCTGGGCGACACAGCGGCAAC 6471
QY 482 AGCGGAGGCTGGCGGAGCGAGCGCCAAAGCGAGGCGGCGAGCGAGCTGACAGCCC 541
DB 6472 AGCGGAGGCTGGCGGAGCGAGCGCCAAAGCGAGGCGGCGAGCGAGCTGACAGCCC 6531
QY 542 AACAGCAAGCGCTCAAGCGCGGAGCGGCAACAGAGAACCGTGAGAACCGCTCCAGCAAC 601
DB 6532 AACAGCAAGCGCTCAAGCGCGGAGCGGCAACAGAGAACCGTGAGAACCGCTCCAGCAAC 6591
QY 602 CAGGACCGAGCAGCGCGCTTCGGGCGACACCCAAAGAGAGAGAGCGGCAAGCTCCAG 661
DB 6592 CAGGACCGAGCAGCGCGCTTCGGGCGACACCCAAAGAGAGAGAGCGGCAAGCTCCAG 6651
QY 662 AAGAGAGAGCGCTCAAGCGGCAAGCGGAGGAGGCGTCCCTGCGGAGCTCCCGCATC 721
DB 6652 AAGAGAGAGCGCTCAAGCGGCAAGCGGAGGAGGCGTCCCTGCGGAGCTCCCGCATC 6711
QY 722 GACCCCAACGAAACCCAGCTACTGTCTGTGCAACCCAGGCTCTCTATGGGAGATGATCGGC 781
DB 6712 GACCCCAACGAAACCCAGCTACTGTCTGTGCAACCCAGGCTCTCTATGGGAGATGATCGGC 6771
QY 782 TCGGACAAACGAGAGTGGCCCATCGAGTGGTTCCACTTCTCTGCGTGGGCTCAATCAT 841
DB 6772 TCGGACAAACGAGAGTGGCCCATCGAGTGGTTCCACTTCTCTGCGTGGGCTCAATCAT 6831
QY 842 AAACCCCAAGGCAAGT 857
DB 6832 AAACCCCAAGGCAAGT 6847
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LOCATION: 16...897
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-968-653A-2

Query Match 70.5%; Score 604; DB 10; Length 2061;
Best Local Similarity 95.4%; Pred. No. 5.3e-145;
Matches 622; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 206 CTAGGCTGTGGAGTGTGTGTCGGCGCGCGGAAATGGAGATCTTGAAGAGCTAGACGAG 265
DB 160 CTGACCCGAGGTTGGCGCGCGCTGGCGTGGAAACAGATCTTGAAGCGCTAGACGAG 219
QY 266 TCTACGAGCGTTTCACTGTCGACAGACAGCGGGGCGGAGAGCGCGGATGTCACATGT 325
DB 220 TCTACGAGCGTTTCACTGTCGACAGACAGCGGGGCGGAGAGCGCGGATGTCACATGT 279
QY 326 GTGACGCGCGCTGATCCGACGACGAGAGCTGGGCGACGAGAAATCCAGATCGTGTAGC 385
DB 280 GTGACGCGCGCTGATCCGACGACGAGAGCTGGGCGACGAGAAATCCAGATCGTGTAGC 339
QY 386 CAGATGTTGAGCTGTGTGAGAACCGACGCGCGGAGGTGGACAGCCAGCTGGAGCTGTT 445
DB 340 CAGATGTTGAGCTGTGTGAGAACCGACGCGCGGAGGTGGACAGCCAGCTGGAGCTGTT 399
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DB 400 GAGGCGACAGAGCTGGGCGACACAGTGCGGCAACAGCGGCAAGGTTGGGCGGACAGG 459
QY 506 CCCAAGGCGAGCGCGGACGAGCTGACAGCCCAACAGCAAGGCTCAGCGGGCAG 565
DB 460 CCCAATGGCGATGCGGTAGCGAGTCTGACAGCCCAACAGCAAGGCTCAGCGGGCAG 519
QY 566 CGCAACCAACAGAACCGTGGAGAACCGCTCCAGCAACACGACGACGAGCGCGCTCG 625
DB 520 CGCAACCAACAGAACCGTGGAGAACCGCTCCAGCAACACGACGACGAGCGCGCTCG 579
QY 626 GGCACACCAAGAGAGAGCGCAAGACTCTCAAGAGAGAGAGGCTCCAGGCGAG 685
DB 580 GGCACACCAAGAGAGAGCGCAAGACTCTCAAGAGAGAGAGGCTCCAGGCGAG 639
QY 686 GCGGAGCGAGAGCGCTCCCTGCGGACCTCCCATCGACCCCAACGAAACCCACGTA 745
DB 640 GCGGAGCGAGAGCGCTCCCTGCGGACCTCCCATCGACCCCAACGAAACCCACGTA 699
QY 746 CTGTGCAACAGGTTCTTATGGGAGATGATCGGTGCGACAAAGAGTGCCCATC 805
DB 700 CTGTGCAACAGGTTCTTATGGGAGATGATCGGTGCGACAAAGAGTGCCCATC 759
QY 806 GAGTGCTTCCACTTCTGTCGTCGTCGTCGTCATATATACCCAGGCAAGT 857
DB 760 GAGTGCTTCCACTTCTGTCGTCGTCGTCGTCATATATACCCAGGCAAGT 811

RESULT 7

US-09-968-653A-6
Sequence 6, Application US/09968653A
Publication No. US20030073084A1

GENERAL INFORMATION:

APPLICANT: Gudkov, Andrey V
Garkavstev, Igor
Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
Pathway

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: 01-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: No. US20030073084Ainan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..630
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-968-653A-6

Query Match 62.4%; Score 534.4; DB 10; Length 633;

Best Local Similarity 98.9%; Pred. No. 3.2e-127;
Matches 538; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 314 ATGTCGACCTGTGTGACGCGCGCTGATCCGACGACGAGCTGGCGACGAGAAGATC 373
DB 1 ATGTCGACCTGTGTGACGCGCGCTGATCCGACGACGAGCTGGCGACGAGAAGATC 60
QY 374 CAGATCTGAGCCAGATGTGTGAGCTGTGTGAGAACCGACGCGGAGGTGGACAGCCAC 433
DB 61 CAGATCTGAGCCAGATGTGTGAGCTGTGTGAGAACCGACGCGGAGGTGGACAGCCAC 120
QY 434 GTGAGCTGTTTCAGGCGGACGAGGAGCTGGGCGACACAGCGGCGCAACAGCGCAAGGCT 493
DB 121 GTGAGCTGTTTCAGGCGGACGAGGAGCTGGGCGACACAGTGGCGACACAGCGCAAGGTT 180
QY 494 GGCCTGACAGCGCCCAAGGCGGAGCGGACGCGAGCTGACAGCCCAACAGCAAGCGC 553
DB 181 GGCCTGACAGCGCCCAATGCGATGCGTAGCGAGTCTGACAAAGCCCAACAGCAAGCGC 240
QY 554 TCACGCGGACGACGCAACAGGAGACCGGTGAGAACCGCTCCAGACACGACGACCGAC 613
DB 241 TCACGCGGACGACGCAACAGGAGACCGGTGAGAACCGCTCCAGACACGACGACCGAC 300
QY 614 GACGCGCTCTCGGCGACACACCAAGGAGAGAGCCCAAGACCTCCCAAGAGAGAGAGCGC 673
DB 301 GACGCGCTCTCGGCGACACACCAAGGAGAGAGAGCCCAAGACCTCCCAAGAGAGAGAGCGC 360
QY 674 TCCAGGCGCAAGCGGAGCGAGAGCGTCCCTGCGACACTCCCATCGACCCCAAGAA 733
DB 361 TCCAGGCGCAAGCGGAGCGAGAGCGTCCCTGCGACACTCCCATCGACCCCAAGAA 420
QY 734 CCCACGTACTGTGTGTGCAACCGAGTCTCTATGGGAGATGATCGGCTCGGACCAAGC 793
DB 421 CCCACGTACTGTGTGTGCAACCGAGTCTCTATGGGAGATGATCGGCTCGGACCAAGC 480
QY 794 GAGTGCCCGCATCGAGTGGTTCCACTTCTGTCGTCGTCGTCGTCATATATACCAAGGCG 853
DB 481 GAGTGCCCGCATCGAGTGGTTCCACTTCTGTCGTCGTCGTCGTCATATATACCAAGGCG 540
QY 854 AAGT 857
DB 541 AAGT 544

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RESULT 8
US-09-738-973-146
; Sequence 146, Application US/09738973
; Patent No. US2002110563A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Algate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Elliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 21021.475C9
; CURRENT APPLICATION NUMBER: US/09/738,973
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-738-973-146

Query Match 41.4%; Score 355; DB 9; Length 451;
Best Local Similarity 99.7%; Pred. No. 2.7e-81;
Matches 366; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 242 GAGATCTCTGAAGGAGCTAGACGAGTGTCTACGAGCGCTTCAGTCGCGAGACAGACAGCGGGCG 301
DB 86 GAGATCTCTGAAGGAGCTAGACGAGTGTCTACGAGCGCTTCAGTCGCGAGACAGACAGCGGGCG 145

QY 302 CAGAAGCGGCGGATGCTGCACTGTGTGACGCGCGCGCTGTATCGGACGCCAGAGCTGGGC 361
DB 146 CAGAAGCGGCGGATGCTGCACTGTGTGACGCGCGCGCTGTATCGGACGCCAGAGCTGGGC 204

QY 362 GACGAGAAGATCCAGATCGTGAGCCAGATGCTGAGCTGGTGGAGAACCGCACGCGCGAG 421
DB 205 GACGAGAAGATCCAGATCGTGAGCCAGATGCTGAGCTGGTGGAGAACCGCACGCGCGAG 264

QY 422 GTGACACGCCACGTGGAGACTGTTGAGCGCGACGAGAGCTGGGGCGACACAGCGGGCGAAC 481
DB 265 GTGACACGCCACGTGGAGACTGTTGAGCGCGACGAGAGCTGGGGCGACACAGCGGGCGAAC 324

QY 482 AGCGCAAGGCTGGCGCGCGACAGAGGCCAAAAGCGAGGCGCGAGCGCGAGCTGACAAAGGCC 541
DB 325 AGCGCAAGGCTGGCGCGCGACAGAGGCCAAAAGCGAGGCGCGAGCGCGAGCTGACAAAGGCC 384

QY 542 AACACGACGGCTACGGCGGCGAGCGCAACACGAGAACCCGTGAGAACCGCTCCAGCGAAC 601
DB 385 AACACGACGGCTACGGCGGCGAGCGCAACACGAGAACCCGTGAGAACCGCTCCAGCGAAC 444

QY 602 CACGACC 608
DB 445 CACGACC 451

RESULT 9
US-09-854-133-146
; Sequence 146, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.

```


QY 661 GAAGGAGAGCGCTCCAGGCGCAAGGGGAGGAGCGCGTCCCTCCGACCTCCCAT 720

Db 561 GAAAGAGAAAGCGCTCCAGGCGCAAGGAGGAGGAGCGCTCCCTTTGATTTGCAAT 620

QY 721 CGACCCCAACGAGCGCTCCAGGCGCAAGGAGGAGGAGCGCTCCCTTTGATTTGCAAT 780

Db 621 AGATCCTAATGAACCTACATCTCTTATGCAACCAAGTGTCTTATGGGAGATGATAG 680

QY 781 CTGGACACGAGCGCTCCAGGCGCAAGGAGGAGGAGCGCTCCCTTTGATTTGCAAT 840

Db 681 ATGGACATGAACGAGTGTCAATTTGATTTGATTTGATTTGATTTGATTTGATTT 740

QY 841 TAAACCCCAAGGCGCAAGT 857

Db 741 TAAACCAAGGCGCAAGT 757

RESULT 13

US-10-115-899-7

Sequence 7, Application US/10115899

Publication No. US20020151025A1

GENERAL INFORMATION:

APPLICANT: Oetuka Pharmaceutical Co., Ltd.

TITLE OF INVENTION: Human TS403 gene and human INGL1 gene

FILE REFERENCE: Q60193

CURRENT APPLICATION NUMBER: US/10/115,899

CURRENT FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: 09/601,478

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: JP H10-134679

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: JP H10-73234

PRIOR FILING DATE: 1998-03-05

PRIOR APPLICATION NUMBER: JP H10-38133

PRIOR FILING DATE: 1998-02-03

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO. 7

LENGTH: 1078

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: human embryonic brain cDNA library

NAME/KEY: CDS

LOCATION: (92)..(931)

US-10-115-899-7

Query Match 16.6%; Score 142.6; DB 14; Length 1078;

Best Local Similarity 55.3%; Pred. No. 6.9e-27;

Matches 341; Conservative 0; Mismatches 244; Indels 32; Gaps 2;

QY 242 GAGATCCTGAAGGAGCTACGAGTGTCTACGAGCGCTTCAGTCGCGAGACAGACGGGCG 301

Db 263 GAAACGTTAAGGAAATTTGATGTCTACGAAATATAGAAAGAGATGATTTAAAC 322

QY 302 CAGAAGCGGAGTGTGCTGCTGTGTGAGCGCGGCTGATCCGAGCGAGAGCTGGGC 361

Db 323 CAGAAGAAACGCTACAGCAGCTTCTCCAGAGAGCACTAAATTAATGTCAGAAATTTGGA 382

QY 362 GACGAGAAATCCAGATCTGAGCAGATGTGTGAGTGTGTGAGAACCGCAGCGGCGAG 421

Db 383 GATGAAAAATACAGATTGTTACAAATGCTCGAATTTGTTGAAAAATCGGCAAGACAA 442

QY 422 GTGGACAGCCAGTGTGAGTGTGTGAGGCGGAGCAGGAGCTGGGCGACACAGCGGGCAAC 481

Db 443 ATGGAGTTACCTACAGTGTGTTCCAGATC----- 473

QY 482 AGCGGAAGGCTGGCGGAGCAGGCGGCGGAGGCGGAGCGGAGCTGACAGCGCC 541

Db 474 --CTGTGAAGTGAACAGCCCTCAGATAAGCAAGATGATTTCCGCCCAACCAAGAG 531

QY 542 AACAGCAAG--CGTCTACGCGGCGAGCGCAACAAACGAGAACCGGTGAGAACCGCTCCAGCAA 600

Db 532 ATCTTTCAAGAAAGACCCCGCAGGCGAGCCAGTGTAAAGCGTGAATTTATGTCAATGGC 591

QY 601 CCACGACACGAGCAGCGCGCTCGGGCACACCCCAAGGAGGAGGAGGAGGAGGAGGAGG 660

Db 592 AAATGGGATTGAGACTGTGATGATCAGCCACCTTAAGAAAGAAATCCAAGTCAGCAA 651

QY 661 GAAGAAAGCGCTCCAGGCGCAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720

Db 652 GAAAAAGAAACCTCCAAAGGCGCAAGCAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAG 711

QY 721 CGACCCCAACGAGCGCTACTGTCTGCAACAGGCTCTCTATGGGAGAGATGATCGG 780

Db 712 AGATCTTAATGAACCTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAGG 771

QY 781 CTGGACACGAGCGAGTGTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

Db 772 ATGTGACATGAACAGTGTCCAATTAATGTTGTTTCACTTTTCACTGTGTGTTTCACTTACCTA 831

QY 841 TAAACCCCAAGGCGCAAGT 857

Db 832 TAAACCAAGGCGCAAGT 848

RESULT 14

US-10-203-532-7

Sequence 7, Application US/10203532

Publication No. US20040058379A1

GENERAL INFORMATION:

APPLICANT: Harris, Curtis C.

APPLICANT: Nagashima, Makoto

APPLICANT: as represented by The Secretary of the

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: New Tumor Suppressor Gene, p47ING3

FILE REFERENCE: 015280-401100US

CURRENT APPLICATION NUMBER: US/10/203,532

CURRENT FILING DATE: 2002-08-08

PRIOR APPLICATION NUMBER: US 60/181,292

PRIOR FILING DATE: 2000-02-09

PRIOR APPLICATION NUMBER: WO PCT/US01/04425

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 1080

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: p33ING2

US-10-203-532-7

Query Match 16.6%; Score 142.6; DB 13; Length 1080;

Best Local Similarity 55.3%; Pred. No. 6.9e-27;

Matches 341; Conservative 0; Mismatches 244; Indels 32; Gaps 2;

QY 242 GAGATCCTGAAGGAGCTACGAGTGTCTACGAGCGCTTCAGTCGCGAGACAGACGGGCG 301

Db 239 GAAACGTTAAGGAAATTTGATGTCTACGAAATATAGAAAGAGATGATTTAAAC 298

QY 302 CAGAAGCGGCGGAGTGTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361

Db 299 CAGAAGAAACGCTACAGCAGCTTCTCCAGAGAGCACTAAATTAATAGTCAAGATTTGGA 358

QY 362 GACGAGAAATCCAGATCTGAGCAGATGTGTGAGTGTGTGAGTGTGTGAGAACCGCAGCGGCGAG 421

Db 359 GATGAAAAATACAGATTGTTACAAATGCTCTGAAATTTGTTGAAAAATTCGGCAAGACAA 418

QY 422 GTGGACAGCCAGTGTGAGTGTGTTGAGGCGGAGGAGCTGGGCGACACAGCGGGCAAC 481

Db 419 ATGGAGTTACCTACAGTGTGTTCCAGATC----- 449

QY 482 AGCGGAAGGCTGGCGGAGCAGGCGGCGGAGGCGGAGGCGGAGGCTGACAGCGCC 541

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Db 450 --CTGCTGAAGTGAACGAGCCTCAGATAAAGCAAAAGATGGATTCCAGCCCAACAGAAAG 507
QY 542 AACAGCAAG-CGCTCACGCGCGCAGCGCAACAAACGAGAACCGTGAGAAACGGGTCCAGCAA 600
Db 508 ATCTTCAAGAACACCCCGCAGCGACCGGACCAAGTCAAAAGCCGTGATTTATGTTCACATGGC 567
QY 601 CCACGACCACGAGCAGCGCGCTCGGCGACACCCAGGAGAGAGAGGCGCAAGCTCCAA 660
Db 568 AATGGGATGAAGACTGTGTATGATCAGCCACCTAAAGAAAGAAATCAAAGTCAGCAAA 627
QY 661 GAAGAAGAGCGCTCCAGGCGCAAGCGGAGCGAGAGGCGTCCCTGCGGACCTCCCCAT 720
Db 628 GAAAGAAACGCTCCAGGCGCAAGCAGGAAAGGAAGCTTCACCTGTGAGTTTGCAAT 687
QY 721 CGACCCCAACGACCACTACTGTCTGTGCAACCAAGTCTCTATGCGGAGATGATCGG 780
Db 688 AGATCCTAATGAACCTACATCTGTATTGCAACCAAGTGTCTTATGGGAGATGATAGG 747
QY 781 CTGCGACCAACGAGTGGCCCATCGAGTGGTTCACATTTCTCGTGGTGGGCTCAATCA 840
Db 748 ATGTGACATGAACAGTGTCCAAATGAATGGTTTCACTTTTCATGTGTTTCACTTACCTA 807
QY 841 TAAACCCAAAGGCAAGT 857
Db 808 TAAACCAAGGGGAAT 824
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RESULT 15

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US-10-027-632-261924/c
; Sequence 261924, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261924
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261924
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Query Match 16.5%; Score 141; DB 13; Length 1890;
Best Local Similarity 61.6%; Pred. No. 1.8e-26;
Matches 322; Conservative 0; Mismatches 175; Indels 26; Gaps 5;

QY 289 GACAGAGCGGCGCAGAACGCGCGATGCTGCACCTGTGTGACGCGCGCGCTGATCCGAG 348
Db 1670 GAGGAGGGGTACCCAGAGAGAGGGGTGTATCCGTGCATCCAGAGAGCCCTGACTCGGAG 1611
QY 349 CCAGGAGCTGGGCGACAGAGATCCAGATCGTGACGAGATGGTGGAGCTGGTGAGAA 408
Db 1610 CCAGGAGCTGGGCGTTGAGAGATCCAGA--CTGAGTCCGACGAGGAGCTGGTGAGAG 1553
QY 409 CCGCAGCGCGCAGGTGGACAGCCACGTCGGAGTGTTCAGAGCGCGCAGCAGGAGCTGGGCGA 468
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Db 1552 CAGGACCGGACAGATGGCGGTCTCCCGAGTCTCTTGGGCGAGCCAGAGATCAGGTT 1493
QY 469 CACAGCGGCGCAACAGCGGCAAGGCTGGCGCGACAGGCCCAAGGCGAGCGCGAGCGCA 528
Db 1492 CCCTGTAGCTGCAGAGCCCGCCACAATCGCGGGAAGATGATAATCAGCAG----- 1440
QY 529 GGCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAGCGCAACACGAGAACCGTGAGAA 588
Db 1439 GGAGAAACGCGGATTAACAAAGTGTTCCTCCGACAGTGCACGATGAGATCGAGAGGA 1380
QY 589 CGGCTCCAGCAACACGACCCACGACCGACGACGCGCGCTCGGCGCACACCCAGGAGAAAGGC 648
Db 1379 TGCATCCAATGATCAGCACCGACGACGAGATCACCAAGGAAACGCGCAAGG-CAAGAAAGC 1321
QY 649 CAAGACCTCCAAGAAAGAGAGCGCTCCAGGCGGAGGCGGAGCGGAGAGCGCTCCCTGC 708
Db 1320 AAAGACCTTGAAGAAAGAAAGAACCACTCCAGTGTCTACAGAGA-----GGCCCCCGC 1270
QY 709 CGACCTCCCCCATCGACCCCAACGAAACCCAGTACTGTGTGTGCAACACGAGTCTCTATGG 768
Db 1269 AGACCTTGCCATGACCGCAAGGAGACAGACAGCGTGTGGTCA-----GGTCTACAG 1217
QY 769 GGAGATGATCGGCTGCGACAAACGACGAGTGGCCCCCATCGAGTGG 811
Db 1216 AGAAGGAGCGGCTGTGACAAACCAACGAGTGGCCCCCAGGAGTGG 1174
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Search completed: May 6, 2004, 14:05:49

Job time : 452.333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 06:27:28 ; Search time 2858.77 Seconds

(without alignments)
8952.060 Million cell updates/sec

Title: US-09-451-739H-4
Perfect score: 857
Sequence: 1 cctccgagacgtgtccat.....tcataaacccaagggaagt 857

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthu:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	71.9	873	13	BQ430264
2	615	71.8	704	29	AY404082
3	606.8	70.8	1110	12	BM457587
4	603.8	70.5	746	9	AV726745

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	592.2	69.1	742	9	AV727365
6	591.4	69.0	982	13	BQ883364
7	589.8	68.8	698	29	AY404083
8	586.8	68.5	959	13	BU166657
9	584.6	68.2	1006	12	BM926787
10	579.8	67.7	1201	13	EX461522
11	574.8	67.1	894	13	BQ883151
12	561.4	65.5	1155	12	BM477126
13	557.8	65.1	722	9	AV727700
14	557	65.0	739	9	AL043324
15	555.4	64.8	897	13	BQ679315
16	528	61.6	757	12	BI523956
17	509.8	59.5	820	12	BI819716
18	492	56.4	651	12	BM042055
19	466.6	54.4	1000	13	BQ677075
20	464.2	54.2	761	12	BM042700
21	462.6	54.0	807	12	BI755594
22	451.6	52.7	803	12	BG394998
23	447.8	52.3	1971	11	AK035490
24	446.4	52.1	975	13	BQ934291
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27	444.8	51.9	664	10	BB614156
28	444.8	51.9	1514	11	AK076482
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30	438.8	51.2	681	14	CB447256
31	432.8	50.5	691	13	BY720374
32	431.4	50.3	627	14	CF791045
33	428	49.9	694	13	BY736023
34	423.2	49.4	582	12	BI898813
35	419	48.9	782	14	CK032035
36	418.8	48.9	556	29	CC544458
37	408.2	47.6	844	12	BG862842
38	406.4	47.4	716	12	BI107722
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40	390.2	45.5	667	9	AI956653
41	389.2	45.4	842	14	CF909709
42	384.2	44.8	1041	13	BU168690
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44	378.4	44.2	729	13	BU622930
45	374.2	43.7	746	10	BF119420

ALIGNMENTS

RESULT 1
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LOCUS BQ430264 873 bp mRNA linear EST 24-MAY-2002
DEFINITION AGENCOURT_7761891 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:5017969
5', mRNA sequence.
ACCESSION BQ430264
VERSION BQ430264.1 GI:21169340
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 873)
AUTHORS NIH-MGC http://mgc.nhl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapps-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNMI3218 row: b column: 18
High quality sequence stop: 731.

FEATURES	Location/Qualifiers		Homo sapiens	
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source	/db_xref="taxon:9606"		Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,	
	/clone="IMAGE:6017969"		Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,	
	/tissue type="epithelioid carcinoma"		Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,	
	/lab host="DH10B (phage-resistant)"		Adams, M.D. and Cargill, M.	
/clone lib="NH MGC 70"				
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: NotI;				
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.				
Average insert size 1.1 kb. Library constructed by Life				
Technologies."				
ORIGIN	71.9%; Score 616; DB 13; Length 873;		Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,	
	Query Match		Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,	
	Best Local Similarity 100.0%; Pred. No. 1.5e-88;		Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,	
	Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Adams, M.D. and Cargill, M.	
QY	242 GAGATCCTGAAGAGCTAGACGAGTGTACGAGCGCTTCACTCGCGACAGACGCGGCG 301		Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,	
	Db		Rockville, MD 20850, USA	
	32 GAGATCCTGAAGAGCTAGACGAGTGTACGAGCGCTTCACTCGCGACAGACGCGGCG 91		This sequence was made by sequencing genomic exons and ordering	
	QY		them based on alignment.	
QY	302 CAGAGCGCGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361		Location/Qualifiers	
	Db		1..704	
	92 CAGAGCGCGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 151		/organism="Homo sapiens"	
	QY		/mol_type="genomic DNA"	
QY	362 GACGAGAGATCCAGATCGTAGCGAGATGTGGAGCTGTGGAGAAACCGCACCGCGCAG 421		/db_xref="taxon:9606"	
	Db		<1..>704	
	152 GACGAGAGATCCAGATCGTAGCGAGATGTGGAGCTGTGGAGAAACCGCACCGCGCAG 211		/gene="ING1"	
	QY		/locus_tag="HCM1772"	
QY	422 GTGGACGCCAGCTGAGAGCTGTTCAGGCGCAGCAGGAGCTGGGCGACACAGCGGGCAAC 481		ORIGIN	
	Db		Query Match	
	212 GTGGACGCCAGCTGAGAGCTGTTCAGGCGCAGCAGGAGCTGGGCGACACAGCGGGCAAC 271		Best Local Similarity 100.0%; Pred. No. 2e-88;	
	QY		Matches 615; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	482 AGCGGCAAGGCTGGCGCGGACAGGCGCCAAAGGCGGAGGCGGCGAGCGCGCTGACAGCCC 541		QY	
	Db		243 AGATCCTGAAGAGCTAGACGAGTGTACGAGCGCTTCACTCGCGACAGACGCGGCGC 302	
	QY		Db	
	272 AGCGGCAAGGCTGGCGCGGACAGGCGCCAAAGGCGGAGGCGGCGAGCGCGCTGACAGCCC 331		1 AGATCCTGAAGAGCTAGACGAGTGTACGAGCGCTTCACTCGCGACAGACGCGGCGC 60	
QY	542 AACAGAGCGCTCAGCGCGGCGAGCGGCGCAACAGAGAACCGTGAAGACCGTCCAGCAAC 601		QY	
	Db		303 AGAAGCGGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 362	
	QY		Db	
	332 AACAGAGCGCTCAGCGCGGCGAGCGGCGCAACAGAGAACCGTGAAGACCGTCCAGCAAC 391		61 AGAAGCGGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120	
QY	602 CACGACCAAGCGCTCGGCGCTTCGGGCGCACACCCAGAGAGAGAGGCGGCGGCGGCGG 661		QY	
	Db		363 ACCGAGAGATCCAGATCGTAGCCAGATGTGGAGTGTGTGGAGAACCGCACCGCGCAGG 422	
	QY		Db	
	392 CACGACCAAGCGCTCGGCGCTTCGGGCGCACACCCAGAGAGAGAGGCGGCGGCGGCGG 451		121 ACCGAGAGATCCAGATCGTAGCCAGATGTGGAGTGTGTGGAGAACCGCACCGCGCAGG 180	
QY	662 AAGAGAGCGCTTCAAGCGCGAGCGGCGAGAGCGGCTGCCCTGCGGACCTCCCGATC 721		QY	
	Db		423 TGGACAGCCACGTGGAGCTGTTCGAGCGCAGCAGAGAGTGGGCGCACAGCGGCGCAACA 482	
	QY		Db	
	452 AAGAGAGCGCTTCAAGCGCGAGCGGCGAGAGCGGCTGCCCTGCGGACCTCCCGATC 511		181 TGGACAGCCACGTGGAGCTGTTCGAGCGCAGCAGAGAGTGGGCGCACAGCGGCGCAACA 240	
QY	722 GACCCCAAGAACCCACGCTACTGTCTGTCAACACCGTCTCTATGGGAGATGATCGGC 781		QY	
	Db		483 GCAGCAAGGCTGGCGCGGCGAGCGCCCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 542	
	QY		Db	
	512 GACCCCAAGAACCCACGCTACTGTCTGTCAACACCGTCTCTATGGGAGATGATCGGC 571		241 GCAGCAAGGCTGGCGCGGCGAGCGCCCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 300	
QY	782 TGGCAACAGCAGAGTGCCTCATTCGAGTGGTTCATCTTCGTCGTGGGGCTCAATCAT 841		QY	
	Db		543 ACAGCAAGCGCTCAGCGCGGCGAGCGGCGCAACAACAGAGAACCGTGAAGACCGTCCAGAAC 602	
	QY		Db	
	572 TGGCAACAGCAGAGTGCCTCATTCGAGTGGTTCATCTTCGTCGTGGGGCTCAATCAT 631		301 ACAGCAAGCGCTCAGCGCGGCGAGCGGCGCAACAACAGAGAACCGTGAAGACCGTCCAGAAC 360	
QY	842 AAACCCCAAGGCAAGT 857		QY	
	Db		603 ACAGCAAGCGCTCAGCGCGGCGAGCGGCGCAACCAGAGAGAGAGGCGGCGGCGGCGGCGG 662	
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	632 AAACCCCAAGGCAAGT 647		361 ACAGCAAGCGCTCAGCGCGGCGAGCGGCGCAACCAGAGAGAGAGGCGGCGGCGGCGGCGG 420	
RESULT 2	AY404082		QY	
	LOCUS		663 AGAAGAGCGCTCAGAGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 722	
	DEFINITION		Db	
	Homo sapiens ING1 gene, VIRTUAL TRANSCRIPT, partial sequence,		421 AGAAGAGCGCTCAGAGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480	
ACCESSION	AY404082		QY	
	VERSION		723 ACCCAAGCAAGACCGTACTGTCTGTCAACACCGTCTCTATGGGAGATGATCGGCT 782	
	KEYWORDS		Db	
	GSS.		481 ACCCAAGCAAGACCGTACTGTCTGTCAACACCGTCTCTATGGGAGATGATCGGCT 540	
SOURCE	Homo sapiens (human)		QY	
	704 bp DNA linear GSS 15-DEC-2003		783 GCAGCAAGCAGAGTGCCTCATTCGAGTGGTTCATCTTCGTCGTGGGGCTCAATCAT 842	
	AY404082			
	Homo sapiens ING1 gene, VIRTUAL TRANSCRIPT, partial sequence,			

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Db      541 GCGACAAACGACGAGTCCCATCGAGTGTTCACCTTCCTCGTGGGCTCAATCATATA 600
      843 AACCCAGGGCAAGT 857
      601 AACCCAAAGGGCAAGT 615

RESULT 3
LOCUS   BM457587 1110 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6407600 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5585127
5', mRNA sequence.
ACCESSION BM457587
VERSION   BM457587.1 GI:18506627
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 1110)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgabsx@mail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM12350 row: 0 column: 16
          High quality sequence stop: 510.
          Location/Qualifiers
            1..1110
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:5585127"
              /tissue_type="embryonal carcinoma, cell line"
              /lab_host="PH10B (phage-resistant)"
              /clone_lib="NIH MGC 92"
              /notes="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
              Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
              Average insert size 2.5 kb. Library enriched for
              full-length clones and constructed by Life Technologies.
              Note: this is a NIH_MGC library."

FEATURES
source
Query Match 70.8%; Score 606.8; DB 12; Length 1110;
Best Local Similarity 95.8%; Pred. No. 4.6e-87;
Matches 623; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY      206 CTAGGCTGTGGAGTGTGTTCGGCGCGGGAATGGAGATCTTGAAGAGCTAGACGAG 265
      67 CTGACCCGAGGGTGGGGCGCGCGTGTGGGAAACAGATCTCTGAAGGAGCTAGACGAG 126
      266 TGCTACGAGCGCTTCAGTCCGAGACAGACGGGGCCGAGAGCGGGGATGTGCACTGT 325
      127 TGCTACGAGCGCTTCAGTCCGAGACAGACGGGGCCGAGAGCGGGGATGTGCACTGT 186
      326 GTCCAGCGCGCTGTATCCGACGCCAGCGAGCTGGGCGAGAGAGATCCAGATCTGTGAGC 385
      187 GTCCAGCGCGCGCTGTATCCGACGCCAGCGAGCTGGGCGAGAGATCCAGATCTGTGAGC 246
      386 CAGATGTGTGAGTGTGGAGAACCCGACCGCGCAGGTGGACAGCCAGCTGGAGCTGTTC 445
      247 CAGATGTGTGAGTGTGGAGAACCCGACCGCGCAGGTGGACAGCCAGCTGTGAGCTGTTC 306
      446 GAGCGCGACGAGAGTGTGGCGACACAGCGGGCAACAGCGGGCAAGGCTGGCGCGACAGG 505

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Db      307 GAGCGCGCAGCAGGAGTGGCGGACACAGCGGGCAACAGCGGCAAGGCTGGCGGGACAG 366
      506 CCACAAAGCGGAGCGGCGAGCGAGGTGTGACAAAGCCCAACAGCAAGCGCTCACGGCGGGCAG 565
      367 CCACAAAGCGGAGCGGCGAGCGGCTGACAGGCCCAACAGCAAGCGCTCACGGCGGGCAG 426
      566 CGCAACAAACGAGAAACCGTGTGAGAACCGTCCAGCAACCAACAGCAAGCGCGGCTCG 625
      427 CGCAACAAACGAGAAACCGTGTGAGAACCGTCCAGCAACCAACAGCAAGCGCGGCTCG 486
      626 GGCACACCCCAAGGAGAGAGGCGCAAGACTCCCAAGAGAGAGCGCTCCCAAGGCGCAAG 695
      487 GGCACACCCCAAGGAGAGAGGCGCAAGACTCCCAAGAGAGAGCGCTCCCAAGGCGCAAG 546
      686 GCGGAGCGAGAGCGTCCCTCGCGACCTCCCATCGACCCCAACCAAGCAAGCGTACTGT 745
      547 GCGGAGCGAGAGCGTCCCTCGCGACCTCCCATCGACCCCAACCAAGCAAGCGTACTGT 606
      746 CTGTGCAACACAGCTCTCTATGCGGAGAGATCGGTGCGACCAACAGCAGTCCCCATC 805
      607 CTGTGCAACACAGCTCTCTATGCGGAGAGATCGGTGCGACCAACAGCAGTCCCCATC 666
      806 GAGTGTGTTCACCTTCTCGTGTGGGGCTCAATCATATAACCCCAAGGGCAA 855
      667 GAGTGTGTTCACCTTCTCGGCGGTGGGGCTCAATCATATAACCCCAAGGGCAA 716

RESULT 4
LOCUS   AV726745 746 bp mRNA linear EST 17-OCT-2000
DEFINITION AV726745 HTC Homo sapiens cDNA clone HTCAQD06 5', mRNA sequence.
ACCESSION AV726745
VERSION   AV726745.1 GI:10836166
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 746)
REFERENCE Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
          Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
          Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
          Chen, J., Chen, Z. and Han, Z.
          Homo sapiens cDNA HTC clones
          Unpublished (2000)
          Contact: Zeguang Han
          Chinese National Human Genome Center at Shanghai
          351 Gao Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
          201203, P. R. China
          Tel: 86-21-50801919 (ex.45)
          Fax: 86-21-50801922
          Email: hanzg@chgc.sh.cn
          This clone is available at CHGC in Shanghai.
          Location/Qualifiers
            1..746
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="HTCAQD06"
              /tissue_type="Hypothalamus"
              /dev_stage="Adult"
              /lab_host="SOLR"
              /clone_lib="HTC"
              /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
              XhoI"

FEATURES
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Query Match 70.5%; Score 603.8; DB 9; Length 746;
Best Local Similarity 95.1%; Pred. No. 1.3e-86;
Matches 520; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY      206 CTAGGCTGTGGAGTGTGTTCGGCGCGGGAATGGAGATCTTGAAGAGCTAGACGAG 265

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Db      6 CTGACCCGAGGGTGGGGCCGCGGTGGCCGTGGGAAACAGATCTTGAAGGAGCTAGACGAG 65
QY      266 TGCTACGAGCGCTTCAGTCGCGAGACACAGCGGGGCGCAGAAAGCGCGGAGTCTGCACCTGT 325
Db      66 TGCTACGAGCGCTTCAGTCGCGAGACACAGCGGGGCGCAGAAAGCGCGGATGCTGCACCTGT 125
QY      326 GTGACGCGCGCTGATCCGAGCGAGAGCTGGCGACGAGAAAGTCCAGATCGTGAGC 385
Db      126 GTGACGCGCGCTGATCCGAGCGAGAGCTGGCGACGAGAAAGTCCAGATCGTGAGC 185
QY      386 CAGATGGTGGAGCTGGTGAGAAACCGCACGCGGCGAGGTGGAGCCACCGTGGAGCTGTTTC 445
Db      186 CAGATGGTGGAGCTGGTGAGAAACCGCACGCGGCGAGGTGGAGCCACCGTGGAGCTGTTTC 245
QY      446 GAGGCGCAGCAGAGCTGGCGACACAGCGGGGCGCAGCGGCAAGGCTGGCGCGCAGG 505
Db      246 GAGGCGCAGCAGAGCTGGCGACACAGCGGGGCGCAGCGGCAAGGCTGGCGCGCAGG 305
QY      506 CCCAAGCGGAGCGGCGAGCGCTGACAAAGCCCAACAGCAGCGCTCAAGCGGCGCAG 565
Db      306 CCCAAGCGGAGCGGCGAGCGCTGACAAAGCCCAACAGCAGCGCTCAAGCGGCGCAG 365
QY      566 GCGACACAGAGAAACCGTGAGAAACCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 625
Db      366 GCGACACAGAGAAACCGTGAGAAACCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 425
QY      626 GGCACACCAAGGAGAGGAGCGGAGCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 685
Db      426 GGCACACCAAGGAGAGGAGCGGAGCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 485
QY      686 GCGGAGCGAGAGCGGCTCCGAGCGGAGCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 745
Db      486 GCGGAGCGAGAGCGGCTCCGAGCGGAGCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 545
QY      746 CTGTGCAACCAAGGAGAGCGGAGCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 805
Db      546 CTGTGCAACCAAGGAGAGCGGAGCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 605
QY      806 GAGTGGTTCACCTTCGTGGTGGGCTCAATCAATAAACCAGGCAAGT 857
Db      606 GAGTGGTTCACCTTCGTGGTGGGCTCAATCAATAAACCAGGCAAGT 857

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RESULT 5
AV727365 742 bp mRNA linear EST 17-OCT-2000
LOCUS
DEFINITION
AV727365 HTC Homo sapiens cDNA clone HTCAHQ9 5', mRNA sequence.
AV727365
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z., and Han, Z.
TITLE
Homo sapiens cDNA HTC clones
JOURNAL
Unpublished (2000)
COMMENT
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. .742
/organism="Homo sapiens"
/mol_type="mRNA"

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FEATURES
source
1. .742
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/mol_type="mRNA"

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RESULT 6
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LOCUS
DEFINITION
AGENCOURT 8071025 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089752
5', mRNA sequence.
ACCESSION
BQ883364
VERSION
BQ883364.1 GI:22275372
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 982)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS

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/db_xref="taxon:9606"
/clone="HTCAHQ9"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="HTC"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
Query Match 69.1%; Score 592.2; DB 9; Length 742;
Best Local Similarity 93.9%; Pred. No. 8.9e-85;
Matches 612; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 206 CTAGGCTGTGGAGTGTGGTCCGCGCGCGGGAATGGAGATCCCTGAGGAGCTAGACGAG 265
Db 6 CTGACCCGAGGGTGGGCGCGCGCTGGCGTGGGAAACAGATCTTGAAGGAGCTAGACGAG 65
QY 266 TGCTACGAGCGCTTCAGTCGCGAGACACAGCGGGGCGCAGAAAGCGCGGATGCTGCACCTGT 325
Db 66 TGCTACGAGCGCTTCAGTCGCGAGACACAGCGGGGCGCAGAAAGCGCGGATGCTGCACCTGT 125
QY 326 GTGACGCGCGCTGATCCGAGCGAGAGCTGGCGACGAGAAAGTCCAGATCGTGAGC 385
Db 126 GTGACGCGCGCTGATCCGAGCGAGAGCTGGCGACGAGAAAGTCCAGATCGTGAGC 185
QY 386 CAGATGGTGGAGCTGGTGAGAAACCGCACGCGGCGAGGTGGAGCCACCGTGGAGCTGTTTC 445
Db 186 CAGATGGTGGAGCTGGTGAGAAACCGCACGCGGCGAGGTGGAGCCACCGTGGAGCTGTTTC 245
QY 446 GAGGCGCAGCAGAGCTGGCGACACAGCGGGGCGCAGCGGCAAGGCTGGCGCGCAGG 505
Db 246 GAGGCGCAGCAGAGCTGGCGACACAGCGGGGCGCAGCGGCAAGGCTGGCGCGCAGG 305
QY 506 CCCAAGCGGAGCGGCGAGCGCTGACAAAGCCCAACAGCAGCGCTCAAGCGGCGCAG 565
Db 306 CCCAAGCGGAGCGGCGAGCGCTGACAAAGCCCAACAGCAGCGCTCAAGCGGCGCAG 365
QY 566 GCGACACAGAGAAACCGTGAGAAACCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 625
Db 366 GCGACACAGAGAAACCGTGAGAAACCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 425
QY 626 GGCACACCAAGGAGAGGAGCGGAGCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 685
Db 426 GGCACACCAAGGAGAGGAGCGGAGCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 485
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Db 546 CTGTGCAACCAAGGAGAGCGGAGCGCTCCAGCAACCAAGCAGCAGCGGCGCTCG 605
QY 806 GAGTGGTTCACCTTCGTGGTGGGCTCAATCAATAAACCAGGCAAGT 857
Db 606 GAGTGGTTCACCTTCGTGGTGGGCTCAATCAATAAACCAGGCAAGT 857

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TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: DCTD/DP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2330 row: a column: 17
High quality sequence stop: 577.
Location/Qualifiers
1. .982
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6089752"
/tissue_type="melanotic melanoma, cell line"
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/clone_lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies kit). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 69.0%; Score 591.4; DB 13; Length 982;
Best Local Similarity 87.2%; Pred. No. 1.3e-84; Indels 1; Gaps 1;
Matches 660; Conservative 0; Mismatches 96;

QY 98 GAAGCAGCTCCCTCTCAGCGCCCTTTGTCTCCAGCCCTTCCAACTGAGTACCGGAG 157
DB 11 GCAGTAGCAGTATCCCGGCGCTGTGGCTCGGGCGCGGTGTCAGTTCGGACCGCTC 70
QY 158 ACACACAAAGGAGGGCGGTGACGATGCGGAGCGGGGAGCGCGCTAGCTGCTGG 217
DB 71 CCGCGACCGCGGGCGCGCTCGGACACAGATTTCAGCGCGCATCTCTGTGACCGCGGG 130
QY 218 GAGTGTGTGTCGGCGCGGATGGAGATCCTGAAGGAGCTAGACGAGTGTACGAGCGC 277
DB 131 TGSGGCGCGGTGGCGGTGGAACAGATCCTGAAGGAGCTAGACGAGTGTACGAGCGC 190
QY 278 TTCAGTCCGAGACAGACGGGGCGCGAGACGGCGGATGCTGCACTGTGTGAGCGCGCG 337
DB 191 TTCAGTCCGAGACAGACGGGGCGCGAGACGGCGGATGCTGCACTGTGTGAGCGCGCG 250
QY 338 CTGATCCGAGCAGGAGCTGGCGGACGAGAGATCCAGATCGTAGCCAGATGTTGGAG 397
DB 251 CTGATCCGAGCAGGAGCTGGCGGACGAGAGATCCAGATCGTAGCCAGATGTTGGAG 310
QY 398 CTGGTGAGAACCGCGCGGAGTGGACAGCCAGCTGTTCAGGCGGACGAG 457
DB 311 CTGGTGAGAACCGCGCGGAGTGGACAGCCAGCTGTTCAGGCGGACGAG 370
QY 458 GAGCTGGGACACAGCGGGCGACAGCGGCAAGGCTGGCGGACAGGCGGCAAGCGAG 517
DB 371 GAGCTGGGACACAGCGGGCGACAGCGGCAAGGCTGGCGGACAGGCGGCAAGCGAG 430
QY 518 GCGGACGCGAGGCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGAGCGCAACACGAG 577
DB 431 GCGGACGCGAGGCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGAGCGCAACACGAG 490
QY 578 AACCGTGAGACGGCTCAGCAACACGAGCAGCGGCGCTTCGGGCAACCCAG 637
DB 491 AACCGTGAGACGGCTCAGCAACACGAGCAGCGGCGCTTCGGGCAACCCAG 550
QY 638 GAGAAAGAGCCCAAGACTCTCCAGAGAGAGAGAGCGTCTCAAGGCCAAGCGGAGGAG 697

DB 551 GAGAGAGAGCCCAAGACCTCCAGAGAGAGAGCGCTCCAGGCCAAGCGGAGCGAGAG 610
QY 598 GCCTCCCTCCCGAGCCTCCCTCCATCGACCCCAACGACCCACCTACTGTCTGTGCAACAG 757
DB 611 GCCTCCCTCCCGAGCCTCCCTCCATCGACCCCAACGACCCACCTACTGTCTGTGCAACAG 670
QY 758 GTCTCTATGGGAGATGATCGGCTCGCAACAGAGTGCCTCCATCGAGTGTGTTCCAC 817
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QY 818 TTCTCTGTGGT-GGGGCTCAATCATTAACCCCAAGGCG 853
DB 731 TTCTCTGTGGTGGGCGCTCATTAACCCCAAGGCG 767

RESULT 7
LOCUS AY404083 698 bp DNA linear GSS 15-DEC-2003
DEFINITION Pan troglodytes INGI gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY404083
VERSION AY404083.1 GI:39760066
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 698)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Infering nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL PUBLISHED 14671302
REFERENCE 2 (bases 1 to 698)
AUTHORS Todd,M.A., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Clark,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source 1..698
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..-698
/gene="ING1"
/locus_tag="HCM1772"

ORIGIN
Query Match 68.8%; Score 589.8; DB 29; Length 598;
Best Local Similarity 96.1%; Pred. No. 2.1e-84;
Matches 591; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 243 AGATCTCTGAGGAGCTAGACGAGTGTACGAGCGCTTCACTCGCGACACAGACGGGCGC 302
DB 1 AGATCTCTGAGGAGCTGACGAGTGTACGAGCGCTTCACTCGCGACACAGACGGGCGC 60
QY 303 AGAAGCGCGGATCTCTGACTGTGTGAGCGCGCTGTATCCGAGCAGCAGAGCTGGCG 362
DB 61 AGAAGCGCGGATCTCTGACTGTGTGAGCGCGCTGTATCCGAGCAGCAGAGCTGGCG 120
QY 363 ACGAGAGATCCAGATCGTGAGCCAGATGTGTGAGCTGTGTGAGAACCGCACCGGCGAG 422
DB 121 ACGAGAGATCCAGATCGTGAGCCAGATGTGTGAGCTGTGTGAGAACCGCACCGGCGAG 180

423 TGGACAGCCAGCTGGAGCTGTTTCAGAGCGCAGCAGAGCTGGCGCAGACAGCGGGCAACA 482
 Db TGGACAGCCAGCTGGAGCTGTTTCAGAGCGCAGCAGAGCTGGCGCAGACAGCGGGCAACA 240
 QY GGGGCAAGCTGGCGCGCAGCAGAGCCAAAGCGGCGCAGCGCGCAGCGCTGACAAGCCCA 542
 Db GGGGCAAGCTGGCGCGCAGCAGAGCCAAAGCGGCGCAGCGCGCAGCGCTGACAAGCCCA 300
 QY ACAGCAAGCGCTACCGCGGCGAGCGCAACACAGAGAACCTGTAGAAACCGTCCAGCAACC 602
 Db ACAGCAAGCGCTACCGCGGCGAGCGCAACACAGAGAACCTGTAGAAACCGTCCAGCAACC 360
 QY AGACACAGCAGACAGCGCGCTCGGCGCACACCAAGGAGAAAGGCGCAAGACCTCCCAAGA 662
 Db AGACACAGCAGCAGCGCGCTCGGCGCACACCAAGGAGAAAGGCGCAAGACCTCCCAAGA 420
 QY AGAAGAAGCGCTCCAAAGCCCAAGCGGCGAGCGCGCTGCCCTGCCGACCTCCCAATCG 722
 Db AGAAGAAGCGCTCCAAAGCCCAAGCGGCGAGCGCGCTGCCCTGCCGACCTCCCAATCG 480
 QY ACCCAACAGAACCCACGCTACTGTCTGTGCAACCGAGTCTCTATGGGAGATGATCGGCT 782
 Db ACCCAACAGAACCCACGCTACTGTCTGTGCAACCGAGTCTCTATGGGAGATGATCGGCT 540
 QY GCGACAAAGCAGAGTGCCTTCAGAGTGGTTCACCTTCTCGTGGCGTGGGGCTCAATCATA 842
 Db GCGACAAAGCAGAGTGCCTTCAGAGTGGTTCACCTTCTCGTGGCGTGGGGCTCAATCATA 600
 QY AACCCAGGCGCACT 857
 Db AACNNNGNGCAAGT 615

RESULT 8
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 LOCUS AGENCOURT_7959357 NIH_MGC_112 Homo sapiens cdna clone IMAGE:6110207
 DEFINITION 5', mRNA sequence.

ACCESSION BUI66657
 VERSION BUI66657.1 GI:22680609
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 959)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 cdna Library Preparation: Rubin Laboratory
 cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM2357 row: e column: 24
 High quality sequence start: 48
 High quality sequence stop: 599.
 Location/Qualifiers

1. .959
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 /lab_host="DH10B (phage-resistant)"
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 /notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:

FEATURES
 source

ORIGIN

Query Match 58.5%; Score 586.8; DB 13; Length 959;
 Best Local Similarity 95.6%; Pred No. 6, 9e-84;
 Matches 625; Conservative 0; Mismatches 27; Indels 2; Gaps 2;

QY 206 CTAGGCTGTGGAGTGTGTTCGGCGCGGGAATGGAGATCTCTGAAGAGCTAGACAG 265
 Db 154 CTGACCCGAGGCTGGGGCGCGCGTGGCGTGGAAACAGATCTCTGAAGAGCTAGACAG 213
 QY 266 TGCTACGAGCGCTTCAGTCCGAGACAGACGCGGCGGAGAGCGCGGATGTGCACTGT 325
 Db 214 TGCTACGAGCGCTTCAGTCCGAGACAGACGCGGCGGAGAGCGCGGATGTGCACTGT 273
 QY 326 GTGACGCGCGCTGATCCGACCGCAGGAGTGGCGGCGAGAGATCCAGATCGTGAGC 385
 Db 274 GTGACGCGCGCTGATCCGACCGCAGGAGTGGCGGCGAGAGATCCAGATCGTGAGC 333
 QY 386 CAGATGCTGAGCTGTGAGAACCGCAGCGCGGAGTGGACAGCAGCTGAGGCTGTTC 445
 Db 334 CAGATGCTGAGCTGTGAGAACCGCAGCGCGGAGTGGACAGCAGCTGAGGCTGTTC 393
 QY 446 GAGCGCAGCAGGAGTGGCGGCGACAGCGGCGCAACAGCGGCAAGGCTGGCGCGGACAG 505
 Db 394 GAGCGCAGCAGGAGTGGCGGCGACAGCGGCGCAACAGCGGCAAGGCTGGCGCGGACAG 453
 QY 506 CCCAAAGGCGGCGCAGCGAGCTGACAGCTGACAGCCACAGCAAGCGTCCAGCGGCGAG 565
 Db 454 CCCAAAGGCGGCGCAGCGAGCTGACAGCTGACAGCCACAGCAAGCGTCCAGCGGCGAG 513
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 Db 514 CGCAACAAAGAGAACCGTGGAGAACCGTCCAGCAACCGACAGCAGCGCGCTCG 573
 QY 626 GGCACACCCAGAGAGAAAGGCGAGACTCCAGAGAGAGAGCGCTCCAGGCGCAAG 585
 Db 574 GGCACACCCAGAGAGAAAGGCGAGACTCCAGAGAGAGAGCGCTCCAGGCGCAAG 633
 QY 686 GCGGAGCAGAGCGCTCCCTCG-CCGACCTCCCATCGACCCCAACGAAACCCACCTACTG 744
 Db 634 GCGGAGCAGAGCGCTCCCTCG-CCGACCTCCCATCGACCCCAACGAAACCCACCTACTG 693
 QY 745 TCTGTGCAACCGAGTCTCTATGGGAGATGATGCGCTCGGCAACAGCAGAGTGCCCAT 804
 Db 694 TCTGTGCAACCGAGTCTCTATGGGAGATGATGCGCTCGGCAACAGCAGAGTGCCCAT 753
 QY 805 CGAGTGGTCCAC-TTCTGTGCGTGGGCTCAATCATAAACCCAGGCGCAAGT 857
 Db 754 CGAGTGGTCCACTTTCTGTGCGTGGGCTCAATCTAAACCCAGGCGCAAGT 807

RESULT 9

BUI66657

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BUI66657 1006 bp mRNA linear EST 12-MAR-2002
 AGENCOURT_6681770 NIH_MGC_121 Homo sapiens cdna clone IMAGE:5767634
 5', mRNA sequence.

ACCESSION BUI66657

VERSION BUI66657.1 GI:19377166

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1006)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12826 row: d column: 03
 High quality sequence stop: 659.
 Location/Qualifiers
 1. .1006
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5767634"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_121"
 /note="Organ: Brain; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
 ORIGIN
 Query Match 68.2%; Score 584.6; DB 12; Length 1006;
 Best Local Similarity 94.6%; Pred. No. 1.6e-83;
 Matches 616; Conservative 0; Mismatches 34; Indels 1; Gaps 1;
 206 CTAGGCTGTGGAGTGTGGTCCGGCCGGGAATGGAGATCTTGAAGAGTACACGAG 265
 102 CTGACCGAGGGTGGGGCCGGCTGGCTGGAAACAGATCTGAAGAGTACACGAG 161
 266 TGCTACGAGCGCTTACGTCCGAGACAGAGGGGGCCAGAGCGGGAGTCTGCACGTG 325
 162 TGCTACGAGCGCTTACGTCCGAGACAGAGGGGGCCAGAGCGGGAGTCTGCACGTG 221
 326 GTGACGCGCGCTGTATCCGACCCAGAGAGTGGGGCCAGAGAGATCCAGATCGTGAC 385
 222 GTGACGCGCGCTGTATCCGACCCAGAGAGTGGGGCCAGAGAGATCCAGATCGTGAC 281
 386 CAGATGGTGAGCTGGTGAGACCCGACGCGGAGTGGACAGCCACGTTGGAGCTGTC 445
 282 CAGATGGTGAGCTGGTGAGACCCGACGCGGAGTGGACAGCCACGTTGGAGCTGTC 341
 446 GAGGCGCAGCAGAGCTGGGGCGACACAGCGGGCAACAGCGGAGCTGGCGGACAGG 505
 342 GAGGCGCAGCAGAGCTGGGGCGACACAGCGGGCAACAGCGGAGCTGGCGGACAGG 401
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 402 CCCAAGGCGAGGCGGAGCGAGGTGACAGCCCAACAGAGCGCTTACGGCGGCGAG 461
 566 CGCAACCAACAGAGACCGTGGAGACCGCTCCAGCAACACAGCAGCAGCGCGCTCG 625
 462 CGCAACCAACAGAGACCGTGGAGACCGCTCCAGCAACACAGCAGCAGCGCGCTCG 521
 626 GGCAACCCCAAGAGAGAGAGGCAAGACCTCCAGAGAGAGAGAGGCTCCAGAGGCGAG 685
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 686 GCGGAGCGAGGCGCTCCCTGCGGACCTCCCATCGACCCCAACAGCCAGCTACTGT 745
 582 GCGGAGCGAGGCGCTCCCTGCGGACCTCCCATCGACCCCAACAGCCAGCTACTGT 641
 746 CTGTGCAACCAAGGTCTCTATGGGAGATGATCGGTGCGAACACAGAGTCCCGCATC 805
 642 CTGTGCAACCAAGGTCTCTATGGGAGATGATCGGTGCGAACACAGAGTCCCGCATC 700

QY 806 GAGTGGTTCACATCTCTGTCGTCGGGCTCAATCAATAACCAAGGCGAAG 856
 DB 701 GAGTGGATCCCTTCTCTGTCGTCGGGCTTCCACGTTAAACCAAGGCGCAG 751
 RESULT 10
 BX461522 1201 bp mRNA linear EST 22-MAY-2003
 LOCUS BX461522 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DF028YP07 5-PRIME, mRNA sequence.
 ACCESSION BX461522
 VERSION BX461522.1 GI:31037156
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polaves, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 was not normalized. Library was constructed by Life Technologies, a
 division of invitrogen. This sequence belongs to sequence cluster
 7164.f For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DF028CH04QP1&cluster=7164.f. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DF028CH04QP1.
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 /clone="CS0DF028YP07"
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 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL BRAIN"
 /note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
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 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."
 ORIGIN

Query Match 67.7%; Score 579.8; DB 13; Length 1201;
 Best Local Similarity 84.7%; Pred. No. 9.6e-83;
 Matches 683; Conservative 1; Mismatches 119; Indels 3; Gaps 3;
 QY 52 AAGCGCCCTTCGGGCTATCCACCTCTTCTGGGGCTCGGACTAGGAAGCAGCTTCCT 111
 DB 33 AAGCAGGCTGNGTACCGGTCGGGAATTCGGGGATCGGATTTATAGCAGTAGCAGTAT 92
 QY 112 CTCAGGCGCCCTTTGTCTCCAGCGGCTTCCAACTGAGTACCGGGAGACGACACAAAGGA 171
 DB 93 CCGCGGCTTGGGGCTCGGGGCGGGCTGCAGTTCGAGCCGCTCCCGACCGCGGG 152
 QY 172 GGGCGGTGACGATGGCGCAGCGCGGAGCGCGCTAGGCTGCTGGGAGTGGTGTGCGG 231
 DB 153 GCGCGCTCGGAGACAGTTTTCAGGCGCATCTCTCTGACCCGAGGGTGGGCGCGGTG 212
 QY 232 CCGCGGAATGGAGATCTCTGAAGGAGCTAGACGAGTGTCTACGAGCGCTTCAGTCCGAGAC 291
 DB 213 GCGGTGGAAACAGATCCTTGAAGGAGCTAGACGAGTGTCTACGAGCGCTTCAGTCCGAGAC 272
 QY 292 AGACGGGCGGACAGAGCGCGGATGCTGCACTGTGTCAGCGCGCGCTGTATCCCGACCA 351
 DB 273 AGACGGGCGGACAGAGCGCGGATGCTGCACTGTGTCGCA-CGCGCGCTGTATCCCGACCA 331

352 GGAGCTGGGCGACGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 411
332 GGAGCTGGGCGACGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 391
412 CACGGGCGAGTGGGACGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 471
392 CACGGGCGAGTGGGACGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 450
472 AGCGGGCAACAGCGGCGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 531
451 AGCGGGCAACAGCGGCGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 510
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511 TGACAGCCCAACAGCGGCGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 570
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571 GTCCAGCAACAGCGGCGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 630
652 GACCTCCAGAGAGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 711
631 GACCTCCAGAGAGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 690
712 CTTCCCTCATCGACCCCAACAGCGGCGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 771
691 CTTCCCTCATCGACCCCAACAGCGGCGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 749
772 GATGATCGGCGACGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 831
750 GATGATCGGCGACGAGGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 809
832 GCTCAATCATAAACCAAGGCAAGT 857
810 GCTCAATCATAAACCAAGGCAAGT 835

RESULT 11
BO683151
LOCUS
DEFINITION
AGENCOURT_8185663 NIH_MGC_112 Homo sapiens cdna clone IMAGE:6262978
5', mRNA sequence.
BO683151
BO683151.1 GI:21795830
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LICM2426 row: c column: 11
High quality sequence stop: 682.
Location/Qualifiers
1. 894
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:6262978"
/tissue_types="melanotic melanoma, cell line"
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FEATURES
source

RESULT 12
BM477126
LOCUS
DEFINITION

BM477126 1155 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6484647 NIH_MGC_85 Homo sapiens cdna clone IMAGE:5553778
5', mRNA sequence.

ORIGIN

Query Match 67.1%; Score 574.8; DB 13; Length 894;
Best Local Similarity 86.9%; Pred. No. 5.6e-82;
Matches 655; Conservative 0; Mismatches 97; Indels 2; Gaps 2;
Qy 98 GAAGGAGCTTCCTCTCAGGCGCCCTTGTCTCCAGCGCGTTCCTCAAACTGAGTACCGGGAG 157
Db 11 GCAGTAGCAGTGTATCCCGGCGCTGTGGGCTCGGGCGCGGGGTGCGAGTTCGAGCCCGCTC 70
Qy 158 ACACACAAAGGAGGAGGCGGTGACGATGCGCGAGCGCGGGAGCGCGCTAGCTGTCTGG 217
Db 71 CCGCGACCCCGCGGGCGCGGTCTGGAGACAGTTTCAGCGCGCATCTCTGCTGACCCGAGG 130
Qy 218 GAGTGTGTGTCGCGCGCGGATGAGATCTTGAAGAGCTAGACGAGTCTTACGAGCGC 277
Db 131 TGGGGCGCGCGCTGGCGCGTGGAAACAGATCTTGAAGAGCTAGACGAGTCTTACGAGCGC 190
Qy 278 TTCACTGCGGAGACAGACGCGCGCGAGAGCGCGGATGCTGCACTGTGTGAGCGCGCG 337
Db 191 TTCACTGCGGAGACAGACGCGCGCGAGAGCGCGGATGCTGCACTGTGTGAGCGCGCG 250
Qy 338 CTGATCGCGAGCAGGAGCTGGGCGCGAGAGATCCAGATCGTGTGAGCAGATGTTGGAG 397
Db 251 CTGATCGCGAGCAGGAGCTGGGCGCGAGAGATCCAGATCGTGTGAGCAGATGTTGGAG 310
Qy 398 CTGTGTGAGAACCGCGCGCGAGGTGGACAGCGCTGTGAGCTGTTCAGGCGCGAGCAG 457
Db 311 CTGTGTGAGAACCGCGCGCGAGGTGGACAGCGCTGTGAGCTGTTCAGGCGCGAGCAG 370
Qy 458 GAGTGTGGCGACACAGCGGCGCAACAGCGGCTGGCGCGGACAGGCGCCAAAGCGGAG 517
Db 371 GAGTGTGGCGACACAGCGGCGCAACAGCGGCTGGCGCGGACAGGCGCCAAAGCGGAG 430
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Db 491 AACCGTGTGAGAACCGCTCCAGCAACACGACCGACCGCGCGCTCGGGGACACCCCAAG 550
Qy 638 GAGAGAGGCGGAGAGCTCCAGAGAGAGAGCGGTCCAGAGCGCGAGCGGAGCGGAGAG 697
Db 551 GAGAGAGGCGGAGAGCTCCAGAGAGAGAGCGGTCCAGAGCGCGAGCGGAGCGGAGAG 610
Qy 698 GCGTCCCTGTGCGGACCTCCCGCATCGACCCCAAGCAACCGTACTGTCTGTGCAACCGAG 757
Db 611 GCGTCCCTGTGCGGACCTCCCGCATCGACCCCAAGCAACCGTACTGTCTGTGCAACCGAG 670
Qy 758 GTCTCTATGAGGAGATGATCGGCTGCGACACAGAGTG-CCCCATCGAGTGTGTCCA 816
Db 671 GTCTCTATGAGGAGATGATCGGCTGCGACACAGAGTGCCCCCATCGAGGAGGTTCCC 730
Qy 817 CTCTCT-GGTGCGTGGGCTCAATCATAAACCCAA 849
Db 731 ATTCTCGTGTGGGCTCAATCATAAACCCCA 764

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ACCESSION   BM477126
VERSION     BM477126.1  GI:18526157
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1155)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaabs-remail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/ILNL at:
            http://image.llnl.gov
            Plate: LLAM12271 row: e column: 11
            High quality sequence stop: 644.
FEATURES    source
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                /clone="IMAGE:5553778"
                /tissue_type="lymphoma, cell line"
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                /clone_lib="NIH_MGC_85"
                /note="Organ: lymph; Vector: pCMV-Sport6; Site 1: Not;
                Site 2: Sali; Cloned unidirectionally; oligo-dT primed.
                Average insert size 1.867 kb. Library enriched for
                full-length clones and constructed by Life Technologies.
                Note: this is a NIH_MGC Library."
ORIGIN
Query Match      65.5%; Score 561.4; DB 12; Length 1155;
Best Local Similarity 98.4%; Pred. No. 8.2e-80;
Matches 609; Conservative 0; Mismatches 6; Indels 4; Gaps 4;
QY 242 GAGATCCTAAGAGAGTACAGAGTCTACGAGCGCTTCAGTCGGAGACAGACGGGGCG 301
DB 211 GAGATCCTAAGAGAGTACAGAGTCTACGAGCGCTTCAGTCGGAGACAGACGGGGCG 270
QY 302 CAGAAGCGCGGATGCTGCTGCTGTCAGCGCGGCTGATCCGAGCGAGAGTGGGCG 361
DB 271 CAGAAGCGCGGATGCTGCTGCTGTCAGCGCGGCTGATCCGAGCGAGAGTGGGCG 330
QY 362 GACGAGAAGATCAGATCCTGAGCCAGATGTTGGAGCTGTTGGAGAACCGGACCGGGCAG 421
DB 331 GACGAGAAGATCAGATCCTGAGCCAGATGTTGGAGCTGTTGGAGAACCGGACCGGGCAG 390
QY 422 GTGGACAGCCAGCTGAGCTGTTTCGAGGCGCAGCAGAGCTGGGCGACACAGCGGGCAAC 481
DB 391 GTGGACAGCCAGCTGAGCTGTTTCGAGGCGCAGCAGAGCTGGGCGACACAGCGGGCAAC 450
QY 482 AGCGGCAAGGCTGGCGCGACAGCGCCCAAGGCGAGCGCGGCGAGCGAGCTGACAGGCC 541
DB 451 AGCGGCAAGGCTGGCGCGACAGCGCCCAAGGCGAGCGCGGCGAGCGAGCTGACAGGCC 510
QY 542 AACAGCAAGCGCTCAGCGGGCAGCGCCCAACAGGAAACCGTGAGAACCGCTCCAGCAAC 601
DB 511 AACAGCAAGCGCTCAGCGGGCAGCGCCCAACAGGAAACCGTGAGAACCGCTCCAGCAAC 570
QY 602 CACGACCAAGCAGCAGCGCGCTCGGGCACAACCCAGGAAAGAGGCCAAGACCTCCAG 661
DB 571 CACGACCAAGCAGCAGCGCGCTCGGGCACAACCCAGGAAAGAGGCCAAGACCTCCAG 630
QY 662 AAGAGAGAGCTCCAGGCGCAGGCGGAGCGCTCCCTGCGGACCTCCCGATC 721
DB 631 AAGAGAGAGCTCCAGGCGCAGGCGGAGCGCTCCCTGCGGACCTCCCGATC 690
QY 722 GACCCCAACGACACGACGAGTCTGTGTCACACAGGTCTCTAT-GGGGAGATGAT-CG 779
DB 691 GACCCCAACGACACGACGAGTCTGTGTCACACAGGTCTCTATGGGGAGATGATCGG 750
QY 780 GCTGCGACACACGACGAGTGTCCCA-TCGAGTGGTTCACATTCCTGCTGCTGGGGC-TCAA 837
DB 751 GCTGCGACACACGACGAGTGTCCCAATTCGAGTGGTTCACATTCCTGCGGCTGCTTCCA 810
QY 838 TCATAAACCCACAGGGCAAG 856
DB 811 TCATAAACCCACAGGGCAAG 829
RESULT 13
AV727700
LOCUS       AV727700 HTC Homo sapiens cDNA clone HTCHO4 5', mRNA linear EST 17-OCT-2000
DEFINITION AV727700
ACCESSION  AV727700
VERSION     AV727700.1 GI:10837121
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 722)
            Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
            Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
            Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
            Chen, J., Chen, Z. and Han, Z.
            Homo sapiens cDNA HTC clones
            Unpublished (2000)
            Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919 (ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
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Best Local Similarity 95.1%; Pred. No. 2.7e-79;
Matches 585; Conservative 0; Mismatches 29; Indels 1; Gaps 1;
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DB 44 AGATCTGAGAGAGCTAGACAGTGTCTACGAGCGCTTCAGTCGGAGACAGACGGGGCG 103
QY 303 AGAAGCGGGCGATGCTCAGCTGTGTGAGCGCGCGCTGTATCCGACGACGAGAGCTGGGCG 362
DB 104 AGAAGCGGGCGATGCTCAGCTGTGTGAGCGCGCGCTGTATCCGACGACGAGAGCTGGGCG 163
QY 363 ACGAGAGATCCAGATCGTAGCCAGATGTGTGAGCTGTGTGAGAGACCGACCGCGGAGG 422
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QY 423 TGGACAGCAGCTGGAGCTGTGTGAGCGCGCAGCAGAGCTGGGCGACACACGCGGGCAACA 482
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laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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Search completed: May 6, 2004, 11:48:46
Job time : 2864.77 secs

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Query Match 64.8%; Score 555.4; DB 13; Length 897;
Best Local Similarity 86.6%; Pred. No. 7e-79;
Matches 658; Conservative 0; Mismatches 97; Indels 5; Gaps 4;

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QY 158 ACACACAAAGGAGGCGGTGACGGATGCGCAGCGCGGGAGCGCCCTAGGCTGTGG 217
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QY 98 CCGCGACCCCGGGCGCGCTCGGAGACAGTTTCAGGCGCATCTCTGTGACCCGAGGG 157
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QY 218 GAGTGTGTTCGGCGCGCGGATGGAGATCTGAGGAGCTAGACGAGTGTACGAGGC 277
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QY 458 GAGCTGGGCGACACAGCGGGCAACAGCGCAAGGTTGGCGCGGACAGGCCCAAGCGCAG 517
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QY 398 GAGCTGGGCGACACAGCGGGCAACAGCGCAAGGTTGGCGCGGACAGGCCCAAGCGCAG 457
DB |||||

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QY 758 CACTTCTCGNGGCGTGGGGGCTCAATCATATAAACCAGGG 797
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: May 6, 2004, 10:18:04 ; Search time 405.667 Seconds
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Title: US-09-451-739H-8

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Total number of hits satisfying chosen parameters: 5983172

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	277.6	36.0	8487	16	US-10-242-515-3454
3	276	35.8	2061	16	US-09-968-653A-2
4	276	35.8	2886	13	US-09-874-347-1
5	276	35.8	2897	13	US-09-874-347-3
6	261.6	33.9	5159	9	US-09-764-877-3707
7	261.6	33.9	5159	16	US-10-242-515-3707
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C 20	254.4	33.0	401616	13	US-10-087-192-1630	Sequence 1630, App
C 21	253.8	32.9	19696	15	US-09-764-891-9327	Sequence 9327, App
C 22	253.8	32.9	19696	10	US-10-091-572-874	Sequence 874, App
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C 28	252.6	32.7	1206	13	US-10-027-632-265025	Sequence 265025, App
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C 31	252.6	32.7	1206	16	US-10-027-632-265026	Sequence 265026, App
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C 35	252.6	32.7	3512	16	US-10-027-632-114279	Sequence 114279, App
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C 40	252.2	32.7	42863	16	US-10-282-798-865	Sequence 865, App
C 41	252.2	32.7	186391	13	US-10-087-192-136	Sequence 136, App
C 42	252	32.6	308	16	US-10-074-024-598	Sequence 598, App
C 43	252	32.6	631	13	US-10-027-632-291223	Sequence 291223, App
C 44	252	32.6	631	13	US-10-027-632-291224	Sequence 291224, App
C 45	252	32.6	631	16	US-10-027-632-291223	Sequence 291223, App

ALIGNMENTS

RESULT 1

US-09-764-877-3454
; Sequence 3454, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3454
; LENGTH: 8487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3454

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 QY 327 CTTGAGAGTCCAGAAAAAACAAGGCTTATACAGGTAGTTTGGGACATCGCTTA 386
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 QY 387 ATAGTGGGAGAACCAATAGACCGTGTGATTACATGCGACCTTCTCGAGTGC 446
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 QY 447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTTGTAGG 488
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US-10-242-515-3454
 ; Sequence 3454, Application US/10242515
 ; Publication No. US20040009488A1
 ; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PC005C1

; CURRENT APPLICATION NUMBER: US/10/242,515

; PRIORITY FILING DATE: 2002-09-13

; PRIOR APPLICATION NUMBER: 09/764,877

; PRIOR FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: 60/179,065

; PRIOR FILING DATE: 2000-01-31

; PRIOR APPLICATION NUMBER: 60/180,628

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: 60/214,886

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/217,487

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/225,758

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/220,963

; PRIOR FILING DATE: 2000-07-26

; PRIOR APPLICATION NUMBER: 60/217,496

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/225,447

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/218,290

; PRIOR FILING DATE: 2000-07-14

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 4031

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3454

; LENGTH: 8487

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-242-515-3454

Query Match 36.0%; Score 277.6; DB 16; Length 8487;

Best Local Similarity 81.0%; Pred. No. 6.3e-75;

Matches 423; Conservative 0; Mismatches 59; Indels 40; Gaps 7;

QY 2 AACGTTCTCGCGGAGCGGACACTAGACCGGTGAGACCGCTCAGCAACCGCAC 61
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 QY 62 CCACGACGAGTCACTCGCGGACCGCCCAAGGAGAGAAAGCCAGACCTCTTAAGAAGAA 121
 Db 6597 CCACGACGAGCGGCGCTCGGGCACACCCCAAGGAGAGAGGCGCAAGACCTCCCAAGAAGAA 6656

QY 122 GCAGGGCTCCATGGCCAAAGCGGTAGCGCAGCGCTCCCGCCAGACCTCCCGCATCGACCC 181
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 QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTGGCA 217
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 QY 218 CA---ACGATGCCCATCGAGTGGTTCGGCTTCTCGTGTGTGAGTCTCAACCAATAAAC 274
 Db 6777 CAACGACGAGTGGCCCATCGAGTGGTTCACCTTCTCGTGTGTGAGTCTCAATCATAAAC 6836
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 QY 327 CTTGAGAGTCCAGAAAAAACAAGGCTTATACAGGTAGTTTGGGACATCGCTTA 386
 Db 6897 CTTGAGAGTCCCA---AAAAGAGAGGCTTACACAGGTAGTTTGTGGACAGCGGCTG 6954
 QY 387 ATAGTGGGAGAACCAATAAGCCAGTGTGTTGATTACATGCCACCTTTGCTAGGTGC 446
 Db 6955 GT-GTGAGGAGGACAAATAAAC--GTGTATTTATTACATGCTGCTTTGAGGTGC 7012
 QY 447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTTGTAGG 488
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RESULT 3

US-09-968-653A-2

; Sequence 2, Application US/09968653A

; Publication No. US20030073084A1

; GENERAL INFORMATION:

; APPLICANT: Gudkov, Andrey V

; Riabowol, Karl

; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

; STREET: 300 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/09/968,653A

; FILING DATE: 01-Oct-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/006,783A

; FILING DATE: 15-JAN-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: NO. US20030073084Ainan, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 97,837

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-913-0001

; TELEFAX: 312-913-0002

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2061 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

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RESULT 6
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; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3707
; LENGTH: 5159
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3707

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Best Local Similarity 87.4%;   Pred. No. 4,6e-70;
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Db	314	CCGGGCGTGTGTGCGGGCTCTGTAGTCCGAGCTCTCGGAGGCTGAGGAGGAGAAATG	373
Qy	687	GCNTGAACCTGGGAGGTGGAGCTTGCANTGAGCCAAGTTCGGGCCACTCGACTCCAGCCT	746
Db	374	CGGTGAACCTGGGAGGCGGAGCTTGCAGTGAGCCGAGATCGCACCCTGACTCTCCAGCCT	433
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Sequence 3707, Application US/10242515
Publication No. US2004009488A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005C1
CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,877
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,896
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3707
LENGTH: 5159
TYPE: DNA
ORGANISM: Homo sapiens
US-10-242-515-3707

	Query Match	33.9%	Score 261.6	DB 16	Length 5159
	Best Local Similarity	87.4%	Pred. No. 4.6e-70		
	Matches 285	Conservative 0	Mismatches 41	Indels 0	Gaps 0
QY	447	ACGAGAGTGAAATGTATATTTTAAAGAAATGTTGTTAGAGCGCGGCGGTGGCTCAC	506		
Db	134	AGGTTTCTTACTCTTGAGACTGTTAAGAGCGTCACAGTGGCCGGGCGGTGGCTCAC	193		
QY	507	GCTGTGTAATCCAGACATTTGGAGGCGCGAGCGGTGGATATCAGAGTCAAGGAGATCGA	566		
Db	194	GCTGTGTGTCACGACATTTGGAGGCGCGAGCGGACGGATATCAGAGTCAAGGAGATCGA	253		

QY 567 GACATCTGCTTAACACGGTGAACCCCGTCTCTACTATAAAATTCAAAAAATTAG 626
 Db 254 GACATCTGCTTAACACGGTGAACCCCGTCTCTACTATAAAATTCAAAAAATTAG 313
 QY 627 CTGGCGGTGGTGGGGGGCGCTGTAGTCCAGCTATTCCGGAGGCTCAGGAGGAGATG 686
 Db 314 CGGGCGGTGGTGGGGGGCGCTGTAGTCCAGCTATTCCGGAGGCTCAGGAGGAGATG 373
 QY 687 GCNTGAACCTGGAGGTGGAGTTCGANTGAGCCAGGTCCGGCCTCAGCTCCAGCCT 746
 Db 374 CGGTGAACCTGGAGGTGGAGTTCGANTGAGCCAGGTCCGGCCTCAGCTCCAGCCT 433
 QY 747 GGGGACAGCGGAGACTCCATCTTA 772
 Db 434 GGGGACAGCGGAGACTCCACTCA 459

RESULT 8
 US-10-027-632-130764
 ; Sequence 130764, Application US/10027632
 ; Publication No. US20020198371A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 130764
 ; LENGTH: 657
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-130764

Query Match 33.7%; Score 260; DB 13; Length 657;
 Best Local Similarity 88.4%; Pred. No. 5.6e-70;
 Matches 281; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 455 TAAATGTATATTTTAAAGAAATGTTGTAGAGCGCGGGCGGTGCTCAGCCTGTAA 514
 Db 72 TAACTATTTCAGTTAAACAAACAAAGAGCGCGGTGCTCAGCCTGTAA 131
 QY 515 TCCAGACATTTGGAGGCGGAGGCGGTGCGATCAGAGTCAGAGATCGAGACCATCC 574
 Db 132 TCCAGACATTTAGGAGGCGGAGGCGGTGCGATCAGAGTCAGAGATCGAGACCATCC 191
 QY 575 TGCTAACACGGTGAACCCCGTCTCTACTATAAAATTCAAAAAATTAGCTGGCGT 634
 Db 192 TGCTAACACGGTGAACCCCGTCTCTACTATAAAATTCAAAAAATTAGCTGGCGT 251
 QY 635 GGTGGCGGGCGCTGTAGTCCAGCTATTTCGGGAGGCTCAGGAGGAGATGGCNTGAAC 694
 Db 252 GGTGGCGGGTGTAGTCCAGCTATTTCGGGAGGCTCAGGAGGAGATGGCNTGAAC 311
 QY 695 CTGGGCGGGCGCTGTAGTCCAGCTATTTCGGGAGGCTCAGGAGGAGATGGCNTGAAC 754
 Db 311 GGTGGCGGGTGTAGTCCAGCTATTTCGGGAGGCTCAGGAGGAGATGGCNTGAAC 371
 QY 695 CTGGGAGGTGGAGTTCGANTGAGCCAGGTCCGCCACTGACCTCCAGCCTGGCGACA 754

Db 312 CCGGAGGCGGAGCTTGCAGTGAGCGGAGATCGGCCACTGCCTCCAGCCTGGCGGACA 371
 QY 755 GAGCGAGACTCCATCTTA 772
 Db 372 GAGCGAGACTCCGCTCTCA 389

RESULT 9
 US-10-027-632-130764
 ; Sequence 130764, Application US/10027632
 ; Publication No. US20030204075A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 130764
 ; LENGTH: 657
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-130764

Query Match 33.7%; Score 260; DB 16; Length 657;
 Best Local Similarity 88.4%; Pred. No. 5.6e-70;
 Matches 281; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 455 TAAATGTATATTTTAAAGAAATGTTGTAGAGCGCGGGCGGTGCTCAGCCTGTAA 514
 Db 72 TAACTATTTCAGTTAAACAAACAAAGAGCGCGGTGCTCAGCCTGTAA 131
 QY 515 TCCAGACATTTGGAGGCGGAGGCGGTGCGATCAGAGTCAGAGATCGAGACCATCC 574
 Db 132 TCCAGACATTTAGGAGGCGGAGGCGGTGCGATCAGAGTCAGAGATCGAGACCATCC 191
 QY 575 TGCTAACACGGTGAACCCCGTCTCTACTATAAAATTCAAAAAATTAGCTGGCGT 634
 Db 192 TGCTAACACGGTGAACCCCGTCTCTACTATAAAATTCAAAAAATTAGCTGGCGT 251
 QY 635 GGTGGCGGGCGCTGTAGTCCAGCTATTTCGGGAGGCTCAGGAGGAGATGGCNTGAAC 694
 Db 252 GGTGGCGGGTGTAGTCCAGCTATTTCGGGAGGCTCAGGAGGAGATGGCNTGAAC 311
 QY 695 CTGGGAGGTGGAGTTCGANTGAGCCAGGTCCGCCACTGACCTCCAGCCTGGCGGACA 754
 Db 312 CCGGAGGCGGAGCTTGCAGTGAGCGGAGATCGGCCACTGCCTCCAGCCTGGCGGACA 371
 QY 755 GAGCGAGACTCCATCTTA 772
 Db 372 GAGCGAGACTCCGCTCTCA 389

RESULT 10
 US-09-764-846-313/c
 ; Sequence 313, Application US/09764846
 ; Patent No. US20020102638A1

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 313
; LENGTH: 10953
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-846-313

Query Match      33.5%; Score 259; DB 9; Length 10953;
Best Local Similarity 91.0%; Pred. No. 4.2e-69;
Matches 274; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 469 TTAAGAATGTTGTTAGAGCGCGGCGGCTCAGCGCTGTAATCCAGCACTTTGG 528
DB 5346 TTTAAGAAAGTAATCTGGCGCGGCGGCTTACGCTGTAAATCCAGCACTTTGG 5287
QY 529 GAGCGCGAGGCGGTCGAGATCAGAGGTCAGAGATCGAGACCATCTGGCTAACAGCGTG 588
DB 5286 GAGCGCGAGGCGGCGGATCATGAGTCAGAGATCGAGACCATCTGGCTAACAGCGTG 5227
QY 589 AAACCCCTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGTGTGGCGGCGCCT 648
DB 5226 AAACCCCTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGTGTGGCGGCGCCT 5167
QY 649 GTAGTCCAGCTATTCGGAGGCTGAGCGAGAGATGGGNTGAACCTGGAGGTGAGC 708
DB 5166 GTAGTCCAGCTATTCGGAGGCTGAGCGAGAGATGGGNTGAACCTGGAGGTGAGC 5107
QY 709 TTGCANTGAGCAGGTCGCGCACTGCACCTCCAGCTGGCGCAGAGAGACTCCAT 768
DB 5106 TTGCAGTGAGCGGAGTTACGCCACTGCATTCAGCTTGGCGGAGAGACTCCGT 5047
QY 769 C 769
DB 5046 C 5046

RESULT 11
US-10-091-483-313/c
; Sequence 313, Application US/10091483
; Publication No. US20030049650A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212C1
; CURRENT APPLICATION NUMBER: US/10/091,483
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 348
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 313
; LENGTH: 10953
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-091-483-313

Query Match      33.5%; Score 259; DB 15; Length 10953;
Best Local Similarity 91.0%; Pred. No. 4.2e-69;
Matches 274; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 469 TTAAGAATGTTGTTAGAGCGCGGCGGCTCAGCGCTGTAATCCAGCACTTTGG 528
DB 5346 TTTAAGAAAGTAATCTGGCGCGGCGGCTTACGCTGTAAATCCAGCACTTTGG 5287
QY 529 GAGCGCGAGGCGGTCGAGATCAGAGGTCAGAGATCGAGACCATCTGGCTAACAGCGTG 588

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DB 5286 GAGCCCGAGGCGGCGGATCATGAGTTCAGGAGATCGAGACCATCTCTGCTAACATGGT 5227
QY 589 AAACCCCTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGTGTGGCGGCGCCT 648
DB 5226 AAACCCCTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGTGTGGCGGCGCCT 5167
QY 649 GTAGTCCAGCTATTCGGAGGCTGAGCGAGAGATGGGNTGAACCTGGAGGTGAGC 708
DB 5166 GTAGTCCAGCTATTCGGAGGCTGAGCGAGAGATGGGNTGAACCTGGAGGTGAGC 5107
QY 709 TTGCANTGAGCAGGTCGCGCACTGCACCTCCAGCTGGCGCAGAGAGACTCCAT 768
DB 5106 TTGCAGTGAGCGGAGTTTACGCCACTGCATTCAGCTTGGCGGAGAGACTCCGT 5047
QY 769 C 769
DB 5046 C 5046

RESULT 12
US-10-074-024-660
; Sequence 660, Application US/10074024
; Publication No. US20030232975A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC001C1
; CURRENT APPLICATION NUMBER: US/10/074,024
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 879
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 660
; LENGTH: 6264
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-074-024-660

Query Match      33.3%; Score 256.8; DB 16; Length 6264;
Best Local Similarity 83.9%; Pred. No. 1.6e-68;
Matches 302; Conservative 0; Mismatches 54; Indels 4; Gaps 1;

QY 413 TGTGTGATTACATTCGCCACCTTTGCTGAGGTGCGAGGAGTGTAAATGTATTTTAA 472
DB 5165 TGTTTTAAGCTAAGTGTATCATATAAAGAGTCAAAAGTTTAAAAAATGTAT 5224
QY 473 AGAATGTTTGTAGAGCGCGGCGGCTGCTCACGCTGTATCCAGCACTTTGGGAGG 532
DB 5225 AAAGTAAAAATATTGCGCGGCGCGGTGCTCACGCTGTATCCAGCACTTTGGGAGG 5284
QY 533 CCGAGGCGGTTCGGATCAGAGGTTCAGGAGATCGAGACCATCTCTGCTAACCGTGAAC 592
DB 5285 CCGAGGCGGCGGATCAGAGGTTCAGGAGATCGAGACCATCTCTGCTAACCGTGAAC 5344
QY 593 CCGCTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGTGTGGCGGCGCCTGTAG 652
DB 5345 CCGCTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGTGTGGCGGCGCCTGTAG 5400
QY 653 TCCAGCTATTCGGAGGCTGAGCGAGAGATGGGNTGAACCTGGGAGGTGGAGCTTGC 712
DB 5401 TCCAGCTATTCGGAGGCTGAGCGAGAGATGGGNTGAACCTGGGAGGTGGAGCTTGC 5460
QY 713 ANTGAGCGAGGTTCGCGCACTGCACCTCCAGCTGGCGCAGAGAGACTCCATCTTA 772
DB 5461 AGTGAGCAAGATCGCGCCACTGCATCCAGCTGGCGGCGAGCAAGACTCCGTCTCA 5520

RESULT 13
US-10-085-117-112/c
; Sequence 112, Application US/10085117
; Publication No. US2003023234A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.

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APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 96597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-112

Query Match 33.3%; Score 256.8; DB 16; Length 96597;
Best Local Similarity 90.4%; Pred. No. 5.5e-68;
Matches 284; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 460 TGTATATTTTAAAGAAATGTTTGTAGAGCCGGCGCGGTGCTCAGCGCTGTAAATCCCA 519
DB 3978 TGGGCACTGTTTCAAGTAGAGCTGAGAGCCGGCGCGGTGCTCGCGCTGTAAATCCCA 3919

QY 520 GCACTTTGGAGCGCGAGCGGTTCGATCAGCAGGTTCAGAGATCGAGACCATCTGGCT 579
DB 3918 GCATTTGGAGCGCGAGCGGTTCGATCAGCAGGTTCAGAGATCGAGACCATCTGGCT 3859

QY 580 AACACGGTGAACCCCGTCTCTACTAAATTC-AAAAAAAAAATTAGTGGCGGTGTG 638
DB 3858 AACACGGTGAACCCCGTCTCTACTAAATTC-AAAAAAAAAATTAGTGGCGGTGTG 3799

QY 639 GCGGGCGCTGTAGTCCAGCTATTCGGAGGCTGAGGAGGAGATGCTGACCTGG 698
DB 3798 GCGGGCGCTGTAGTCCAGCTATTCGGAGGCTGAGGAGGAGATGCTGACCTGG 3739

QY 699 GAGGTGAGCTTGCAATGAGCAAGGTTCGCGCACTGCACTCCAGCTGGCGACAGAGC 758
DB 3738 GAGGCGAGCTTGCAATGAGCAAGGTTCGCGCACTGCACTCCAGCTGGCGACAGAGC 3679

QY 759 GAGACTCCATCTTA 772
DB 3678 GAGACTCCGCTCA 3665

RESULT 14
US-10-087-192-688
; Sequence 688, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 688
; LENGTH: 97247
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(97247)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-688

Query Match 33.1%; Score 255.6; DB 13; Length 97247;
Best Local Similarity 93.0%; Pred. No. 3e-68;
Matches 266; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 487 GCGCGCGCGGTGGCTCAGCGCTGTAAATCCAGCACTTTGGAGCGCGGCGGCGGA 546
DB 2219 GCGCGCGCGGTGGCTCAGCGCTGTAAATCCAGCACTTTGGAGCGCGGCGGCGGA 2160

QY 547 TCAGGAGTCAGGAGATCGAGACCATCTGGCTAAACACCGGTGAAACCCCGTCTCTACTAA 606
DB 2159 TCAGGAGTCAGGAGATCGAGACCATCTGGCTAAACCCCGGTGAAACCCCGTCTCTACTAA 2100

QY 607 AAATTCAAAAAATAGTGGCGGTGTGGCGCGCGCTGTAGTCCAGCTATTTCGG 666
DB 2099 AAATTCAAAAAATAGTGGCGGTGTGGCGCGCGCTGTAGTCCAGCTATTTCGG 2040

QY 667 GAGGTCAGGAGGAGATGCGNTGAACTGGAGGTGGAGCTTGCANTGAGGCAAGGTC 726
DB 2039 GAGGTCAGGAGGAGATGCGNTGAACTGGAGGTGGAGCTTGCANTGAGGCAAGGTC 1980

QY 727 GCGCACTGCACTCCAGCTGGCGGACAGAGCGAGACTCCATCTTA 772
DB 1979 GCGCACTGCACTCCAGCTGGCGGACAGAGCGAGACTCCATCTTA 1934

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 07:44:53 ; Search time 72.9822 Seconds
(without alignments)
5870.227 Million cell updates/sec

Title: US-09-451-739H-8
Perfect score: 772
Sequence: 1 aaagcgtctcggcgagc.....cagagcgagactccattta 772

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	276	35.8	1902	2	US-09-258-257-1 Sequence 1, Appli
2	276	35.8	1902	2	US-09-258-371-1 Sequence 1, Appli
3	276	35.8	1902	3	US-08-569-721A-1 Sequence 1, Appli
4	276	35.8	1902	3	US-08-751-230-1 Sequence 1, Appli
5	276	35.8	1902	3	US-09-499-082-1 Sequence 1, Appli
6	276	35.8	1902	3	US-09-258-372-1 Sequence 1, Appli
7	276	35.8	2061	2	US-09-258-371-9 Sequence 9, Appli
8	276	35.8	2061	3	US-08-751-230-9 Sequence 9, Appli
9	276	35.8	2061	3	US-09-499-082-9 Sequence 9, Appli
10	276	35.8	2061	3	US-09-258-372-9 Sequence 2, Appli
11	276	35.8	2061	4	US-09-006-783A-2 Sequence 1, Appli
12	272.8	35.3	2061	4	US-09-159-871-1 Sequence 6, Appli
13	249.8	32.4	14636	3	US-09-173-914-6 Sequence 6, Appli
14	248.6	32.2	15328	2	US-08-888-497-33 Sequence 33, Appli
15	248.6	32.2	15328	4	US-09-362-230-33 Sequence 33, Appli
16	248.6	32.2	15328	5	PCT-US94-07926-33 Sequence 33, Appli
17	248.4	32.2	148567	4	US-09-801-876B-3 Sequence 3, Appli
18	248.4	32.2	148567	4	US-10-254-869-3 Sequence 3, Appli
19	248	32.1	319608	4	US-09-539-333D-1 Sequence 1, Appli
20	248	32.1	319608	4	US-09-579-409-1 Sequence 1, Appli
21	247.2	32.0	1268	4	US-09-369-247-42 Sequence 42, Appli
22	246.4	31.9	1712	3	US-09-058-389A-12 Sequence 12, Appli
23	246.4	31.9	1712	4	US-09-611-781-12 Sequence 12, Appli
24	246.4	31.9	6354	3	US-09-058-389A-5 Sequence 5, Appli
25	246.4	31.9	6354	4	US-09-611-781-5 Sequence 5, Appli
26	246.4	31.9	14796	3	US-08-975-080-35 Sequence 35, Appli
27	246.4	31.9	14796	3	US-09-630-706-10 Sequence 10, Appli

28	246.4	31.9	14796	4	US-09-496-694B-3 Sequence 3, Appli
29	244.8	31.7	320	1	US-08-629-933-5 Sequence 5, Appli
30	244.8	31.7	320	1	US-08-759-873-5 Sequence 5, Appli
31	244.6	31.7	14581	4	US-08-520-373D-4 Sequence 4, Appli
32	244.6	31.7	22481	4	US-08-367-841A-43 Sequence 43, Appli
33	244.6	31.7	22481	5	PCT-US95-07201-43 Sequence 43, Appli
34	244.6	31.7	22484	4	US-09-875-223-2 Sequence 2, Appli
35	244.6	31.7	22484	4	US-09-875-114-2 Sequence 2, Appli
36	244.2	31.6	246240	2	US-08-724-394A-20 Sequence 20, Appli
37	244.2	31.6	246240	2	US-08-724-394A-21 Sequence 21, Appli
38	244.2	31.6	246240	2	US-08-724-394A-22 Sequence 22, Appli
39	243.4	31.5	84495	4	US-09-797-906-3 Sequence 3, Appli
40	242.4	31.4	193303	4	US-09-497-855A-37 Sequence 37, Appli
41	242.4	31.4	193303	4	US-09-497-855A-44 Sequence 44, Appli
42	242	31.3	392000	4	US-10-027-983-11 Sequence 11, Appli
43	241.8	31.3	3742	1	US-08-694-915-5 Sequence 5, Appli
44	241.8	31.3	23187	4	US-09-499-522-1 Sequence 1, Appli
45	241.6	31.3	70000	4	US-09-851-896-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-258-257-1
; Sequence 1, Application US/09258257
; Patent No. 5965398
; GENERAL INFORMATION:
; APPLICANT: GARKAVTSEV, Igor
; APPLICANT: RIAZOMOL, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/258,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 854-7400
; TELEFAX: (650) 854-8275
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1902 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..738
; US-09-258-257-1
Query Match 35.8%; Score 276; DB 2; Length 1902;
Best Local Similarity 80.8%; Pred. No. 2.7e-68;


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;
; TELEPHONE: 415-854-7400
;
; TELEFAX: 415-854-8275
;
; INFORMATION FOR SEQ ID NO: 1:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 1902 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: double
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA
;
; FEATURE:
;
; NAME/KEY: CDS
;
; LOCATION: 109..741
;
US-09-258-371-1

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RESULT 3
US-08-569-721A-1
; Sequence 1, Application US/08569721A
; Patent No. 6037121
; GENERAL INFORMATION:
; APPLICANT: GARKAVTSEV, Igor
; APPLICANT: RIABOWOL, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,721A
FILING DATE: 08-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 028722-128
TELEPHONE: (650) 854-7400
TELEFAX: (650) 854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 109..738
US-08-569-721A-1

Query Match 35.8%; Score 276; DB 3; Length 1902;
Best Local Similarity 80.8%; Pred. No. 2.7e-68;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY 2 AAGCGTTCCTCGGGCAGCGCAACACTAGAACCGGTGAGAACCGTCCAGCAACCGGAC 61
Db 343 AAGCGTTCACGGCGGCGGCAACACGAGAACCGGTGAGAACCGTCCAGCAACCGGAC 401
QY 62 CCACGACGAGTCACTCTCGGCGACGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAG 121
Db 402 CCACGACGAGTCACTCTCGGCGACGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAG 461
QY 122 GCAGGGCTCCATGGCCCAAGCGGTAGCGGAGCGGCTCCCGCGAGAGCTCCCATCGACCC 181
Db 462 GAAGCGTCCAGGCCAAGCGGAGCGGAGCGGCTCCCGCGAGAGCTCCCATCGACCC 521
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCGCTCGGA 217
Db 522 CAACGAAACCCACGTAAGTCTGTGTGCAACCGAGTCTCTATGGGGAGATGATCGCTCGGA 581
QY 218 CA---ACGAATGCCCATCGAGTGGTTCGCGTTCCTCGTGTGAGTCTCAACCATAAACC 274
Db 582 CAACGACGAGTCCCGCATCGAGTGGTTCCTCGTGTGAGTCTCAACCATAAACC 641
QY 275 AAGCGCAAGTGTACTGTTCAGATGCGGGGAAAGAACG-----ATGGGCAAGC 326
Db 642 CAAGGGCAAGTGTACTGTTCAGATGCGGGGAAAGAACG-----ATGGGCAAGC 701
QY 327 CCTTGAGAGTCCAGAAATAAGCCAGTGTGTGATTAATGCACTTGTGAGGTC 386
Db 702 CCTTGAGAGTCCAGAAATAAGCCAGTGTGTGATTAATGCACTTGTGAGGTC 759
QY 387 ATAGTGAGGAGAACAAATAAGCCAGTGTGTGATTAATGCACTTGTGAGGTC 446
Db 760 GT-GTGAAGAGGACAAATAAGCCAGTGTGTGATTAATGCACTTGTGAGGTC 817
QY 447 AGAAGTGAATGATGATATTTTAAAGATGTTGTAGAGG 488
Db 818 AAGAGTGAATGATGATATTTTAAAGATGTTGTAGAGG 859

RESULT 4

US-08-751-230-1
; Sequence 1, Application US/08751230
; Patent No. 6117633
; GENERAL INFORMATION:

APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 109..741
US-08-751-230-1

Query Match 35.8%; Score 276; DB 3; Length 1902;
Best Local Similarity 80.8%; Pred. No. 2.7e-68;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY 2 AAGCGTTCCTCGGGCAGCGCAACACTAGAACCGGTGAGAACCGTCCAGCAACCGGAC 61
Db 343 AAGCGTTCACGGCGGCGGCAACACGAGAACCGGTGAGAACCGTCCAGCAACCGGAC 401
QY 62 CCACGACGAGTCACTCTCGGCGACGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAG 121
Db 402 CCACGACGAGTCACTCTCGGCGACGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAG 461
QY 122 GCAGGGCTCCATGGCCCAAGCGGTAGCGGAGCGGCTCCCGCGAGAGCTCCCATCGACCC 181
Db 462 GAAGCGTCCAGGCCAAGCGGAGCGGAGCGGCTCCCGCGAGAGCTCCCATCGACCC 521
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCGCTCGGA 217
Db 522 CAACGAAACCCACGTAAGTCTGTGTGCAACCGAGTCTCTATGGGGAGATGATCGCTCGGA 581
QY 218 CA---ACGAATGCCCATCGAGTGGTTCGCGTTCCTCGTGTGAGTCTCAACCATAAACC 274
Db 582 CAACGACGAGTCCCGCATCGAGTGGTTCCTCGTGTGAGTCTCAACCATAAACC 641
QY 275 AAGCGCAAGTGTACTGTTCAGATGCGGGGAAAGAACG-----ATGGGCAAGC 326
Db 642 CAAGGGCAAGTGTACTGTTCAGATGCGGGGAAAGAACG-----ATGGGCAAGC 701
QY 327 CCTTGAGAGTCCAGAAATAAGCCAGTGTGTGATTAATGCACTTGTGAGGTC 386
Db 702 CCTTGAGAGTCCAGAAATAAGCCAGTGTGTGATTAATGCACTTGTGAGGTC 759

Db 702 CTGGAGAAATCCA--AAAAAGAGAGGCTTACAAAGGTAGTTTGTGGACAGGCGCTG 759
Qy 387 ATAGTGAGGAGAAACAAATAAGCCAGTGTGTGATTACATTGCCACCTTTGCTGAGGTGC 446
Db 760 GT-GTGAGGAGACAAATAAACC-GTGTATTATTACATTGCTGCTTTGTTGAGGTGC 817
Qy 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 488
Db 818 AAGGAGTGTAAATGTATATTTTAAAGATGTTAGAAAAGG 859

RESULT 5
US-09-499-082-1
; Sequence 1, Application US/09499082
; Patent No. 6143522
; GENERAL INFORMATION:
; APPLICANT: Helbing, Caren C.
; APPLICANT: Riabowol, Karl
; APPLICANT: Johnston, Randall N.
; APPLICANT: Garkavtsev, Igor
; TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/499,082
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,158
; FILING DATE: 27-VAR-1997
; APPLICATION NUMBER: US 08/751230
; FILING DATE: 15-NOV-1996

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-854-7400
; TELEFAX: 650-854-8275
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1902 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..741
US-09-499-082-1

Query Match 35.8%; Score 276; DB 3; Length 1902;
Best Local Similarity 80.8%; Pred. NO. 2.7e-68;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
Qy 2 AAGCGTCTCGGCGGAGCGGACAACTAGAACCGGTGAGACCGGTCCAGCAACCGGAC 61
Db 343 AAGCGTCTCGGCGGAGCGGACAACTAGAACCGGTGAGACCGGTCCAGCAACCGA- 401

Qy 62 CCAGCAGCGTCACTCGGCGCGCCCAAGGAGAGAAAGCCAGACCTCTTAAGAGAA 121
Db 402 CCAGCAGCGCGCGCTCGGCGCACCCAGGAGAGAGAGCCAGACCTCTTAAGAGAA 461
Qy 122 GCAGGGCTCCATGGCCAAAGCGGTAGCGGAGGCGTCCCGCGAGACCTCCCGATCGACCC 181
Db 462 GAAGCGCTCCAAGGCCAAAGCGGAGGAGGCGTCCCGTCCCGACCTCCCGATCGACCC 521
Qy 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTCGGA 217
Db 522 CAACGAACCCACGTACTGTGTGCAACAGGTCTCTTATGGGAGATGATCGCTCGGA 581
Qy 218 CA---ACGAATGCCCATCGAGTGGTTCCTCGTGTGTAGTCTCAACCAATAAAC 274
Db 582 CAACGACGAGTGCCTCCAGTGGTTCCTCTCGTGGGAGTCAATCATATAAAC 641
Qy 275 AAAGCGCAAGTGTACTGTTCCAGTGCCTGGGAGAAAGCG-----ATGGGCAAGC 326
Db 642 CAAGGCGAAGTGTACTGTTCCAGTGCCTGGGAGAAAGCG-----ATGGGCAAGC 701
Qy 327 CCTTGAGAAAGTCCAGAAAAAAGAGGCTTTATACAGGTAGTTTGGGAGACATCGTCTA 386
Db 702 CTGGAGAAATCCA--AAAAGAGAGGCGCTTACACAGGTAGTTTGTGACAGCGCGCTG 759
Qy 387 ATAGTGAGGAGAAACAAATAAGCCAGTGTGTGATTACATTGCCACCTTTGCTGAGGTGC 446
Db 760 GT-GTGAGGAGACAAATAAACC-GTGTATTTTATTCATTGCTGCTCTTTGTTGAGGTGC 817
Qy 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 488
Db 818 AAGGAGTGTAAATGTATATTTTAAAGATGTTAGAAAAGG 859

RESULT 6
US-09-258-372-1
; Sequence 1, Application US/09258372
; Patent No. 6238918
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,372
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1902 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..741
; US-09-258-372-1

Query Match      35.8%  Score 276; DB 3; Length 1902;
Best Local Similarity 80.8%; Pred. No. 2.7e-68;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY 2 AAGCGTCTCGGCGGAGCGGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAACCGCGAC 61
Db 343 AAGCGTCTCGGCGGAGCGGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAACCGCGAC 401
QY 62 CCACGACGAGCGTCACTCTCGGCGGAGCGGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAAC 121
Db 402 CCACGACGAGCGGCGCTCGGCGGAGCGGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAAC 461
QY 122 GCAGGCGTCCATGGCCCAAGCGGTAGCGGAGCGGTCCTCCCGGAGACCTCCCGCATCGACCC 181
Db 462 GAAGCGTCTCAAGGCCCAAGCGGAGCGGAGCGGTCCTCCCGGAGACCTCCCGCATCGACCC 521
QY 182 CACGCGAGCC-----CTCTACTGGGAGATGATCGGTGCGA 217
Db 522 CAACGAAACCACTACTGTCTGTGCAACCGAGTCTCTATGGGAGATGATCGGTGCGA 581
QY 218 CA---ACGAATGCCCATCGAGTGGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 274
Db 582 CAACGACGAGTGGCCCATCGAGTGGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 641
QY 275 AAGCCCAAGTGTACTGTCTCAGATGCCGCGGGAAGAGCG-----ATGGGCAAGC 326
Db 642 CAAAGGCAAGTGTACTGTCTCAGATGCCGCGGGAAGAGCG-----ATGGGCAAGC 701
QY 327 CCTTGAGAGATGCCAGAAAAAAGAGCGGCTTAAACAGGTAGTTTGGGACATGCGTCTA 386
Db 702 CCTTGAGAGATGCCA-----AAAAAGAGAGCGCTTAAACAGGTAGTTTGGGACATGCGTCTA 759
QY 387 ATAGTGAGAGAACAAATAAGCCAGTGTGTGATTTACATTTGCGACCTTTGCTGAGGTGC 446
Db 760 GT-GTGAGGAGGACAAATAAACC-GTGATTTATTACATTTGCTGCTTTGTTGAGGTGC 817
QY 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTGTAGAG 488
Db 818 AAGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAG 859

RESULT 7
US-09-258-371-9
; Sequence 9, Application US/09258371
; Patent No. 5986078
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,371

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..900
; US-09-258-371-9

Query Match      35.8%  Score 276; DB 2; Length 2061;
Best Local Similarity 80.8%; Pred. No. 2.8e-68;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY 2 AAGCGTCTCGGCGGAGCGGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAACCGCGAC 61
Db 502 AAGCGTCTCGGCGGAGCGGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAACCGCGAC 560
QY 62 CCACGACGAGTCACTCTCGGCGGAGCGGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAAC 121
Db 561 CCACGACGAGCGGCGCTCGGCGGAGCGGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAAC 620
QY 122 GCAGGCGTCCATGGCCCAAGCGGTAGCGGAGCGGTCCTCCCGGAGACCTCCCGCATCGACCC 181
Db 621 GAAGCGTCTCAAGGCCCAAGCGGAGCGGAGCGGTCCTCCCGGAGACCTCCCGCATCGACCC 680
QY 182 CACGCGAGCC-----CTCTACTGGGAGATGATCGGTGCGA 217
Db 681 CAACGAAACCACTACTGTCTGTGCAACCGAGTCTCTATGGGAGATGATCGGTGCGA 740
QY 218 CA---ACGAATGCCCATCGAGTGGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 274
Db 741 CAACGACGAGTGGCCCATCGAGTGGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 800
QY 275 AAGCGCAAGTGTACTGTCTTCCAGATGCCGCGGGAAGAGCG-----ATGGGCAAGC 326
Db 801 CAGGGCAAGTGTACTGTCTTCCAGATGCCGCGGGAAGAGCG-----ATGGGCAAGC 860
QY 327 CCTTGAGAGTCCAGAAAAAAGAGCGGCTTAAACAGGTAGTTTGGGACATGCGTCTA 386
Db 861 CCTTGAGAGATCCA-----AAAAAGAGAGCGGCTTAAACAGGTAGTTTGGGACATGCGTCTA 918
QY 387 ATAGTGAGAGAACAAATAAGCCAGTGTGTGATTTACATTTGCGACCTTTGCTGAGGTGC 446
Db 919 GT-GTGAGGAGGACAAATAAACC-GTGATTTATTACATTTGCTGCTTTGTTGAGGTGC 976
QY 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTGTAGAG 488
Db 977 AAGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAG 1018

RESULT 8
US-09-751-230-9
; Sequence 9, Application US/08751230
; Patent No. 6117633
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
```


QY 122 GCAGGGCTCCATGGCCAGAGCGTAGCGCAGCGCTCCCGCAGACCTCCCATCGACCC 181
Db 621 GAAGCGCTCCAGGCGCAAGCGGAGAGCGCTCCCTGCGACCTCCCATCGACCC 680
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCCGCTGCGA 217
Db 681 CAACGAACCCAGCTACTGCTGTGCAACCCAGGCTCTCTATGGGAGATGATCGGCTGCGA 740
QY 218 CA---ACGAATGCCATCGAGTGTTCGGCTTCTCGTGTGTGAGTCTCAACCATAAACC 274
Db 741 CAACGACGAGTGGCCCATCGAGTGTTCACCTTCGTGCGTGGGCTCAATCATAAACC 800
QY 275 AAAGCGCAAGTGTACTGTTCAGATGCGCGGGAAGAAGC-----ATGGGCAAAAGC 326
Db 801 CAAGGCGCAAGTGTACTGTGCTCCCAAGTGCAGGCGGAGAACGAGAGAACCATGGAACAAAGC 860
QY 327 CTTGAGAGTCCAGAAAACAGGCGTTATACAGTAGTGTGGGACATCGGTCTA 386
Db 861 CTTGAGAAATCCA---AAAAAGAGAGGCGTTTACACAGTAGTGTGGACAGGCGGCTG 918
QY 387 ATAGTGAGGAGAACAAATPAAGCCAGTGTGTTGATTACATTGCCACCTTTGCTGAGGTGC 446
Db 919 GT-GTGAGGAGCAAAATAAACCC-GTGATATTATTACATTGCTGCTTTGTTGAGGTGC 976
QY 447 AGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 488
Db 977 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGAAAGG 1018

RESULT 10

US-09-258-372-9
; Sequence 9, Application US/09258372
; Patent No. 6238918
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,372
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..900
US-09-258-372-9

Query Match 35.8%; Score 276; DB 3; Length 2061;
Best Local Similarity 80.8%; Pred. No. 2.8e-68;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
QY 2 AAGCGTTCTCGGCGCAGGCGCAACACTAGAACCGGTGAGAACCGTCCAGCAACCGCGAC 61
Db 502 AAGCGTCTCAGCGGCGAGCGCAACACGAGAACCGGTGAGAACCGTCCAGCAACCGACGA- 560
QY 62 CACGACGAGCTCACCTCGGCGACGCCCAAGAGAGAGAAAGCCAGACCTCTAAGAGAA 121
Db 561 CCACGACGAGCGGCGCTCGGCGCACCCCAAGGAGAGAAAGGCGCAAGACCTCCAAGAGAA 620
QY 122 GCAGGGCTCCATGCCCAAGCGGTAGCGGCGAGGCGTCCCGCAGACCTCCCATCGACCC 181
Db 621 GAAGCGTCTCAAGGCCCAAGCGGAGCGAGGCGTCCCTGCGACCTCCCATCGACCC 680
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCGGCTGCGA 217
Db 681 CAACGAACCCAGCTACTGCTGTGTGCAACCCAGGCTCTCTATGGGAGATGATCGGCTGCGA 740
QY 218 CA---ACGAATGCCATCGAGTGTTCGGCTTCTCGTGTGTGAGTCTCAACCATAAACC 274
Db 741 CAACGACGAGTGCCTCCCATCGAGTGTTCACCTTCGTGCGTGGGCTCAATCATAAACC 800
QY 275 AAAGCGCAAGTGTACTGTTCAGATGCGCGGGAAGAAGC-----ATGGGCAAAAGC 326
Db 801 CAAGGCGCAAGTGTACTGTGCTCCCAAGTGCAGGCGGAGAACGAGAGAACCATGGAACAAAGC 860
QY 327 CTTGAGAGTCCAGAAAACAGGCGTTATACAGTAGTGTGGGACATCGGTCTA 386
Db 861 CTTGAGAAATCCA---AAAAAGAGAGGCGTTTACACAGTAGTGTGGACAGGCGGCTG 918
QY 387 ATAGTGAGGAGAACAAATPAAGCCAGTGTGTTGATTACATTGCCACCTTTGCTGAGGTGC 446
Db 919 GT-GTGAGGAGCAAAATAAACCC-GTGATATTATTACATTGCTGCTTTGTTGAGGTGC 976
QY 447 AGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 488
Db 977 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGAAAGG 1018

RESULT 11

US-09-006-783A-2
; Sequence 2, Application US/09006783A
; Patent No. 6297366
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrey V
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
; TITLE OF INVENTION: Pathway
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,783A
; FILING DATE: 15-JAN-1998
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: No. 6297366nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..897
US-09-006-783A-2

Query Match 35.8%; Score 276; DB 3; Length 2061;
Best Local Similarity 80.8%; Pred. No. 2.8e-68;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
QY 2 AAGCGTTCTCGCGCGCAGCGCAACCTAGAACCGGTGAGAACCGGTCCAGCAACCGCGAC 61
Db |||||
502 AAGCGTCTACGCGCGCAGCGCAACCTAGAACCGGTGAGAACCGGTCCAGCAACCGCGA- 560
QY 62 CCACGACGACGTCACCTCGGCGCAGCGCAACCTAGAACCGGTGAGAACCGGTCCAGCAACCG 121
Db |||||
561 CCACGACGACGCGCTCGGCGCAGCGCAACCTAGAACCGGTGAGAACCGGTCCAGCAACCG 620
QY 122 GCAGGCGTCCATGCGCAAGCGGTAGCGGCGAGCGTCCCGCGAGACCTCCCGCATCGACCC 181
Db |||||
621 GAAGCGTCCAAAGGCCAAGCGGCGAGCGCGTCCCGCGACCTCCCGCATCGACCC 680
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCCGTGGGA 217
Db |||||
681 CAACGACCGACGCTACTGCTGTGCAACAGCGTCTCTATGGGAGATGATCGGCTGGGA 740
QY 218 CA---ACGAATGCCCATCGAGTGTCCGCTTCTCGTGTGTGAGTCTCAACCATATAACC 274
Db |||||
741 CAACGACGAGTGCCTCATCGAGTGTCCACCTTCTCGTGTGTGAGTCTCAATCATAAACC 800
QY 275 AAAGCGCAAGTGTACTGTTCCAGATGCGCGGGAAGAACG-----ATGGCGCAAGC 326
Db |||||
801 CAAGGCAAGTGTACTGTTCCAGTGCCTGCGGCGGAGAACGAGAACCATGGACAAAGC 860
QY 327 CCTTGAGAACTCCAGAAAAAACAAGGCTTATAACAGTAGTGTGGGACATGCGTCTA 386
Db |||||
861 CCTGGAATAATCCA--AAAAAGAGAGGCTTACACAGTAGTGTGGACAGGCGCTG 918
QY 387 ATAGTGAGAGAACAAATAAGCCAGTGTGTGATTACATTCACCTTGTGAGGTGC 446
Db |||||
919 GT-GTGAAGGAGCAAAATAAACC-GTGTAATTATTACATTGCTGCTCTTGTGAGGTGC 976
QY 447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTAGAGG 488
Db |||||
977 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGAAAGG 1018

RESULT 12
US-09-159-871-1
Sequence 1, Application US/09159871A
Patent No. 6420136
GENERAL INFORMATION:
APPLICANT: RIABOWOL, Karl T.
TITLE OF INVENTION: METHOD OF MODULATING P53 ACTIVITY
FILE REFERENCE: 028722-181
CURRENT APPLICATION NUMBER: US/09/159,871A
CURRENT FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: US 60/060,138
PRIOR FILING DATE: 1997-09-26
PRIOR APPLICATION NUMBER: US 09/006,783

PRIOR FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1
LENGTH: 2061
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: CDS
LOCATION: (16)..(897)
US-09-159-871-1

Query Match 35.3%; Score 272.8; DB 4; Length 2061;
Best Local Similarity 80.5%; Pred. No. 2.2e-67;
Matches 420; Conservative 0; Mismatches 62; Indels 40; Gaps 7;
QY 2 AAGCGTTCTCGCGCGCAGCGCAACCTAGAACCGGTGAGAACCGGTCCAGCAACCGCGAC 61
Db |||||
502 AAGCGTCTACGCGCGCAGCGCAACCTAGAACCGGTGAGAACCGGTCCAGCAACCGCGA- 560
QY 62 CCACGACGACGTCACCTCGGCGCAGCGCAACCTAGAACCGGTGAGAACCGGTCCAGCAACCG 121
Db |||||
561 CCACGACGACGCGGTGCGGCGACACCCAGGAGAGAACGCCAAGACCTCCAGCAAGAA 620
QY 122 GCAGGCGTCCATGCGCAAGCGGTAGCGGCGAGCGTCCCGCGAGACCTCCCGCATCGACCC 181
Db |||||
621 GAAGCGTCCAAAGGCCAAGCGGCGAGCGCGTCCCGCGACCTCCCGCATCGACCC 680
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCCGTGGGA 217
Db |||||
681 CAACGACCGACGCTACTGCTGTGCAACAGCGTCTCTATGGGAGATGATCGGCTGGGA 740
QY 218 CA---ACGAATGCCCATCGAGTGTCCGCTTCTCGTGTGTGAGTCTCAACCATATAACC 274
Db |||||
741 CAACGACGAGTGCCTCATCGAGTGTCCACCTTCTCGTGTGTGAGTCTCAATCATAAACC 800
QY 275 AAAGCGCAAGTGTACTGTTCCAGATGCGCGGGAAGAACG-----ATGGCGCAAGC 326
Db |||||
801 CAAGGCAAGTGTACTGTTCCAGTGCCTGCGGCGGAGAACGAGAACCATGGACAAAGC 860
QY 327 CCTTGAGAACTCCAGAAAAAACAAGGCTTATAACAGTAGTGTGGGACATGCGTCTA 386
Db |||||
861 CCTGGAATAATCCA--AAAAAGAGAGGCTTACACAGTAGTGTGGACAGGCGCTG 918
QY 387 ATAGTGAGAGAACAAATAAGCCAGTGTGTGATTACATTCACCTTGTGAGGTGC 446
Db |||||
919 GT-GTGAAGGAGCAAAATAAACC-GTGTAATTATTACATTGCTGCTCTTGTGAGGTGC 976
QY 447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTAGAGG 488
Db |||||
977 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGAAAGG 1018

RESULT 13
US-09-173-914-6
Sequence 6, Application US/09173914
Patent No. 6171857
GENERAL INFORMATION:
APPLICANT: Hendrickson, Eric
TITLE OF INVENTION: A No. 6171857el Leucine Zipper, kARP-1 and
FILE REFERENCE: B0877/7017/HK
CURRENT APPLICATION NUMBER: US/09/173,914
CURRENT FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: 60/064,557
EARLIER FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 14636
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-173-914-6

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Query Match      32.4%; Score 249.8; DB 3; Length 14636;
Best Local Similarity 82.8%; Pred. No. 1.6e-60;
Matches 284; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 430 CACCTTTGCTGAGTGCAGGAAGTCTAAATGATATATTTTAAAGAAATGTTTGTAGAGGC 489
DB 9844 CAACCTTGGTGTAGTGTATATTTATATTAAGGCTGCTTGAACCCGTTGCAACCTTGGC 9903
QY 490 CGGGCGCGGTGGCTCACGCTGTAATCCAGGACATTTCGGAGGCGCGGCGGTGGATCA 549
DB 9904 CAGGCGCGGTGGCTCACGCTGTAATCCAGGACATTTCGGAGGCGCGGCGGTGGATCG 9963
QY 550 CGAGTGCAGGAGATCGAGACCATCTCGGTACACGGTGAACCCCGCTCTCTACTAAAAA 609
DB 9964 TGAGTGCAGGATCGAGACCATCTCGGTACACGGTGAACCCCGCTCTCTACTAAAAA 10023
QY 610 TTTAAAAAAAATTAGTGGCGGTGGTGGCGGCGCTGTAGTCCAGCTATTTCGGGAG 669
DB 10024 TACAAAAAAAATTAGCGGCGCATGGTGGTGGCGACCTTTAGTCCAGCTACTTGGGAG 10083
QY 670 GCTGAGGAGGAGAAATGGGNTCAACTCGGAGGTGAGCTTGCANTGAGCCAAAGTCCG 729
DB 10084 GCTGAGATAGGAAATGGGNTGAAACCCGGAGCGGAGGTTGCAGTGAAGCGAGATCCG 10143
QY 730 CCAGTGCATCCAGCTCGGCGGACAGAGCGAGACTCCATCTTA 772
DB 10144 CCGCTGCATCCAGCTCGGCGGACAGAGCGAGACTCCATCTCA 10186

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RESULT 14
US-08-888-497-33
; Sequence 33, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,497
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,405
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 15328 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-888-497-33

Query Match      32.2%; Score 248.6; DB 2; Length 15328;
Best Local Similarity 90.8%; Pred. No. 3.6e-60;
Matches 275; Conservative 0; Mismatches 26; Indels 2; Gaps 1;

QY 470 TAAAGAAATGTTGTAGAGCCCGGCGGTGGCTTACGCTGTATATCCAGACACTTTGGG 529
DB 5679 TAAAGAAATGTTGTAGAGCCCGGCGGTGGCTTACGCTGTATATCCAGACACTTTGGG 5738
QY 530 AGCCCGAGGCGGTGCGGATCACGAGGTCAGAGATCGAGACCATCTGGGTAAACACGCTGA 589
DB 5739 AGCCCGAGGCGGCGGATCACGAGGTCAGAGATCGAGACCATCTGGGTAAACACGCTGA 5798
QY 590 AACCCCGTCTCTACTAAAAATTCAAAAAATTAAGCTGGGCGTGGTGGCGGCGCCCTG 649
DB 5799 AACCCCGTCTCTACTAAAAAT--ACAAAAAATTAAGCCGCGCTGATGTTGGCGCCCTG 5856
QY 650 TAGTCCCGAGCTATTCGGGAGGCTGAGGAGGAGATGGGNTGAACCTGGAGGTGGAGCT 709
DB 5857 TAGTCCCGAGCTATTCGGGAGGCTGAGGAGGAGATGGGNTGAACCTGGAGGTGGAGCT 5916
QY 710 TGCANTGAGCCAAAGGTGCGGCCACTGCATCCAGCTGGGCGGACAGGCGAGACTCCATC 769
DB 5917 TGCAGTGAGCCGAGATTGGCCACTGCACTCCCGCTGGGCCACAGAGCGAGACTCCGTC 5976
QY 770 TTA 772
DB 5977 TCA 5979

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RESULT 15
US-09-362-230-33
; Sequence 33, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,230
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/888,497
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264

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REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 15328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-362-230-33

Query Match 32.2%; Score 248.6; DB 4; Length 15328;
Best Local Similarity 90.8%; Pred. No. 3.6e-60;
Matches 275; Conservative 0; Mismatches 26; Indels 2; Gaps 1;
QY 470 TAAAGATGTTGTAGAGCGCGCGGTGGCTCAGCCCTGTAAATCCAGCACTTTGGG 529
Db |||||
QY 530 AGGCGAGGCGGTGGATCAGAGGTCAGGAGATCGAGACCATCTGGCTAACACGGTGA 589
Db |||||
QY 5739 AGGCGAGGCGGCGGATCAGAGGTAGGAGATCGAGACCATCTGGCTAACACGGTGA 5798
Db |||||
QY 590 AACCCCGTCTCTACTTAAATAATCAAAAAAATTTAGCTGGGCGTGGTGGCGGCGCTG 649
Db |||||
QY 5799 AACCCCGTCTCTACTTAAAT -ACAAAAAATTTAGCGGGCGTGATGGTGGCGGCTG 5856
Db |||||
QY 650 TAGTCCAGCTATTCCGAGGCTAGGCGAGAGATGGCNTGACCTGGGAGGTGGAGCT 709
Db |||||
QY 5857 TAGTCCAGCTACTCGGAGGCTAGGCGAGAGATGGCGTGAACCCGAGGCGGAGCT 5916
Db |||||
QY 710 TGCANTGAGCGAAGGTCCGCGCACTGCACCTCCAGCTGGGCGACAGAGCGGAGACTCCATC 769
Db |||||
QY 5917 TGCAGTGGCCGAGATTGGCCACTGCACTCCGCGCTGGGCCACAGAGCGGAGACTCCGTC 5976
Db |||||
QY 770 TTA 772
Db |||||
QY 5977 TCA 5979

Search completed: May 6, 2004, 11:51:30
Job time : 75.9822 secs

	1	770	99.7	772	4	Ah28482	Nucleotid
	2	277.6	36.0	8487	4	Ah137089	Human mus
	3	277.6	36.0	9487	7	AhX60077	CDNA enco
	4	276	35.8	1143	4	Ah28479	Nucleotid
	5	276	35.8	1533	4	Ah28478	Nucleotid
	6	276	35.8	1902	2	Ah28478	Nucleotid
	7	276	35.8	1902	2	Ah28478	Nucleotid
	8	276	35.8	1905	6	Ah28478	Nucleotid
	9	276	35.8	2061	2	Ah28478	Nucleotid
	10	276	35.8	2061	2	Ah28478	Nucleotid
	11	276	35.8	2886	6	Ah28478	Nucleotid
	12	276	35.8	2887	6	Ah28478	Nucleotid
	13	276	35.8	16350	6	Ah28478	Nucleotid
	14	272.8	35.3	2061	2	Ah28478	Nucleotid
	15	266.2	34.5	322	4	AhX84420	Human imm
	16	266.2	34.5	322	4	AhX84419	Human imm
	17	261.6	33.9	5159	4	Ah137342	Human mus
	18	261.6	33.9	5159	7	AhX60330	CDNA enco
	19	260	33.7	136284	6	AhX83575	Human cDN
	20	259.4	33.6	110000	6	AbS55320 ¹	Continuatio
	21	259.4	33.6	141511	6	AbS55200	Genomic D
	22	259	33.5	10953	5	Ah629204	Genomic S
	23	259	33.5	10953	6	Ah629204	Genomic S
	24	259	33.5	10953	6	AbS68344	Human DNA

Query Match		99.7%; Score 770; DB 4; Length 772;
Best Local Similarity		100.0%; Pred. No. 9.9e-197;
Matches 772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	AAAGCGTTCTCGGCGGAGCGGCAACAACTAGAACCGTGAGAACCGTCCAGCAACCGCGA 60
DB	1	AAAGCGTTCTCGGCGGAGCGGCAACAACTAGAACCGTGAGAACCGTCCAGCAACCGCGA 60
QY	61	CCACGAGCAGCTCACCTCGGCGGAGCGGCAACAACTAGAACCGTCCAGCAACCGCGA 120
DB	61	CCACGAGCAGCTCACCTCGGCGGAGCGGCAACAACTAGAACCGTCCAGCAACCGCGA 120
QY	121	AGCAGGCTCCATGGCCCAAGCGTAGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGG 180
DB	121	AGCAGGCTCCATGGCCCAAGCGTAGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGG 180
QY	181	CCAGGAGCCCTCTCTATCGGAGATGATCCGCTCGGAGCAAGATGCCCATCGAGTGGT 240
DB	181	CCAGGAGCCCTCTCTATCGGAGATGATCCGCTCGGAGCAAGATGCCCATCGAGTGGT 240
QY	241	TCCGCTCTCTGTTGTGAGTCTCAACCAATAACCAAGCGCAAGTGGTACTGTTCCAGAT 300
DB	241	TCCGCTCTCTGTTGTGAGTCTCAACCAATAACCAAGCGCAAGTGGTACTGTTCCAGAT 300
QY	301	GCCTGGGAAAGAACGATGGGCAAGCCCTTGAGAGTCCAGAAAAAAGGCGCTTATA 360
DB	301	GCCTGGGAAAGAACGATGGGCAAGCCCTTGAGAGTCCAGAAAAAAGGCGCTTATA 360
QY	361	ACAGTGTGTTGGGACATGGTCTAATAGTGAGGAGAACAAATAAGCCAGTGTGTGA 420
DB	361	ACAGTGTGTTGGGACATGGTCTAATAGTGAGGAGAACAAATAAGCCAGTGTGTGA 420
QY	421	TTACATGCCACCTTGTGAGGTCAGGAGTGTAAATGTATATTTTAAAGATGTT 480
DB	421	TTACATGCCACCTTGTGAGGTCAGGAGTGTAAATGTATATTTTAAAGATGTT 480
QY	481	GTTAGAGCGCGCGCGTGGTCTACGCTGTAAATCCAGCACTTGGAGGCGCGAGCG 540
DB	481	GTTAGAGCGCGCGCGTGGTCTACGCTGTAAATCCAGCACTTGGAGGCGCGAGCG 540
QY	541	GTCGGATCACGAGTCAGGATCAGACCATCTGGGTAAACAGCGTGAACCCCGCTC 600
DB	541	GTCGGATCACGAGTCAGGATCAGACCATCTGGGTAAACAGCGTGAACCCCGCTC 600
QY	601	TACTAAATTTCAAAAAAATTTAGTGGGCGTGGTGGGCGGCGGCGTGTAGTCCAGCT 660
DB	601	TACTAAATTTCAAAAAAATTTAGTGGGCGTGGTGGGCGGCGGCGTGTAGTCCAGCT 660
QY	661	ATTCGGGAGCTGAGGAGGAGATGGTGAACCTGGGAGTGGAGCTTGCANTGAGCC 720
DB	661	ATTCGGGAGCTGAGGAGGAGATGGTGAACCTGGGAGTGGAGCTTGCANTGAGCC 720
QY	721	AAGGTGCGCCACTGCACTCCAGCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 772
DB	721	AAGGTGCGCCACTGCACTCCAGCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 772
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AAL37089		
ID	AAL37089	standard; DNA; 8487 BP.
XX	XX	
AC	AC	
XX	XX	
DT	DT	08-JAN-2002 (first entry)
XX	XX	
DE	DE	Human musculoskeletal system related polynucleotide SEQ ID NO 3454.
XX	XX	
KW	KW	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW	KW	antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW	KW	vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW	KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW	KW	neurological disease; infection; human; secreted protein;

KW	musculoskeletal system; ds.
XX	Homo sapiens.
XX	WC200155367-Al.
PD	02-AUG-2001.
XX	17-JAN-2001; 2001WO-US001338.
XX	31-JAN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.
PR	24-FEB-2000; 2000US-0184664P.
PR	02-MAR-2000; 2000US-0186350P.
PR	16-MAR-2000; 2000US-0189874P.
PR	17-MAR-2000; 2000US-0190076P.
PR	18-APR-2000; 2000US-0198123P.
PR	19-MAY-2000; 2000US-0205515P.
PR	07-JUN-2000; 2000US-0209467P.
PR	28-JUN-2000; 2000US-0214888P.
PR	30-JUN-2000; 2000US-0215135P.
PR	07-JUL-2000; 2000US-0216647P.
PR	07-JUL-2000; 2000US-0216880P.
PR	11-JUL-2000; 2000US-0217487P.
PR	11-JUL-2000; 2000US-0217496P.
PR	14-JUL-2000; 2000US-0218290P.
PR	26-JUL-2000; 2000US-0220363P.
PR	26-JUL-2000; 2000US-0220564P.
PR	14-AUG-2000; 2000US-0224518P.
PR	14-AUG-2000; 2000US-0224519P.
PR	14-AUG-2000; 2000US-0225213P.
PR	14-AUG-2000; 2000US-0225214P.
PR	14-AUG-2000; 2000US-0225266P.
PR	14-AUG-2000; 2000US-0225267P.
PR	14-AUG-2000; 2000US-0225268P.
PR	14-AUG-2000; 2000US-0225270P.
PR	14-AUG-2000; 2000US-0225477P.
PR	14-AUG-2000; 2000US-0225757P.
PR	14-AUG-2000; 2000US-0225758P.
PR	14-AUG-2000; 2000US-0225759P.
PR	18-AUG-2000; 2000US-0228279P.
PR	22-AUG-2000; 2000US-0228681P.
PR	22-AUG-2000; 2000US-0228688P.
PR	22-AUG-2000; 2000US-0227182P.
PR	23-AUG-2000; 2000US-0227009P.
PR	30-AUG-2000; 2000US-0228924P.
PR	01-SEP-2000; 2000US-0229287P.
PR	01-SEP-2000; 2000US-0229343P.
PR	01-SEP-2000; 2000US-0229344P.
PR	01-SEP-2000; 2000US-0229345P.
PR	05-SEP-2000; 2000US-0229509P.
PR	06-SEP-2000; 2000US-0229513P.
PR	06-SEP-2000; 2000US-0230437P.
PR	06-SEP-2000; 2000US-0230438P.
PR	08-SEP-2000; 2000US-0231242P.
PR	08-SEP-2000; 2000US-0231243P.
PR	08-SEP-2000; 2000US-0231244P.
PR	08-SEP-2000; 2000US-0231413P.
PR	08-SEP-2000; 2000US-0231414P.
PR	08-SEP-2000; 2000US-0232080P.
PR	12-SEP-2000; 2000US-0232081P.
PR	14-SEP-2000; 2000US-0232387P.
PR	14-SEP-2000; 2000US-0232388P.
PR	14-SEP-2000; 2000US-0232399P.
PR	14-SEP-2000; 2000US-0232400P.
PR	14-SEP-2000; 2000US-0232401P.
PR	14-SEP-2000; 2000US-0233063P.
PR	14-SEP-2000; 2000US-0233064P.
PR	14-SEP-2000; 2000US-0233065P.
PR	21-SEP-2000; 2000US-0234223P.
PR	21-SEP-2000; 2000US-0234274P.
PR	25-SEP-2000; 2000US-0234997P.

PR	25-SEP-2000;	2000US-0234998P.	XX	(HUMA-) HUMAN GENOME SCI INC.
PR	26-SEP-2000;	2000US-0235484P.	PA	
PR	27-SEP-2000;	2000US-0235834P.	XX	Rosen CA, Barash SC, Ruben SM;
PR	29-SEP-2000;	2000US-0235836P.	PI	
PR	29-SEP-2000;	2000US-0236327P.	XX	WPI; 2001-451937/48.
PR	29-SEP-2000;	2000US-0236367P.	DR	
PR	29-SEP-2000;	2000US-0236368P.	XX	Isolated polypeptide for treating, preventing and/ or prognosing
PR	29-SEP-2000;	2000US-0236369P.	PT	disorders related to the musculoskeletal system including musculoskeletal
PR	29-SEP-2000;	2000US-0236370P.	PT	cancers and also for testing and detection e.g. diagnosis.
PR	02-OCT-2000;	2000US-0236802P.	XX	
PR	02-OCT-2000;	2000US-0237037P.	PS	Example 2; SEQ ID NO 3454; 781pp + Sequence Listing; English.
PR	02-OCT-2000;	2000US-0237038P.	XX	
PR	02-OCT-2000;	2000US-0237039P.	XX	The invention relates to novel genes (AAU34669-AAU37666) and proteins
PR	13-OCT-2000;	2000US-0237040P.	CC	(ABO3087-ABO4109) associated with the musculoskeletal system useful for
PR	13-OCT-2000;	2000US-0239933P.	CC	preventing, treating or ameliorating medical conditions e.g. by protein
PR	13-OCT-2000;	2000US-0239937P.	CC	or gene therapy. The genes are isolated from a range of human tissues
PR	20-OCT-2000;	2000US-0240960P.	CC	disclosed in the specification. The nucleic acids, proteins, antibodies
PR	20-OCT-2000;	2000US-0242211P.	CC	and (ant)agonists are useful in the diagnosis, treatment and prevention
PR	20-OCT-2000;	2000US-0241785P.	CC	of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
PR	20-OCT-2000;	2000US-0241786P.	CC	lung, or urogenital; (b) immune disorders e.g. Addison's disease,
PR	20-OCT-2000;	2000US-0241808P.	CC	allergies, autoimmune haemolytic anaemia, multiple sclerosis, rheumatoid
PR	20-OCT-2000;	2000US-0241822P.	CC	diabetes mellitus, Crohn's disease, (c) cardiovascular disorders such as
PR	01-NOV-2000;	2000US-0244617P.	CC	arthritis and ulcerative colitis; (d) wound healing; (e) neurological disorders such as
PR	08-NOV-2000;	2000US-0246474P.	CC	myocardial ischaemias; (f) infectious diseases such as viral,
PR	08-NOV-2000;	2000US-0246475P.	CC	cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
PR	08-NOV-2000;	2000US-0246476P.	CC	bacterial, fungal and parasitic infections. Note: the sequence data for
PR	08-NOV-2000;	2000US-0246477P.	CC	this patent did not form part of the printed specification, but was
PR	08-NOV-2000;	2000US-0246478P.	CC	obtained in electronic format directly from WIPO at
PR	08-NOV-2000;	2000US-0246523P.	CC	ftp.wipo.int/pub/published_pct_sequences
PR	08-NOV-2000;	2000US-0246524P.	XX	
PR	08-NOV-2000;	2000US-0246525P.	XX	Sequence 8487 BP; 1948 A; 1987 C; 2408 G; 2144 T; 0 U; 0 Other;
PR	08-NOV-2000;	2000US-0246526P.	SQ	
PR	08-NOV-2000;	2000US-0246527P.		Query Match 36.0%; Score 277.6; DB 4; Length 8487;
PR	08-NOV-2000;	2000US-0246528P.		Best Local Similarity 81.0%; Pred. No. 48-64;
PR	08-NOV-2000;	2000US-0246532P.		Matches 423; Conservative 0; Mismatches 59; Indels 40; Gaps 7;
PR	08-NOV-2000;	2000US-0246609P.	QY	2 AAGCGTTCTCGCGGCGAGCGCAACACTAGAACCGTGTGAGAACCGTCCAGAACCGCGAC 61
PR	08-NOV-2000;	2000US-0246610P.	Db	5538 AAGCGTCTACGGCGGCGAGCGCAACAGAGAACCGTGTGAGAACCGTCCAGAACCGCA- 6596
PR	17-NOV-2000;	2000US-0249207P.	QY	62 CCACGACGAGCTCACTCTCGGCGACGCCCAAGAGAGAAAGCCCGAGACCTCTTAAGAGAA 121
PR	17-NOV-2000;	2000US-0249208P.	Db	6597 CCACGACGAGCGGCGCTCGGCGACACCCAAAGAGAGAAAGGCGCAAGACCTCCAAGAAGAA 6656
PR	17-NOV-2000;	2000US-0249210P.	QY	122 GCAGGGCTCCATGGCCCAAGCGGTAGCGGCGAGCGGCTCCCGCAGAGCTCCCATCGACCC 181
PR	17-NOV-2000;	2000US-0249211P.	Db	6657 GAAGCGCTCCAGGCCAAGCGGAGCGAGGCGTCCCTTCCGACCTCCCATCGACCC 6716
PR	17-NOV-2000;	2000US-0249212P.	QY	182 CAGCGAGCC-----CTCTACTGGAGATGATCGGTGGA 217
PR	17-NOV-2000;	2000US-0249213P.	Db	6717 CAACGAACCCACGCTACTGTGTGCAACCCAGGCTCTCTATGGGAGATGATCGGTGGA 6776
PR	17-NOV-2000;	2000US-0249244P.	QY	218 CA---AGCAATGCCCATCGAGTGGTTCGGCTTCTGTGTGTGAGTCTCAACCAATAACC 274
PR	17-NOV-2000;	2000US-0249245P.	Db	6777 CAACGACGAGTGGCCCATCGAGTGGTTCACATCTCTGTGTGGGCTCAATCATTAACCC 6836
PR	17-NOV-2000;	2000US-0249297P.	QY	275 AAAGCGCAAGTGGTACTGTTCAGATGCGCGGGGAAAGAACG-----ATGGGCAAGC 326
PR	17-NOV-2000;	2000US-0249299P.	Db	6837 CAAGGCGAAGTGGTACTGTTCAGATGCGCGGGGAGAACGAGAGACCATGACAAAGC 6896
PR	01-DEC-2000;	2000US-0250160P.	QY	327 CTTGAGAGTCCAGAAAAAAGAGGGCTTATAACAGTAGTCTTGGGACATGGCTCTA 386
PR	01-DEC-2000;	2000US-0250161P.	Db	6897 CTTGGAGAAATCCA--AAAAAGAGAGGGCTTACACAGTAGTCTTGGAGAGGGCCCTG 6954
PR	05-DEC-2000;	2000US-0251030P.	QY	387 ATAGTGAGGAGAAACAAATAAGCCAGTGTGTGATTACATTTGCCACTTTGTGAGGTGC 446
PR	05-DEC-2000;	2000US-0251030P.	Db	6955 GT-GTGGAGGAGCAAAATAAACCC-GTGTATTATTATACATTTGTCTCTTTGTGAGGTGC 7012
PR	05-DEC-2000;	2000US-0251988P.	QY	447 AGGAAGTGTAATGTATATATTTTAAAGATGTGTGTAGG 488
PR	11-DEC-2000;	2000US-0251990P.	Db	7013 AAGGAGTGTAAATGTATATTTTAAAGATGTGTAGTAAAG 7054

RESULT 3

ABX60077
 ID ABX60077 standard; cDNA; 8487 BP.
 XX
 AC ABX60077;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE cDNA encoding novel human musculoskeletal system antigen #2421.
 XX
 KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
 KW re-vascularization; thrombosis; arteriosclerosis; mineral content;
 KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
 KW post-operative tissue repair; limb regeneration; neuronal growth;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW AIDS-related complex; chondrocyte growth; bone regeneration;
 KW periodontal regeneration; tissue transport; bone graft; skin aging;
 KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
 KW cell growth; organ transplant; cell differentiation; body height; weight;
 KW hair colour; eye colour; skin; percentage of adipose tissue;
 KW pigmentation; cosmetic surgery; metabolism; biorhythm; cardiac rhythm;
 KW depression; tendency for violence; pain; reproductive capability;
 KW hormone level; endocrine level; appetite; libido; memory; stress;
 KW storage capability; fat content; lipid content; protein content;
 KW carbohydrate content; vitamin content; cofactor content;
 KW nutritional component.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US2002147140-A1.
 PN
 XX
 PD 10-OCT-2002.
 XX
 XX 17-JAN-2001; 2001US-00764877.
 PF
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0215647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 22-AUG-2000; 2000US-0225758P.
 PR 30-AUG-2000; 2000US-0226868P.
 PR 01-SEP-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 05-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 23-SEP-2000; 2000US-0234997P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0237040P.
 PR 20-OCT-2000; 2000US-0239935P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241805P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 XX Rosen CA, Ruben SM, Barash SC;
 XX WPI; 2003-128199/12.
 XX
 PT Isolated nucleic acid molecules encoding musculoskeletal system
 associated polypeptides, useful for detecting disorders, e.g. cancer.
 XX
 PS Disclosure; SEQ ID NO 3454; 321pp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule comprising a
 sequence encoding musculoskeletal system associated polypeptides useful
 for detecting disorders, e.g., cancer or cancer metastases, in animals or
 humans. The nucleic acid stimulates re-vascularisation of ischaemic
 tissues associated with conditions such as thrombosis, arteriosclerosis,
 and other cardiovascular conditions; treats wounds due to injuries,
 burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
 and limb regeneration; stimulates neuronal growth; can treat and prevent
 neuronal damage occurring in certain disorders or neurodegenerative
 conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-
 related complex; stimulates chondrocyte growth, thus they can be used to
 enhance bone and periodontal regeneration and aid in tissue transports or
 bone grafts; prevents skin aging due to sunburn by stimulating
 keratinocyte growth; prevents hair loss, since RGF family members
 activate hair-forming cells and promotes melanocyte growth; stimulates
 growth and differentiation of hematopoietic cells and bone marrow cells
 when used in combination with other cytokines; maintains organs before
 transplantation or for supporting cell culture of primary tissues;
 CC induces tissue of mesodermal origin to differentiate in early embryos;
 CC increases or decreases the differentiation or proliferation of embryonic
 stem cells, besides, hematopoietic lineage; modulates mammalian
 characteristics, such as, body height, weight, hair colour, eye colour,
 skin, percentage of adipose tissue, pigmentation, size, and shape (e.g.,
 cosmetic surgery); modulates mammalian metabolism; changes mammal's metal
 state or physical state by influencing biorhythms, cardiac rhythms,
 depression, tendency for violence, tolerance for pain, reproductive
 capabilities, hormonal or endocrine levels, appetite, libido, memory, or
 stress; increases or decreases storage capabilities, fat content, lipid,
 protein, carbohydrate, vitamins, minerals, cofactors or other nutritional
 components. This sequence encodes a novel human musculoskeletal system
 antigen. Note: The sequence data for this patent did not form part of the
 printed specification, but was obtained in electronic format directly
 from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID=20020147140
 XX
 SQ Sequence 8487 BP; 1948 A; 1987 C; 2408 G; 2144 T; 0 U; 0 Other;

Query Match 36.0%; Score 277.6; DB 7; Length 8487;
 Best Local Similarity 81.0%; Pred. No. 4e-64;
 Matches 423; Conservative 0; Mismatches 59; Indels 40; Gaps 7;
 QY 2 AAGCGTTCTCGGGGAGCGCAACACTAGAACCGTGAGAACCGTCCAGCAACCGGAC 61
 |||||
 DB 6538 AAGCGCTCAGCGGCGGAGCGCAACAGAGAACCGTGAGAACCGTCCAGCAACCGA- 6596

62 CCACGACGAGTCACTCGGCACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGAA 121
 6597 CCACGACGAGCGCGCTCGGCACACCCCAAGGAGAGAGAGGCAAGACCTCCAAAGAA 6656
 122 CGAGGCTCATGGCCCAAGCGTAGAGCGAGCGTCCCGCAGACCTCCCGATCGACCC 181
 6657 GAAGCGCTCCAAAGCGCAAGCGGAGCGAGAGCGTCCCGTCCGACCTCCCGATCGACCC 6716
 182 CAGCGAGCC-----CTCTACTGGGAGATGATCCGCTGGGA 217
 6717 CAACGAACCCACGTACTGTCTGTGCAACCAAGTCTCTATGGGAGATGATCGGCTGGGA 6776
 218 CA---ACGAATGCCCATCGAGTGTTCGCTTCCAGTCTCTATGGGAGATGATCGGCTGGGA 274
 6777 CAACGACGAGTCCCGCATCGAGTGTTCACCTTCTCGTGGTGGGCTCAATCATAAACC 6836
 275 AAAGCGCAAGTGTACTGTTCAGATGCGCGGGAAGAACG-----ATGGGCAAGC 326
 6837 CAAGGCAAGTGTACTGTCCCAAGTCCCGGAGAGAGAGACCAATGACCAAGC 6896
 327 CTTTGAGAGTCAGAAAAAACAAGGCTTATAACAGGTAGTTTGGGACATGCGTCTA 386
 6897 CTTGAGAAATCCA--AAAAAGAGAGGCTTACAACAGGTAGTTTGGGACAGGCGCTG 6954
 387 ATAGTGAGGAGACAAATAAGCCAGTGTGTGATTACATTCGCCACCTTGTGAGGTGC 446
 6955 GT-GTGGAGGACAAATAAACC-GTGATTATTATACATTCTGCTGCTTTGTTGAGGTGC 7012
 447 AGGAAGTGAATAATGATATTTTAAAGAAATGTTGTAGAGG 488
 7013 AAGGAGTGAATAATGATATTTTAAAGAAATGTTGTAGAGG 7054

RESULT 4
 AAH28479
 ID AAH28479 standard; DNA; 1143 BP.
 XX AC AAH28479;
 XX DT 17-SEP-2001 (first entry)
 XX DE Nucleotide sequence of a human cancer associated antigen.
 XX KW Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX CDS 16..900
 XX FT /*tag= a
 XX FT /transl_except= (pos: 25..30, aa: Cys)
 XX FT /transl_except= (pos: 124..126, aa: Pro, Ala)
 XX FT /product= cancer associated antigen
 XX PN WO200147959-A2.
 XX XX
 XX 05-JUL-2001.
 XX XX
 XX 29-NOV-2000; 2000WO-US042334.
 XX XX
 XX 30-NOV-1999; 99US-00451739.
 XX PR 24-OCT-2000; 2000US-00602362.
 XX XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX PA (CORR) CORNELL RES FOUND INC.
 XX XX
 XX Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;
 XX WPI; 2001-441706/47.
 XX DR P-PSDB; AAB84697.
 XX XX
 XX Isolated cancer associated nucleic acid molecule identified by SEREX

(serological identification of antigens by recombinant expression cloning) technique, useful in nucleic acid based therapies to treat cancer.
 XX Example 4; Page 44; 62pp; English.
 XX The present sequence encodes a human cancer associated antigen. The sequence is the wildtype of the INGI gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines
 XX Sequence 1143 BP; 289 A; 291 C; 366 G; 197 T; 0 U; 0 Other;
 SQ
 Query Match 35.8%; Score 276; DB 4; Length 1143;
 Best Local Similarity 80.8%; Pred. No. 5.6e-64;
 Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
 QY 2 AAGCGTTCTCGGCGGAGCGCAACACTAGAACCGTGAACCGTCCAGCACCGCGAC 61
 DB 502 AAGCGTTCTACGCGGCGAGCGCAACAGAGAACCGTGAACCGTCCAGCACCGACGA - 560
 QY 62 CCACGACGAGTCACTCGGCGCAGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGAA 121
 DB 561 CCACGACGAGCGGCTCGGCGCACACCCAGGAGAGAGAGGCAAGACCTCCAGAGAA 620
 QY 122 GCAGGGTCCATGGCAAGCGTAGCGGAGGCGTCCCGCAGAGCTCCCGATCGACCC 181
 DB 621 GAAGCGTCCAGGCCAAGCGGAGGCGGCTCCCTGCGGAGCTCCCATCGACCC 680
 QY 182 CAGCGAGCG-----CTCTACTGGGAGATGATCGGTCGGA 217
 DB 681 CAACGAACCCACGTACTGTCTGTGCAACCAAGTCTCTATGGGAGATGATCGGTCGGA 740
 QY 218 CA---ACGAATGCCCATCGAGTGTTCGCTTCTCGTGTGAGTCTCAACCATAAACC 274
 DB 741 CAACGACGAGTGGCGCCATCGAGTGTTCACCTTCTCGTGGTGGGCTCAATCATAAACC 800
 QY 275 AAAGCGCAAGTGTACTGTTCAGATGCGCGGGAAGAACG-----ATGGGCAAGC 326
 DB 801 CAAGGCGAGTGTACTGTTCAGATGCGCGGAGAGAGAGACCAATGACCAAGC 860
 QY 327 CTTTGAGAGTCCAGAAAAAACAAGGCTTATAACAGGTAGTTTGGGACATGCGTCTA 386
 DB 861 CTTGAGAAATCCA--AAAAAGAGAGGCTTACAACAGGTAGTTTGGGACAGGCGCTG 918
 QY 387 ATAGTGAGGAGACAAATAAAGCCAGTGTGTGATTACATTCGCCACCTTGTGAGGTGC 446
 DB 919 GT-GTGGAGGACAAATAAACC-GTGATTATTATACATTGCTGCTTTGTTGAGGTGC 976
 QY 447 AGGAAGTGAATAATGATATTTTAAAGAAATGTTGTAGAGG 488
 DB 977 AAGGAGTGAATAATGATATTTTAAAGAAATGTTGTAGAGG 1018
 RESULT 5
 AAH28478
 ID AAH28478 standard; DNA; 1533 BP.
 XX AC AAH28478;
 XX DT 17-SEP-2001 (first entry)
 XX DE Nucleotide sequence of a human cancer associated antigen.
 XX KW Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX CDS 451..1290
 XX FT /*tag= a

PA (UYTE-) UNIV TECHNOLOGIES INT INC.
XX Garkavteev I, Riabowol K;
PI WPI, 1997-332781/30.
XX P-PSDB; AAW18119.
DR Isolated tumour suppressor gene, INGI - useful to develop products for
XX inhibiting or increasing cell proliferation, in particular for treatment
XX or diagnosis of cancer.
XX Claim 11; Fig 3; 63pp; English.
PS A full-length cDNA clone (AAT69652), designated INGI, codes for a novel
XX 33 kDa tumour suppressor protein p33ING1 (AAW19119), formerly p33IG1,
XX that is a potent inhibitor of cell growth. A partial clone (AAT69651) was
XX isolated by subtractive hybridisation between normal mammary and
XX transformed epithelial cDNAs, isolation of an antisense INGI cDNA insert
XX that caused increased cell proliferation, and use of the insert to screen
XX normal human fibroblast and HeLa cDNA libraries. The complete INGI
XX cDNA sequence was then obtained by 5'RACE. INGI is localised to the 13q33-34
XX chromosome region, to which a number of human cancers have been mapped.
XX INGI nucleic acids can be used in the diagnosis of breast cancer; a
XX decreased level of INGI mRNA indicates cancerous cells. They can also be
XX used in gene therapy methods to block the proliferation of cancer cells
XX
SQ Sequence 2061 BP; 602 A; 439 C; 515 G; 505 T; 0 U; 0 Other;
Query Match 35.8%; Score 276; DB 2; Length 2061;
Best Local Similarity 80.8%; Pred. No. 6.7e-64;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
QY 2 AAGCGTTCTCGCGGAGGCAACCACTAGAACCGCTGAGAACCGCTCCAGCAACCGCGAC 61
Db 502 AAGCGCTACGCGGAGGCGGACACACGACGACCGCTGAGAACCGCTCCAGCAACCGCA- 560
QY 62 CCACGACGAGTCACTCTCGGCGACCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
Db 561 CCACGACGAGTCACTCTCGGCGACCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 620
QY 122 CGAGGCTCCATGGGCAAGCGCTAGCGGAGGCGTCCCGGAGAGAGAGAGAGAGAGAGAG 181
Db 621 GAAGCGCTCAAGGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 680
QY 182 CAGCGAGGCC-----CTCTACTGGGAGATGATCGGTGCGA 217
Db 681 CAACGAAACCCACTACTGTGTGCAACCAAGCTCTCTATGGGAGATGATCGGTGCGA 740
QY 218 CA---ACGATGCCCATCGAGTGGTTCGCTTCTGCTGTGTGAGTCTCAACCATAAACC 274
Db 741 CAACGACGAGTGCCTCATCGAGTGGTTCACCTCTCTGCTGGGCTCAATCATAAACC 800
QY 275 AAAGCGCAAGTGTACTGTCTCCAGATGCCGGGGAAGAACG-----ATGGGCAAGC 326
Db 801 CAGGGCAAGTGTACTGTCTCCAGTGCAGGTCGGGGGAGAGACGAGACCATGACAAAGC 860
QY 327 CTTTGAAGTCCAGAAAAAAGAGGCTTATAACAGTAGTTTGGGACATGGCTCTA 386
Db 861 CTTGGAAGATCCA--AAAAAGAGGGGCTTACACAGGTAGTTTGTGACAGGGCGCTG 918
QY 387 ATAGTGAAGAGAAACAAATAAGCCAGTGTGTGATTACATTGTCACCTTTGTGAGGTGC 446
Db 919 GT-GTGAGGAGGACAAATAAACCC-GTGTATTATTATGCTGCTTTGTGAGGTGC 976
QY 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTGTAGAG 488
Db 977 AAGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAAAG 1018
RESULT 10
AAV62292
ID AAV62292 standard; cDNA; 2061 BP.
XX

AC AAV62292;
XX 18-JAN-1999 (first entry)
DT XX
DE XX
DE Human INGI full-length cDNA sequence.
DE XX
KW INGI gene; p33ING1; human; apoptosis; cell death; breast cancer;
KW brain tumour; gene therapy; tumour suppressor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 16..900
FT CDS /*tag= a
FT
FT
FT WO9844102-A2.
PN
XX
XX 08-OCT-1998.
XX
XX 26-MAR-1998; 98WO-CA000277.
XX
XX 27-MAR-1997; 97US-00828158.
XX
XX (UYTE-) UNIV TECHNOLOGIES INT INC.
XX
XX Helbing CC, Riabowol K, Johnston RN, Garkavteev I;
XX
XX WPI; 1998-542700/46.
XX
XX P-PSDB; AAW79675.
XX
XX Modulating eukaryotic apoptosis by increasing p33ING1 activity - using
XX p33ING1 derivatives, to induce apoptosis in cancer cells, and in the
XX investigation of apoptotic pathways.
XX
XX Claim 7; Fig 3; 66pp; English.
XX
XX This is the nucleotide sequence of a human INGI (INHIBITOR OF GROWTH)
XX that codes for a p33ING1 polypeptide (see AAW79675), a novel inhibitor
XX of cell growth and a candidate tumour suppressor. INGI is a new gene that
XX is expressed in normal mammary epithelial cells, but which is expressed
XX only at lower levels in several cancerous mammary epithelial cell lines
XX and is not expressed in many primary brain tumours. To isolate INGI, a
XX subtractive hybridisation of breast cancer cell line cDNAs was performed
XX with cDNA from normal mammary epithelial cells, and subtracted cDNAs were
XX cloned into retrovirus vector pLNCX. Following passage through a
XX packaging line, normal mouse mammary epithelial cells were infected, and
XX infected cells were injected into nude mice. Putative transforming
XX fragments from tumours were isolated by PCR (see AAV62290-91) and
XX subcloned into LNCX. An INGI fragment was obtained and used to screen
XX normal human fibroblast and HeLa cell cDNA libraries. 2 Clones were
XX sequenced to obtain a partial INGI sequence (see AAV62285). The complete
XX cDNA sequence was then obtained by RACE. A claimed method to potentiate
XX apoptosis in a eukaryotic cell involves administering an active p33ING1
XX peptide or an oligonucleotide encoding such as a peptide. A claimed
XX method for inhibiting apoptosis in a eukaryotic cell involves
XX administering an antisense oligonucleotide. Also claimed are a method for
XX determining the apoptotic characteristics of a eukaryotic cell, an assay
XX for determining the level of p33ING1 activity in a eukaryotic cell, and
XX an isolated eukaryotic cell substantially free of p33ING1 biological
XX activity. The invention discloses INGI derivatives or variants that may
XX be used to induce apoptosis in eukaryotic cancer cells
XX
SQ Sequence 2061 BP; 602 A; 439 C; 515 G; 505 T; 0 U; 0 Other;
Query Match 35.8%; Score 276; DB 2; Length 2061;
Best Local Similarity 80.8%; Pred. No. 6.7e-64;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
QY 2 AAGCGTTCTCGCGGAGGCGGACCAACTAGAACCGCTGAGAACCGCTCCAGCAACCGCGAC 61
Db 502 AAGCGCTCACGCGGAGGCGGACACACGACGACCGCTGAGAACCGCTCCAGCAACCGCA- 560
QY 62 CCACGACGAGTCACTCTCGGCGACCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
Db 561 CCACGACGAGTCACTCTCGGCGACCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 620
QY 122 CGAGGCTCCATGGGCAAGCGCTAGCGGAGGCGTCCCGGAGAGAGAGAGAGAGAGAGAG 181
Db 621 GAAGCGCTCAAGGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 680
QY 182 CAGCGAGGCC-----CTCTACTGGGAGATGATCGGTGCGA 217
Db 681 CAACGAAACCCACTACTGTGTGCAACCAAGCTCTCTATGGGAGATGATCGGTGCGA 740
QY 218 CA---ACGATGCCCATCGAGTGGTTCGCTTCTGCTGTGTGAGTCTCAACCATAAACC 274
Db 741 CAACGACGAGTGCCTCATCGAGTGGTTCACCTCTCTGCTGGGCTCAATCATAAACC 800
QY 275 AAAGCGCAAGTGTACTGTCTCCAGATGCCGGGGAAGAACG-----ATGGGCAAGC 326
Db 801 CAGGGCAAGTGTACTGTCTCCAGTGCAGGTCGGGGGAGAGACGAGACCATGACAAAGC 860
QY 327 CTTTGAAGTCCAGAAAAAAGAGGCTTATAACAGTAGTTTGGGACATGGCTCTA 386
Db 861 CTTGGAAGATCCA--AAAAAGAGGGGCTTACACAGGTAGTTTGTGACAGGGCGCTG 918
QY 387 ATAGTGAAGAGAAACAAATAAGCCAGTGTGTGATTACATTGTCACCTTTGTGAGGTGC 446
Db 919 GT-GTGAGGAGGACAAATAAACCC-GTGTATTATTATGCTGCTTTGTGAGGTGC 976
QY 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTGTAGAG 488
Db 977 AAGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAAAG 1018
RESULT 10
AAV62292
ID AAV62292 standard; cDNA; 2061 BP.
XX

PI Gong F, Yan C;
 XX WPI: 2002-698658/75.
 DR P-PSDB; AA28633.
 XX New human tumor suppressor proteins, useful for developing human
 PT therapeutic agents, or preventing or treating inflammation, or disorders
 PT associated with cell proliferation, e.g. bone cancer, brain cancer,
 PT leukemia or lymphoma.
 XX
 XX Claim 4; Fig 3; 200pp; English.
 PS The invention relates to human tumor suppressor polypeptides and
 XX polynucleotides. Sequences of the invention are useful for diagnosing,
 CC preventing or treating inflammation, or disorders associated with cell
 CC proliferation and apoptosis e.g. bone cancer, brain cancer, cervix
 CC cancer, adenocarcinoma, leukemia, lymphoma or melanoma. They are
 CC particularly useful as models for developing human therapeutic targets,
 CC identifying therapeutic proteins, or serving as targets for the
 CC development of human therapeutic agents that modulate tumor suppressor
 CC protein activity in cells and tissues that express the tumor suppressor
 CC protein. Polypeptides of the invention are useful for identifying agents
 CC that modulate their activity. They are useful for raising antibodies or
 CC eliciting an immune response; as a reagent in assays designed to
 CC quantitatively determine levels of the protein (or its binding partner or
 CC ligand) in biological fluids; or as markers for tissues in which the
 CC corresponding protein is preferentially expressed. The invention is also
 CC used as vaccines. The present sequence is human tumor suppressor gene
 CC located on chromosome 13
 XX
 SQ Sequence 163350 BP; 40430 A; 36356 C; 37002 G; 39020 T; 0 U; 10542 Other;
 Query Match 35.8%; Score 276; DB 6; Length 163350;
 Best Local Similarity 80.8%; Pred. No. 2.8e-63;
 Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
 QY 2 AAGCGTTCGCGGAGGCGGACAACTAGACCGGTGAGAACCGGTCCAGCAACCGAC 61
 Db 160113 AAGCGTTCGCGGAGGCGGACAACTAGACCGGTGAGAACCGGTCCAGCAACCGAC 160171
 QY 62 CCACGACGAGTCTACCTCGGCGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAGAA 121
 Db 160172 CCACGACGAGTCTACCTCGGCGACGCCCAAGGAGAGAGGCGACCTCTAAGAGAA 160231
 QY 122 GCAGGGCTCCATGGCCCAAGCGGTAGCGGAGGCGTCCCGGAGACCTCCCATGACCC 181
 Db 160232 GAAGCGCTCCAGGCGCAAGCGGAGGCGGCGTCCCGGAGACCTCCCATGACCC 160291
 QY 182 CAGCGAGCC-----CTCTACTGGGAGATCATCGCTGCGA 217
 Db 160292 CAACGAAACCCAGTACTGTCTGTGCACACGAGTCTCTATGGGAGATCATCGCTGCGA 160351
 QY 218 CA---ACGAAATGCCCATCGAGTGGTTCGCTTCTGTGTGTGAGTCTCAACCATTAACC 274
 Db 160352 CAACGACGAGTGGCCCATCGAGTGGTTCCTACTTCTGTGTGTGAGTCTCAATCATTAACC 160411
 QY 275 AAGCGCAAGTGTACTGTTCAGATGCCCGGGAAGAACG-----ATGGGCAAGC 326
 Db 160412 CAGGGCAAGTGTACTGTTCCTCAAGTCCCGGGGGAGAACGAAACCATGACCAAAAC 160471
 QY 327 CTTTGAAGTCCAGAAAAAAGAGGGCTTATAACAGGTAGTTTGGGACATGCTCTA 386
 Db 160472 CTTGGAGAAATCCA--AAAAGAGAGGGCTTACACAGGTAGTTTGGGACAGGCGCTG 160529
 QY 387 ATAGTGGAGAACAAATAGCAGTGTGTGTTTACATTGCCACTTTGCTGAGGTGC 446
 Db 160530 GT-GTGAGGAGGACAAATAAAC-GTGTATTATTACATGTGCTTGTGAGGTGC 160587
 QY 447 AGGAAGTGTAAATGTATATTTTAAAGAATGTTGTAGAGG 488
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 ID AAX28688 standard; cDNA; 2061 BP.
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 AC AAX28688;
 XX
 DT 26-AUG-1999 (first entry)
 DE Nucleotide sequence of the human p33-ING1 gene.
 XX
 KW Human; p33-ING1 protein; growth regulation; apoptosis; DNA damage;
 KW inhibition; anchorage independent growth; cytotoxic drug;
 KW transcriptional activation; cancer; immortal cell line; ss.
 XX
 OS Homo sapiens.
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 FH Key Location/Qualifiers
 FT CDS 16..900
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 XX WO9916790-A1.
 XX 08-APR-1999.
 XX 24-SEP-1998; 98WO-US018179.
 XX 26-SEP-1997; 97US-0060138P.
 XX 14-JAN-1998; 98US-00006783.
 XX (UNITE-) UNIV TECHNOLOGIES INT INC.
 XX (UNII) UNIV ILLINOIS BOARD OF TRUSTEES.
 XX Riabowol K, Garkavtsev I, Gudkov A;
 WPI: 1999-263685/22.
 P-PSDB; AAY03244.
 Use of p33-ING1 peptides to modulate activity of, isolate or detect p53.
 Disclosure; Fig 1; 64pp; English.
 This is the nucleotide sequence encoding the human p33-ING1 protein, used
 in the method of the invention. The ING1 gene encodes p33-ING1 which can
 be used to modulate the activity of, isolate or detect p53. Expression of
 the ING1 and p53 genes in a mammalian cell results in normal growth
 regulation anchorage-dependent growth and apoptosis as a response to
 irreversible DNA damage and other cellular insult. Inhibition of
 expression of either gene results in a loss of cellular growth control,
 anchorage independent growth, inhibition of apoptosis and resistance to
 radiation and cytotoxic drugs. The p33-ING1 is a component of the p53
 signalling pathway that cooperates with p53 in negative regulation of
 cell proliferation by modulating p53 dependent transcriptional
 activation. Biological function of p53 signalling pathway can therefore
 be regulated (both enhanced or suppressed) by modulating p33-ING1
 activity. The modulation of p33-ING1 activity can be used for the
 stimulation or restoration of the p53 pathway in anti cancer therapy or
 for the suppression of the p53 pathway to defend sensitive tissues from
 genotoxic stress or for the generation of immortal cell lines
 Sequence 2061 BP; 600 A; 437 C; 518 G; 506 T; 0 U; 0 Other;
 Query Match 35.3%; Score 272.8; DB 2; Length 2061;
 Best Local Similarity 80.5%; Pred. No. 4.9e-63;
 Matches 420; Conservative 0; Mismatches 62; Indels 40; Gaps 7;
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 Db 502 AAGCGTTCGCGGAGGCGGACAACTAGAACCGGTCCAGCAACCGCGAC 560
 QY 62 CCACGACGACGTTCACCTCGGCGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAGAA 121
 Db 561 CCACGACGACGCGCGTCCGCGACACCCAGGAGAGAAAGCCAGACCTCTAAGAGAA 620

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 6, 2004, 15:57:18 ; Search time 642 Seconds
(without alignments)
3612.703 Million cell updates/sec

Title: US-09-451-739H-16

Perfect score: 2599

Sequence: 1 MKVSIPIKALELMDVQTEFA.....IAGDACLQRKNVDVSSTDI 512

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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1	2589	99.6	4047	14	US-10-007-805-566	Sequence 566, App
2	2589	99.6	4047	15	US-10-076-622-566	Sequence 566, App
3	2589	99.6	4047	15	US-10-124-805-566	Sequence 566, App
4	2589	99.6	4458	13	US-10-058-270A-3	Sequence 3, Appli
5	2589	99.6	4458	14	US-10-007-805-564	Sequence 564, App
6	2589	99.6	4458	15	US-10-076-622-564	Sequence 564, App
7	2589	99.6	4458	15	US-10-177-293-333	Sequence 333, App
8	2589	99.6	4458	15	US-10-124-805-564	Sequence 564, App
9	2578	99.2	3288	14	US-10-007-805-490	Sequence 490, App
10	2578	99.2	3288	15	US-10-076-622-490	Sequence 490, App
11	2578	99.2	3288	15	US-10-124-805-490	Sequence 490, App
12	2578	99.2	3865	9	US-09-604-287A-474	Sequence 474, App
13	2578	99.2	3865	10	US-09-551-621-474	Sequence 474, App
14	2578	99.2	3865	14	US-10-007-805-474	Sequence 474, App
15	2578	99.2	3865	15	US-10-076-622-474	Sequence 474, App
16	2578	99.2	3865	15	US-10-124-805-474	Sequence 474, App
17	2576	99.1	3045	14	US-10-007-805-548	Sequence 548, App
18	2576	99.1	3045	15	US-10-076-622-548	Sequence 548, App
19	2576	99.1	3045	15	US-10-124-805-548	Sequence 548, App
20	2227.5	85.7	2307	9	US-09-825-301-24	Sequence 24, Appl
21	2227.5	85.7	2307	9	US-09-604-287A-468	Sequence 468, App
22	2227.5	85.7	2307	10	US-09-551-621-468	Sequence 468, App
23	2227.5	85.7	2307	14	US-10-007-805-468	Sequence 468, App
24	2227.5	85.7	2307	15	US-10-076-622-468	Sequence 468, App
25	2227.5	85.7	2307	15	US-10-124-805-468	Sequence 468, App
26	2227.5	85.7	2307	15	US-10-033-527-24	Sequence 24, Appl
27	2224.5	85.6	3681	9	US-09-825-301-19	Sequence 19, Appl
28	2224.5	85.6	3681	9	US-09-604-287A-463	Sequence 463, App
29	2224.5	85.6	3681	10	US-09-551-621-463	Sequence 463, App
30	2224.5	85.6	3681	14	US-10-007-805-463	Sequence 463, App
31	2224.5	85.6	3681	15	US-10-076-622-463	Sequence 463, App
32	2224.5	85.6	3681	15	US-10-124-805-463	Sequence 463, App
33	2224.5	85.6	3681	15	US-10-033-527-19	Sequence 19, Appl
34	2125	81.8	1337	9	US-09-825-301-23	Sequence 23, Appl
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ALIGNMENTS

RESULT 1

US-10-007-805-566

; Sequence 566, Application US/10007805

; Publication No. US20020150581A1

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yugu

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Durham, Margarita

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER

; FILE REFERENCE: 210121.470C10

; CURRENT APPLICATION NUMBER: US/10/007,805

; CURRENT FILING DATE: 2001-12-07

; NUMBER OF SEQ ID NOS: 593

; SOFTWARE: FastSeq for Windows Version 4.0


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; SEQ ID NO 566
; LENGTH: 4047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-805-566

Alignment Scores:
Pred. No.: 1.82e-225 Length: 4047
Score: 2589.00 Matches: 510
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.62% Indels: 0
DB: 14 Gaps: 0

US-09-451-739H-16 (1-512) x US-10-007-805-566 (1-4047)

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DB 2053 ATGAAGATTCTATTCCAACTAAGCCTTAGAATTGATGGACATGCCAACTTTCARAGCA 2112
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
DB 2113 GAGCCTCCGAGAGCCATCTGCCCTTCGAGCCTGCCATTGAATGCCAAAGCTCTGTCCA 2172
QY 41 LenLysAlaLeuGluLysLeuLysAsnGlnThrLysAlaGluAspGluLysLeuProSer 60
DB 2173 AATAAAGCCTTGAATTGAGATGGAACAAACATTGAGAGCAGATGATGATCTCCATCA 2232
QY 61 GluSerLysGlnLysAspTyrGluGluSerTrpAspSerGluSerLysLeuGluThr 80
DB 2233 GAATCCAAACAAAGAGCTATGAAGAAAGTTCTTGGGATTCCTGAGAGTCTCTGTGAGACT 2292
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLeuLysLys 100
DB 2293 GTTTCACAGAGAGATGTGGTTTACCAGGCTACACATCAAAAGAAATAGATTAATA 2352
QY 101 AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
DB 2353 AATGAAATATTAGAAGATCTCTGATAATGATGCTTTCTGAAGCTCCCTCGAGAATG 2412
QY 121 LysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAlaGlu 140
DB 2413 AAGATTCTTATCCAACTTAAGCCTTAGAATTGATGGACATGCCAACTTTCARAGCAG 2472
QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
DB 2473 CCTCCGAGAGCCATCTGCCCTTCGAGCCTGCCATTGAATGCCAAAGTCTGTCCAAAT 2532
QY 161 LysAlaLeuGluLysLeuLysAsnGlnThrLysAlaGluAspGlnMetPheProSerGlu 180
DB 2533 AAGCCTTGAATTGAAGATGAACAAACATTGAGAGCAGATCAGATGTCCCTTCAGAA 2592
QY 181 SerLysGlnLysLysValGluGluLysSerTrpAspSerGluSerLysLeuArgLysVal 200
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QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysLeuSer 220
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QY 221 GlyLysLeuGluAspSerThrSerLysSerLysLysLeuAspThrValHisSerCysGlu 240
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QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280
DB 2833 AAAAAGAGTTTGTGTACTGAAGAAACAACTGTGAGAGCAAAAGAAATTAATACAG 2892
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RESULT 2

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US-10-076-622-566
; Sequence 566, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 566
; LENGTH: 4047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-566

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Alignment Scores:
Pred. No.: 1.82e-225 Length: 4047
Score: 2589.00 Matches: 510
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

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Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer 60
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Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLysGluThr 80
Db 2233 GAATCCAAACAAGAGACTATGAAGAAGTCTTGGATTCGAGAGTCTCTGTGAGAT 2292
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuLeuLysLys 100
Db 2293 GTTTCACAGAGGATGTGTGTTTACCACAGCTACACATCAAAAGAAATAGATAAATA 2352
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 2353 AATGGAAATATAGAAGAGTCTCTGATAATGATGATGTTTCTGAAGGCTCCCTCAGAAATG 2412
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
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Qy 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
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Qy 181 SerLysGlnLysLysValGluGluLysSerTyrAspSerGluSerLeuArgGluThrVal 200
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Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysLysSer 220
Db 2653 TCACAGAGGATGTGTGTACCCAGGCTACACATCAAAAGAAATGGATAAATAAGT 2712
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Qy 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluLysSerGln 280
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Qy 281 LeuGluAsnGlnLysValLysTyrGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 2893 TTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2952
Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysLysLeuArgGluGluLeu 320
Db 2953 CAAGAAGAAGAGAGAGAAATGCCATATATTAATGAATAAATTAGGGAAGAATTA 3012
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnLeuGluGlnAla 340
Db 3013 GGAAGAATCGAAGACAGCATAGGAAGATTAGAGTGAACACACACTTGAACAGCT 3072
Qy 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 3073 CTCAGATACAGATATAGATTGAAGAGTGTAGAAGTAATTTGAATCAGGTCTCTCAC 3132
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380
Db 3133 ACTCATGAAGATGAAGATTTATCTTATGAAATTCATGTTGAAAGAAAGAAATTCGCC 3192
Qy 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 3193 ATGCTAAACTGGAAATACCCACACTGAACACCAATACCAGGAAGAAAGAAATAAATAAC 3252

Qy 401 PheGluAspIleLysLysLysLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 3253 TTTGAGGACATTAGATTTTAAAGAAAAGAACTTCAGATGACCTTAAAACTG 3312
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 3313 AAAGAGGAATCATTAACATAAAGGGCATCTCAATATAGTGGCAGCTTAAAGTCTGATA 3372
Qy 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
Db 3373 GCTGAGAACACATCTCTACCTTCTTAATTCAGGAAAAACAAGCAAGAAATACATAGAG 3432
Qy 461 AlaGluLeuGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 3433 GCAGAAATTTGAATCACACCATCTCTAGACTGGCTTCTGCTACAGACCATGATCAAT 3492
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
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Qy 501 ArgLysMetAsnValAspValSerThr 510
Db 3553 AGAAAAATGAATGTGATGTGAGTAGTACG 3582

RESULT 4

US-10-058-270A-3
; Sequence 3, Application US/10058270A
; Publication No. US20040029114A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Afar, Daniel
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer
; FILE REFERENCE: 018501-005210US
; CURRENT APPLICATION NUMBER: US/10/058,270A
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,965
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/265,928
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/829,472
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/282,698
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/288,590
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,443
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-058-270A-3

Alignment Scores:
Pred. No.: 2,06e-225 Length: 4458
Score: 2589.00 Matches: 510
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.62% Indels: 0
DB: 13 Gaps: 0

US-09-451-739H-16 (1-512) x US-10-058-270A-3 (1-4458)

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QY	21	GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro	40
DB	2188	GAGCCTCCCGAGAAGCCATCTGCTTCGAGCGTCCCATCAATGCAATGCAAAAGTCTGTTC	2247
QY	41	AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer	60
DB	2248	AATAAAGCCTTGGAAATGAAGAATGAACAACATTGAGAGCAGATGAGATCTCCCATCA	2307
QY	61	GluSerLysGlnLysAspTyrGluGluSerSerTriaAspSerGluSerLeuCysGluThr	80
DB	2308	GAATCCAAACAAAGAGACTATGAAGAAGTCTCTGGATTCTGAGAGTCTCTGTGAGACT	2367
QY	81	ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle	100
DB	2368	GTITTCACAGAAGGATGTGTGTTTACCAGAGCTACACATCAAAAGAAATAGATAAAATA	2427
QY	101	AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet	120
DB	2428	AATGGAAATTAGAAGAGTCTCTGTATAATGATGGTITTTCTGAAGGCTCCCTCAGAAATG	2487
QY	121	LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu	140
DB	2488	AAAGTTTCTATTCCAACTAAAGCCTTAGAATGTATGGACATGCAAACTTTTCAAGAGCAGAG	2547
QY	141	ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn	160
DB	2548	CCTCCGAGAGCCATCTGGCTTCGAGCCTGCCATTGAATGACAAAGTCTGTTCCTCAAT	2607
QY	161	LysAlaLeuGluLysAsnGluGlnThrIleuArgAlaAspGlnMetPheProSerGlu	180
DB	2608	AAAGCCTTGGAAATGAAGAATGAACAACATTTAGAGCAGATCAGATGTTCCTTCAGAA	2667
QY	181	SerLysGlnLysLysValGluGluAsnSerTriaAspSerGluSerLeuArgGluThrVal	200
DB	2668	TCAAAACAAAGAGAGTTGAAGAAATTTCTTGGATTCTGAGAGTCTCCGTGAGACTGTT	2727
QY	201	SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer	220
DB	2728	TCACAGAAGGATGTGTGTGTACCCAGGCTACACATCAAAAGAAATGGATATAAATAAGT	2787
QY	221	GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu	240
DB	2788	GGAAATTTAGAAGATTCAACTAGGCTATCAAAATCTTGGATACAGTTCATTCTTTGAA	2847
QY	241	ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet	260
DB	2848	AGACCAAGGAACTTCAAAAAGATCACTGTGAACAACGTACAGGAAATGGACAAATG	2907
QY	261	LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluIleLysSerGln	280
DB	2908	AAAAAGAAATTTGTGTACTGAAAAGAAACTGTTCAGAGCAAAAGAAATATAAATTCACAG	2967
QY	281	LeuGluAsnGlnLysValLysTyrGluGlnGluLeuCysSerValArgLeuThrLeuAsn	300
DB	2968	TTAGAACCAAAAAGTTAATGGGAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAAC	3027
QY	301	GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu	320
DB	3028	CAAGAAGAAGACAGAGAAGAAATGCCGATATATTAATGAAAAATTAGGGAAGAAATTA	3087
QY	321	GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnLeuGluGlnAla	340
DB	3088	GGAGAATTCGAAGACGACATAGGAAGAGTTAGAGTGAACAACAACCTTGAACAGGCT	3147
QY	341	LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis	360
DB	3148	CTCAGAAATACAGATATAGAAATTTGAAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCAC	3207
QY	361	ThrHisGluAsnGluAsnTyrLeuHisGluAsnCysMetLeuLysLysGluIleAla	380
DB	3208	ACTCATGAAATGAAATATATCTCTTACATGAAATTCATGTGTGAAAGAAATGTGCC	3267
QY	381	MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr	400

Db	3368	ATGCTAAACTGGAAATAGCCACACTGAAACCAATACCGAGAAAGGAATAAATAC	3327
Qy	401	PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu	420
Db	3328	TTTGAGCACATTAAAGATTTTAAAGAAAGAAAGATGCTGAACCTTCAGATGACCCATAAATCG	3387
Qy	421	LysGluCysSerLeuThrLysArgAlaSerGlnThrSerGlyGlnLeuLysValLeuIle	440
Db	3388	AAAGAGAAATCATTAACATAAAGGGCATCTCAATATAGTGGCAGCTTAAAGTTCGTGATA	3447
Qy	441	AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu	460
Db	3448	GCTGAGAACACATGCTCACTTCTAAATTGAAGGAAAAACAAGACAAAGAAATACTAGAG	3507
Qy	461	AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle	480
Db	3508	GCAGAAATTTGAATCACACCACTCTAGACTGGCTTCTGCTGTACAGACCAATGATCAAAAT	3567
Qy	481	ValThrSerArgLysSerGlnGluProAlaIlePheHisIleAlaGlyAspAlaCysLeuGln	500
Db	3568	GTGACATCAGAAAAAAGTCAAGAACCTGCTTCCACATTCAGGAGATGCTTGTTTGCAA	3627
Qy	501	ArgLysMetAsnValAspValSerSerThr	510
Db	3628	AGAAAAATGATGTTGATGTGTCAGTAGTACG	3657

RESULT 5

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US-10-007-805-564
; Sequence 564, Application US/10007805
; Publication No. US20020150581A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Jiang, Yugu
;
; APPLICANT: Dillon, Davin C.
;
; APPLICANT: Mitcham, Jennifer L.
;
; APPLICANT: Xu, Jiangchun
;
; APPLICANT: Harlocker, Susan L.
;
; APPLICANT: Hepler, William T.
;
; APPLICANT: Henderson, Robert A.
;
; APPLICANT: Fanger, Gary R.
;
; APPLICANT: Vedvick, Thomas S.
;
; APPLICANT: McNeill, Patricia D.
;
; APPLICANT: Durham, Margaria
;
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF BREAST CANCER
;
; FILE REFERENCE: 210121.470C10
;
; CURRENT APPLICATION NUMBER: US/10/007,805
;
; CURRENT FILING DATE: 2001-12-07
;
; NUMBER OF SEQ ID NOS: 593
;
; SOFTWARE: Fast-SEQ for Windows Version 4.0
;
; SEQ ID NO 564
;
; LENGTH: 4458
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
US-10-007-805-564

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Alignment Scores:		
Pred. No.:	2,066-235	Length:
Score:	2589.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	99.63%	Indels:
DB:	14	Gaps:
		4458
		510

US-09-451-739H-16 (1-512) x US-10-007-805-564 (1-4458)

Qy	1	MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla	20
Db	2128	ATGAAGTTTCTATTCCAACTAAAGCCTTGAATGTGACATGCAACCTTCAAAGCA	2187
Qy	21	GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro	40
Db	2188	GAGCCTCCCGAAGACCATCTGCCTCGAGCTGCCATTGAAATGCAAAAGTCGTGCCA	2247

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QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuProSer 60
Db 2248 AATAAGCCTTGATTTGAAGATGACAAACATTGAGAGCAGATGAGATCTCCATCA 2307
QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLysGluThr 80
Db 2308 GAATCCAAACAAAGGACTATGAGAAAGTCTCTGGGATCTGAGAGTCTCTGTGAGACT 2367
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysIle 100
Db 2368 GTTTCACAGAGAGATGTTGTTTACCCAGGCTACACATCAAAAGAAATAGATAAATA 2427
QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 2428 AATGGAAAATTAGAAAGTCTCTGATATATGATGGTCTTCTGAAGGCTCCCTCAGAAATG 2487
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 2488 AAAGTTTCTATTCCAACTAAGCCTTAGAATTGATGACATGCNAACCTTCAAGCAGAG 2547
QY 141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 2548 CCTCCGAGAGCCATCTGCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCAAAT 2607
QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2608 AAAGCCTTGGAAATGGAAGATGAACAAACATTGAGAGCAGATCAGATGCCCTTCAGAA 2667
QY 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 2668 TCAAACAAAGAGAGTTGAGAAATTTCTTGGCATCTGAGAGTCTCCGTGAGACTGTT 2727
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2728 TCACAGAGAGTGTGTGTACCCAGGCTACATCAAAAGAAATGGATAAATAAGT 2787
QY 221 GlyLysLeuGluAspSerThrSerLysLysIleLeuAspThrValHisSerCysGlu 240
Db 2788 GGAAATATTAGAGATTCAACTAGCTATCAAAATCTTGGATACAGTTCACTTCTGTGAA 2847
QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2848 AGAGCAAGGGAACTTCAAAAAGATCACTGTGAACACGTACAGGAAATGGAAACAATG 2907
QY 261 LysLysLysPheCysValLeuLysLysLysLysLeuSerGluAlaLysGluLysSerGln 280
Db 2908 AAAAAGAACTTTTGTGTACTGAAAAGAACTGTCAAGAGCAAAAGAAATTAATTCACAG 2967
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 2968 TTAGAGAACCAAAAAGTTAAATGGGAACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 3027
QY 301 GlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 3028 CAAGAAGAAGAGAGAGAAATGCCGATATATTAAATGAAAAAATTAGGAGAAATTA 3087
QY 321 GlyArgIleGluGlnGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
Db 3088 GGAAGAATCGAGAGCAGCATAGGAAGAGTTAGAAGTGAACAACAACAACTTGAACAGGCT 3147
QY 341 LeuArgIleGluAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 3148 CTCAGAAATCAAGATATAGATTGAAGAGTGTAGAAGTAAATTTGAATCAGGTTTCTCAC 3207
QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 3208 ACTCATGAAATGAAATATCTCTTACATGAAATTCATGTAATTCGAAAAAGGAAATGCC 3267
QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 3268 ATGCTAAACTGGAAATAGCCACTGAAACCAATACAGGAAAGGAAATTAATATAC 3327
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QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 3328 TTTGAGACATTAAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATGACCTTAAACCTG 3387
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 3388 AAAGAGGAAATCAATTAACATAAAGGCGCATCTCAATATAGTGGCAGCTTAAAGTCTTGATA 3447
QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
Db 3448 GCTGAGAACCAATGCTCACTTCTAAATTTGAAGAAANAACAAGCAAGAAATCTAGAG 3507
QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 3508 GCAGAAATTTGAATCACACCATCTCTAGACTGGCTTCTGCTGTACAAGACCATGATCAAT 3567
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 3568 GTGACATCAAGAAAGATCAAGAACCTGCTTTCACATTGCAGGAGATGCTTGTTCGAA 3627
QY 501 ArgLysMetAsnValAspValSerSerThr 510
Db 3628 AGAATAATGAATGTTGATGTAGTAGTACG 3657

RESULT 6
US-10-076-622-564
; Sequence 564, Application US/1007622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 564
; LENGTH: 4458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-564

Alignment Scores:
Pred. No.: 2,06e-225 Length: 4458
Score: 2589.00 Matches: 510
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.62% Indels: 0
DB: 15 Gaps: 0

US-09-451-739H-16 (1-512) x US-10-076-622-564 (1-4458)
QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
Db 2128 ATGAAGATTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCAAACTTCAAGCA 2187
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 2188 GAGCCTCCGAGAGCCTCTGCTTCGAGCCTGCCATTTGAATGCAAAAGTCTGTTCCTCA 2247
QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 2248 AATAAGCCTTGGAAATTTGAAGATGAACAAACATTGAGAGCAGATGAGATCTCCCATCA 2307
QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLysGluThr 80
Db 2308 GAATCCAAACAAAGGACTATGAGAAAGTCTCTGGGATCTGAGAGTCTCTGTGAGACT 2367
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
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Db 2368 GTTTCACAGAGGATGTGTGTTTACCAAGGCTACACATCAAAAAGAAATAGATAAATA 2427
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 2428 AATGGAAAATAGAGAGTCTCCTGATATATGATGTTTCTGAAGGCTCCTCGAGAAATG 2487
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 2488 AAAGTTTCTATTCACACTAAAGCCTTAGAATTGATGGACATGCCAACTTTCARAGCAGAG 2547
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 2548 CTTCCGAGAGGCCATCTGCTTCAGGCTCCCAATTGAAATGCCAAAAGTCTGTTTCCAAAT 2607
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2608 AAAGCTTTGGAATTGGAAGATGAACAACATTTGAGAGATCAGATGTTCCCTTCAGAA 2667
Qy 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 2668 TCAAAACAAAAGAGGTTTGAAGAAATTTCTTGGGATTTCTGAGAGTCTCCGTGAGAGCTTT 2727
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Db 2728 TCACAGAGGATGTGTGTGTTGATCCCAAGGCTACACATCAAAAAGAAATGGATAAATAGT 2787
Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
Db 2788 CGAAAATTTAGAGATTCAACTAGCCTATCAAAAATCTTGGATACAGTTCACTTCTGTGAA 2847
Qy 241 ArgAlaArgGluLeuGluLysPheHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2848 AGAGCAAGGGAACCTTCAAAAAGATCACTGTGAAACAGCTACAGGAAAATGGACAAATG 2907
Qy 261 LysLysLysPheCysValLeuLysLysLysLysLeuSerGluAlaLysGluLysSerGln 280
Db 2908 AAAAGAGAGTTTGTGTACTGAGAAAGAACTGTGAGAGCAAGAAATAAATCAACAG 2967
Qy 281 LeuGluAsnGlnLysValTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 2968 TTAGAGAACCAAAAAGTTAAATGGGAACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 3027
Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 3028 CAAGAGAGAGAGAGAGAGAAATGCCGATATATTAAATGAAGAAATTTAGGAGAAATTA 3087
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
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Qy 341 LeuArgIleGluAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 3148 CTCAGAAATCAAGATATAGATTTAGAGAGTGTAGAAAGTAAATTTGAATCAGGTTTCTCAC 3207
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 3208 ACTCATGAAATGAAAATTTATCTTTACATGAAATTTGCATTTGAAAAGAGAAATGCCC 3267
Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 3268 ATCTAAATCTGGAATAGCCACCTGAAACCAACCATACACGAGAAAGAAATTAATATAC 3327
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 3328 TTTGAGCAGATTAAAGATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCCCTAAACATG 3387
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 3388 AAAGAGGAATCATTAACATAAGGGATCTCAATATAGTGGGAGGCTTAAAGTTCTGATA 3447
Qy 441 AlaGluAsnThrMetLeuThrSerLysLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
Db 3448 GCTGAGAACACATGCTCACTTCTTAATTCAGGAAACAAACAGACAAAGAAATCTAGAG 3507

Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 3508 GCAGAAATGATATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAAT 3567
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 3568 GTGACATCAAGAAAAAGTCAAGAACCTCTTCCACATTCGAGGAGATGCTTTGTTGCA 3627
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 3628 AGAAAATGATGTTGATGTGAGTAGTACG 3657
RESULT 7
US-10-177-293-333
; Sequence 333, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatc, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysgul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 333
; LENGTH: 4458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-333
Alignment Scores:
Pred. No.: 2,06e-225 Length: 4458
Score: 2589.00 Matches: 510
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.62% Indels: 0
Gaps: 15
US-09-451-739H-16 (1-512) x US-10-177-293-333 (1-4458)
Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20

Db 2128 ATGAAAGTTTCTATTCCAACTAAAGCCTTGAAGATTGATGGACATGCCAAACTTTCAAGCA 2187
Qy 21 GluProGluLysProSerAlaPheGluProAlaileGluMetGlnLysSerValPro 40
Db 2188 GAGCCTCCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTC 2247
Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer 60
Db 2248 AATAAAGCCTTGGAAATGGAAGATGAACAACATTGAGACGATGATGATCTCCCATCA 2307
Qy 61 GluSerLysGlnLysAspLysGluLysSerTrpAspSerGluSerLysGluThr 80
Db 2308 GAATCCAAACAAAGGACTATGAAGAAGTCTTGGGATTCTGAGAGTCTCTGTGAGACT 2367
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysIle 100
Db 2368 GTTTCACAGAAGGATGTGTGTATCCCAAGCCTACATCAAAAAGAAATGATTAATA 2427
Qy 101 AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 2428 AATGGAAATATGAAGAGTCTCTGATTAATGATGTTTCTGAAGGCTCTGTCGAGATG 2487
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 2488 AAAGTTTCTATTCCAACTAAAGCCTTGAATGATGACATGCAAACTTTCAAGCAGAG 2547
Qy 141 ProProGluLysProSerAlaPheGluProAlaileGluMetGlnLysSerValProAsn 160
Db 2548 CTTCCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTC 2607
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2608 AAAGCCTTGGAAATGAAGAATGAACAAACATTGAGACGATGATGTTCCCTTCAGAA 2667
Qy 181 SerLysGlnLysLysValGluLysSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 2668 TCAAAACAAAGAAGTTGAAGAAATCTTGGGATCTGAGATCTCCGTGAGACGTT 2727
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2728 TCACAGAAGGATGTGTGTATCCCAAGCCTACATCAAAAGAAATGGATAAATAAGT 2787
Qy 221 GlyLysLeuGluAspSerThrSerLysSerLysLysLeuAspThrValHisSerCysGlu 240
Db 2788 GGAATAATTAGAAATTAAGTAACTAGCTATCAAAAATCTTGGATACAGTTTCATCTTG 2847
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2848 AGAGCAAGGGAATTCAAAAGATCACTGTGAACCACTGACGAGGAAATGGAACAAATG 2907
Qy 261 LysLysLysPheCysValLysLysLysLysLysSerGluAlaLysGluLysSerGln 280
Db 2908 AAAAAGAAATTTGTGTACTGAAAAGAAATGTGAGAGGCAAAAGAAATTAATCAAG 2967
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnLysCysSerValArgLeuThrLeuAsn 300
Db 2968 TTAGAGAACCAAAAGTTAAATGGGAACAAAGAGCTCTGAGTGTGAGATTGACTTTAAC 3027
Qy 301 GlnGluGluLysArgGlnAlaPheLysLeuAsnGluLysLysLysLysLysLysLys 320
Db 3028 CAGAAGAGAGAGAGAGAGAAATGCCGATATATTAAATGAATAAATTTAGGAAGANTA 3087
Qy 321 GlyArgIleGluGlnHisArgLysGluLysGluValLysGlnGlnLeuGluGlnAla 340
Db 3088 GGAAGAATCGAAGAGCAGCATAGGAAGAGTTAGAGTGAACCAACAACTTGAACAGGCT 3147
Qy 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 3148 CTCAGAATCAAGATATGAATGGAAGTGTAGAAAGTAATTTGAATCAGGTTTCTCAC 3207
Qy 361 ThrHisGluAsnGluAsnThrLeuLeuHisGluAsnCysMetLysLysGluLeuAla 380
Db 3208 ACTCATGAATGAAATATCTCTTACATGAAATTTGCATGTAATGCAATTTGCAAAAGGAAATGCC 3267

Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnThrGlnGluLysGluAsnLysTyr 400
Db 3268 ATGCTAAACCTGGAAATATAGCCACTGAAACCACTATCCAGGAAAGGAAATAAATAC 3327
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 3328 TTTGAGGACATTAAGATTTTAAAGAGAAAGAAATGCTGAACTTCCAGATGACCCCTAAACTG 3387
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnThrSerGlyGlnLeuLysValLeuIle 440
Db 3388 AAAGAGGAATCATTAACCTAAAGGCGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 3447
Qy 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluLysLeuGlu 460
Db 3448 GCTGAGAACACAACTTCTCACTTCTAAATTTGAAGGAAACCAAGCAAGAAATACTAGAG 3507
Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 3508 GCAGAAATGGAATCACACCTTACCTTCTGCTGTACAGACCATGATCAATTT 3567
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 3568 GTGACATCAAGAAAGGTCAGAACCTGCTTTCCACATTCGAGGAGATGCTTTGTTGCA 3627
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 3628 AGAAATGAATGATGTGATGTGAGTAGTACG 3657

RESULT 8
US-10-124-805-564
; Sequence 564, Application US/10124805
; Publication No. US2003016022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10/124,805
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 564
; LENGTH: 4458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-564

Alignment Scores:
Pred. No.: 2,06e-225 Length: 4458
Score: 2589.00 Matches: 510
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.62% Indels: 0
DB: 15 Gaps: 0

US-09-451-739H-16 (1-512) x US-10-124-805-564 (1-4458)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
Db 2128 ATGAAAGTTTCTATTCCAACTAAAGCCTTGAAGATTGATGGACATGCCAAACTTTCAAGCA 2187
Qy 21 GluProGluLysProSerAlaPheGluProAlaileGluMetGlnLysSerValPro 40
Db 2188 GAGCCTCCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTC 2247
Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer 60
Db 2248 AATAAAGCCTTGGAAATGGAAGATGAACAACATTGAGACGATGATGATCTCCCATCA 2307
Qy 61 GluSerLysGlnLysAspLysGluLysSerTrpAspSerGluSerLysGluThr 80
Db 2308 GAATCCAAACAAAGGACTATGAAGAAGTCTTGGGATTCTGAGAGTCTCTGTGAGACT 2367

Db 2308 GAATCCAAACAAAGGACTATGAAGAAAGTTCTGGGATTCGAGAGTCTCTGTGAGACT 2367
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysLeu 100
Db 2368 GTTTCACAGAAGGATGTGTGTTTATCCCAAGGCTACACATCAAAAGAAATAGATAAATA 2427
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 2428 AATGGAAATAGAAAGAGTCTCTGATATGATGTTTTCTGAAGGCTCCCTGCAGAAATG 2487
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 2488 AAGATTTCTATTCCAACTAAAGCCCTTAGAATTGATGGACATGCCAACTTTTCAAGCAGAG 2547
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 2548 CCTCCCGAGAGCCATCTGCCTTCGAGCTGCCATTGAATGCAAAAGTCTGTTCCAAAT 2607
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2608 AAGAGCTTTGGAATTGAAGANTGAACAAACATTTGAGAGCAGATCGATGTTCCCTTCAGAA 2667
Qy 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 2668 TCAAAACAAAGAAGGTTGAAGAAATTTCTTGGGATTCGAGAGTCTCCGTGAGACTGTT 2727
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2728 TCACAGAAGGATGTGTGTATCCCAAGGCTACACATCAAAAGAAATGATGATAAATAGT 2787
Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
Db 2788 GGAAATTTAGAGATTCAACTAGCTATCAAAATCTTGGATACAGTTCACTCTGTGAA 2847
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2848 AGAGCAAGGAACTTCAAAAGATCACTCTGAACACGTACAGGAAAAATGGAACAATG 2907
Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLeuLysSerGln 280
Db 2908 AAAAAGAGTTTTGTGTACTGAAAAGAACTGTGAGAGCAAAAGAAATTAATCAATCAG 2967
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 2968 TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 3027
Qy 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluLeu 320
Db 3028 CAAGAAGAGAGAGAGAGAAATCCGATATATTAAATGAAAAAATTAGGGAAGAAATTA 3087
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
Db 3088 GGAAGAAATCGAAGAGCAGCATAGGAAGAGTTAGAAGTGAACACAACTTGAACAGGCT 3147
Qy 341 LeuArgIleGluAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 3148 CTCAGAATACAGATATAGATTGAAGAGTGTAGAAGTAATTTGAATCAGGTTTTCTCAC 3207
Qy 361 ThrHisGluAsnGluAsnTrpLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 3208 ACTCATGAATGAAATTTATCTTACATGAATTTGATGTTGAAAAGGAATTTGCC 3267
Qy 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTrpGlnGluLysGluAsnLysTrp 400
Db 3268 ATGCTAAAACCTGGAATAGCCACTGAAACCAATACCAAGAAAAAGAAATAAATAC 3327
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 3328 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATGATCCCTAAATCG 3387
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTrpSerGlyGlnLeuLysValLeuIle 440

Db 3388 AAAGAGGAATCAATTAACTAAAGGCGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 3447
Qy 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGlnAspLysGlnAspLysGlnLeuLeu 460
Db 3448 GCTGAGACACCAATGCTCACCTTCTAAATTGAAGGAAAAACAAGACAAAGAAATACTAGAG 3507
Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 3508 GCAGAAATTTGAATCACACCATCTAGATGGCTTCTGCTGACAAGACCATGATCAAAAT 3567
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 3568 GTGACATCAAGAAAGATCARGAACCTGTTTCCACATTCGAGGAGATGCTTGTGTTGCAA 3627
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 3628 AGAAAAATGAATGTTGATGTGAGTAGTAGC 3657

RESULT 9
US-10-007-805-490
; Sequence 490, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillion, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO 490
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-805-490

Alignment Scores:
Pred. No.: 1.4e-224 Length: 3288
Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservative: 2
Best Local Similarity: 99.61% Mismatches: 0
Query Match: 99.19% Indels: 0
DB: Gaps: 0

US-09-451-739H-16 (1-512) x US-10-007-805-490 (1-3288)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspValGlnThrPheLysAla 20
Db 1291 ATGAAAGTTTCTATTCCAACTAAAGGCTTAGAATTCAGACATGCAAACTTTCAAAGCA 1350
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1351 GAGCTCCCGAAGAGCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTCCA 1410
Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuProSer 60
Db 1411 AATAAGCCTTGAATTTGAAGAATGAACAACATTGAGAGCAGATGAGATCTCCCATCA 1470
Qy 61 GluSerLysGlnLysAspTrpGluSerSerTrpAspSerGluSerLeuCysGluThr 80
Db 1471 GAATCCAAACAAAGGACTATGAAGAAAGTTCTTGGAGTCTCTGTGAGACT 1530

QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuLeuLeuLys 100
Db 1531 GTTTCAGAGAGGATGTGTGTATACCAAGGCTRCRCATCAAAAGAAATAGATAAATA 1590
QY 101 AsnGlyLysLeuGluGlnSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 1591 AATGGAAATTAAGAGAGCTCTCGTAAATGATGATGTTTCTGAAGGCTCCCTGCGAAGT 1650
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 1651 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTCATGACATGCACAACTTTCAAGCAGAG 1710
QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetCysLeuSerValProAsn 160
Db 1711 CTTCCCGAGAGGACATCTGCTTCGAGCCTGCCATTGAAATGCAGAAATCTGTTCACAT 1770
QY 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 1771 AAAGCCTTGGAAATGAAGATGAACAAACATTCAGAGCAGATCAGATGTTCCCTTCAGAA 1830
QY 181 SerLysGlnLysLysValGluGlnLysAsnSerTrpAspSerGluSerLeuArgGlnThrVal 200
Db 1831 TCAAAACAAAGAAAGTGTGAAGAAATCTTGGATTCGAGAGTCTCCGTGAGACTGTT 1890
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 1891 TCACAGAGGATGTGTGTATCCCAAGGCTACACATCAAAAGAAATGCATAAATTAAGT 1950
QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
Db 1951 GGAATTAAGAGATTCACATGACCTATCAAAATCTTGATACAGTTCATCTTGTGA 2010
QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2011 AGACCAAGGACCTTCAAAAGATCACTGTGAACACGTACAGCAAAATGGAACAAATG 2070
QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluLysLysGluLysSerGln 280
Db 2071 AAAAAGAGTTTGTGTACTGAAAGAAATCTGTCAAGCAAAAGAAATTAATCACAG 2130
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 2131 TTAGAGAACCAAAAGTTAATGGACACAGCTCTGCAGTGTGAGATTGACTTTAATC 2190
QY 301 GlnGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2191 CAAGAGAGAGAGAGAGAGAAATCCGATATTAATGAATAATAGGAGAAATTA 2250
QY 321 GlyArgIleGluGlnGlnHisArgLysGluLeuValLysGlnGlnGluGlnAla 340
Db 2251 GGAAGATCGAAGAGCAGCATAGAAAGAGTTAGAGTGAACAACTTGACAGGCT 2310
QY 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2311 CTCAGATACAGATATAGAATTCAGAGTGTAGAAAGTAAATTTGAATCAGGTTCTCAC 2370
QY 361 ThrHisGluAsnGluLysLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 2371 ACTCATGAAATGAAATTAATCTTACATGAAATTTGCATGTTGAAAGAAATTCGC 2430
QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTrpGlnGluLysGluAsnLysTyr 400
Db 2431 ATGCTAAACTGGAAATAGCCACACTGAAACCAATACAGGAGAAAGAAATAAATAC 2490
QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2491 TTTGAGGACATTAAGATTATAAGAAAGAAATCTGAACCTTCAGATGACCTTAAGACTG 2550
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTrpSerGlyGlnLeuLysValLeuIle 440
Db 2551 AAAGAGGATCATTAACCTAAAGGACATCTCAATATAGTGGCAGCTTAAGTTCTGATA 2610
QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGlnAspLysGluIleLeuGlu 460

Db 2611 GCTGAGAACCAATGCTCACTTCTAAATTCAGAGAAACCAAGAAATACATAGAG 2670
QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisGlnIle 480
Db 2671 CGAGAAATTCATCACACCATCTAGACTGGCTTCGTGTACAGACCATGATCAAT 2730
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGluAspAlaCysLeuGln 500
Db 2731 GTGACATCAGAGAAAGTCAAGAACTGCTTTCCATTCGAGAGATGCTGTGTGCA 2790
QY 501 ArgLysMetAsnValAspValSerSerThr 510
Db 2791 AGAAATGAATGTTGATGTAGTAGTACG 2820
RESULT 10
US-10-076-622-490
; Sequence 490, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Sleath, Paul R.
; APPLICANT: Peising, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076.622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 490
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-490
Alignment Scores:
Pred. No.: 1,48-224 Length: 3288
Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.19% Indels: 0
Gaps: 15
US-09-451-739H-16 (1-512) x US-10-076-622-490 (1-3288)
QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
Db 1291 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTCAGACATGCAAACTTTCAAGCA 1350
QY 21 GluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1351 GAGCCTCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGCAATGCAAAAGTCTGTCCA 1410
QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 1411 AATAAGCCTTGGATTGAAGATGAACAAACATTCAGAGCAGATGAGATCTCCCATCA 1470
QY 61 GluSerLysGlnLysAspTyrCysLeuSerTrpAspSerGluSerLeuCysGluThr 80
Db 1471 GAATCAAAACAAAGAGACTATGAGAAAGTTCTTGGATTCTGAGAGTCTCTGTGAGACT 1530
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
Db 1531 GTTTCAGAGAGGATGTGTGTATACCAAGGCTRCRCATCAAAAGAAATAGATAAATA 1590
QY 101 AsnGlyLysLeuGluGlnSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 1591 AATGGAAATTAAGAGAGTCTCTGATTAATGATGTTTCTGAGGCTCCCTGCGAAGT 1650
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 1651 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTCAGAGTGTGAGACTTTCAAGCAGAG 1710

QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
DB 1711 CCTCCGAGAGCCATCTGCTTGGAGCTCCCATTTGAATGCAAAAGTCTGTTCCTCAAT 1770

QY 161 LysAlaLeuGluLysLeuLysGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
DB 1771 AAAGCCTTGAATGAAGATGAACACATTTGAGAGCAGATCAGATGTTCCCTTCAGAA 1830

QY 181 SerLysGlnLysLysValGluLysSerTrpAspSerGluSerLeuArgGluThrVal 200
DB 1831 TCACAAACAAAGAGGTTGAAGAAATTCCTGGAGTCTCGGTGAGAGCTGT 1890

QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
DB 1891 TCACAGAGGATGTGTGTACCCAGGCTACACATCAAAAGAAATGGATAAATAAGT 1950

QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysLysLeuAspThrValHisSerCysGlu 240
DB 1951 GGAAATTTAGAGATTCACATAGCCTATCAAAAATCTTGGATACAGTTTCATCTGTGAA 2010

QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
DB 2011 ACAGCAAGGAACTTCAAAAGATCCTGTGACACAGTACAGGAAATGCAACAATG 2070

QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280
DB 2071 AAAAAGAGTCTTGTGTACTGAAAAAGAACTGTGAGAGCAAAAGAAATTAATCAAG 2130

QY 281 LeuGluAsnGlnLysValIleTrpGluGlnLysCysSerValArgLeuThrLeuAsn 300
DB 2131 TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTGAGTGTGAGATTGACTTTAATC 2190

QY 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
DB 2191 CAAGAAGAAGAGAGAGAGAAATCCCGATATATTAAATGAAAAATTAGGGAAGATTA 2250

QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnLeuGluAla 340
DB 2251 GGAAGATCGAAGAGCAGATAGGAAGAGTTAGAAAGTGAACACAACTTTGAACAGCT 2310

QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
DB 2311 CTCAGATACAGATATAGATTGAAGAGTGTAGAAAGTAAATTTGAATCAGGTTCTCAC 2370

QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLysAla 380
DB 2371 ACTCATGAAATGAAATTTATCTTTACATGAAATTCATGTGTAAGAAAGAAATTGCC 2430

QY 381 MetLeuLysLeuGluLysAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
DB 2431 ATGCTAAAGTGAATAGCCACACTGAAACACCATACCAGGAAAGAAATTAATATAC 2490

QY 401 PheGluAspIleLysLysLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
DB 2491 TTTGAGGACATTAAGATTTAAAGAAAGAAATGCTGAATTCAGATGACCTTAAAGCTG 2550

QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
DB 2551 AAAGAGGAATCATTAACATAAGGGCACTCATATAGTGGCAGCTTAAGTTCTGATA 2610

QY 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluLysLeuGlu 460
DB 2611 GCTGAGAACACAAATGCTCACTTCTAAATTAAGGAAAGAAACAGACAAAGAAATATAG 2670

QY 461 AlaGluLysSerHisIleProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
DB 2671 GCAGAAATTAATCACACCATCTAGCTGGTCTCTGTGTACAAAGACCATGATCAAAAT 2730

QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
DB 2731 GTGACATCAAGAAAGTCAAGAACTGCTTTCCACATTCAGGAGATGCTGTGTTGCAA 2790

QY 501 ArgLysMetAsnValAspValSerSerThr 510
DB 2791 AGAAAAATGAATGTTGATGTGAGTAGTAGC 2820

RESULT 11

US-10-124-805-490
; Sequence 490, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Sersing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10/124,805
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 490
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-490

Alignment Scores: 1.4e-224 Length: 3288
Pred. No.: 2578.00 Matches: 508
Score: 2578.00
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.19% Indels: 0
DB: 15 Gaps: 0

US-09-451-739H-16 (1-512) x US-10-124-805-490 (1-3288)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
DB 1291 ATGAAAGTTTCTATTCCAACTAAAGCTTAGAATTTAGTGGACATGCAAACTTTCAAGCA 1350

QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
DB 1351 GAGCCTCCCGAAGGACATCTGCTTCGAGCTGCCATTTGAAATGAAAGTCTGTTC 1410

QY 41 AsnLysAlaLeuLysLysAsnGluGlnThrLeuArgAlaAspGluLysLeuProSer 60
DB 1411 AATAAGCCTTGAATTTGAAGATGAACAAACATTTGAGAGCAGATGAGATCTCCATCA 1470

QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80
DB 1471 GAATCAAAACAAAGGACATATGAAGAAAGTCTTGGGATTTCTGAGAGTCTCTGAGACT 1530

QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLysIle 100
DB 1531 GTTTCACAGAGAGTGTGTGTTTACCAAGCTTCRCATCAAAAGAAATGATATAAATA 1590

QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
DB 1591 AATGGAATTTAGAGAGTCTCTGATAATGATGTTTCTGAAGGCTCCCTGCAAGATG 1650

QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
DB 1651 AAGTTTCTATTCCAACTTAAGCTTAGAATTTAGTGGACATGCAAACTTTCAAGCAGAG 1710

QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
DB 1711 CCTCCGAGAGGACATCTGCTTCGAGCTGCCATTTGAAATGAAAGTCTGTTCCTCAAT 1770

QY 161 LysAlaLeuLysLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
DB 1771 AAGCCTTGAATTTGAAGATGAACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAA 1830

QY 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200

```
Db 1831 TCAAAACAAAAGAGAGTGAAGAAAATCTTGGGATCTCGAGAGTCTCCGTGAGACTGTT 1890
Qy SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 1891 TCAGAGAGGATGTGTGTGTACCAAGCTACACATCAAAAGAAATGGATAAAATAGT 1950
Qy GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
Db 1951 GGAATAATTAGAAAGATTCACTAGGCTATCAAAAATCTTGATACAGTTCACTTTGAA 2010
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGlnArgThrGlyLysMetGluGlnMet 260
Db 2011 AGAGCAAGGGAACCTCAAAAAGATCACTGTGAACAACGTACAGGAAAAATGGAACAAATG 2070
Qy 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluLysSerGln 280
Db 2071 AAAAAGAAGTTTGTGTACTGAAAAGAAATCTGCAAGAACAAAGAAATAAAATCACAG 2130
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 2131 TTAGAGAACCAAAAAGTTAATGGGAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2190
Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGlnLysIleArgGluGluLeu 320
Db 2191 CAAGAGAAGAGAGAGAGAAATGCCGATATATTAATGAAAATTTAGGGAAGATTA 2250
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340
Db 2251 GGAAGATCGAAGAGCAGCATAGAAAGATTAGAACTGAACACAACTTTGAACAGCT 2310
Qy 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2311 CTCAGAATACAGATATAGAAATGGAAGAGTGAAGAAATTAATTTGAATCAGGTTCTCAC 2370
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 2371 ACTCATGAAATGAATATCTCTTACATGAATATTCATGTGAAAGAAAGAAATGTC 2430
Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 2431 ATGCTAAACCTGAATATAGCCACACTGAACACCAATACCAGGAAAAAGAAATAAATAC 2490
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2491 TTTGAGGCATTAAGATTTTAAAGAAAGAAATGCTGAATCTGAGATGACCTTAAACTG 2550
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 2551 AAAGAGGAATCATTAACCTAAAAGGCACTCTCAATATAGTGGGACGCTTAAAGTTCTGATA 2610
Qy 441 AlaGluAsnThrMetLeuThrSerLysLysLysGlnAspLysGluIleLeuGlu 460
Db 2611 GCTGAGAACACAAATGCTCACTTCTAAATTGAAGGAAAAACAAGACAAAGAAATACTAGAG 2670
Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2671 GCAGAAATTTGAATCACACCATCTAGACTGCTTCTGCTGTACAGACCATGATCAATTT 2730
Qy 481 ValThrSerArgLysSerGlnProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 2731 GTGACATCAAGAAAAAGTCAAGAACCTGCTTTCACATTCGAGAGATGCTTGTGTTGCAA 2790
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 2791 AGAAAAATGAATGTTGATGTGAGTAGTACG 2820
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RESULT 12

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US-09-604-287A-474
; Sequence 474, Application US/09604287A
; Patent No. US20020064872A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
```

```
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
```

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; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
```

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; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
```

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; SEQ ID NO 474
; LENGTH: 3865
```

```
; TYPE: DNA
```

```
; ORGANISM: Homo sapien
```

```
; FEATURE:
```

```
; NAME/KEY: misc feature
```

```
; LOCATION: (2448)...(2631)
```

```
; OTHER INFORMATION: 184 bp insert of B726P splice form
```

```
US-09-604-287A-474
```

Alignment Scores:

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Pred. No.: 1,728-224 Length: 3865
Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.19% Indels: 0
DB: 9 Gaps: 0
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US-09-451-739H-16 (1-512) x US-09-604-287A-474 (1-3865)
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Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
```

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Db 1563 ATGAAAGTTTCTATTCCAACTAAAGCCCTTAGAATTGATGGACATGCAAACTTTCAAAGCA 1622
```

```
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
```

```
Db 1623 GAGCCTCCGAGAGCCATCTGCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCA 1682
```

```
Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
```

```
Db 1683 AATAAAGCCTTGGAATTCGAAGATGACAAACATTTGAGCAGATGAGACTCCCATCA 1742
```

```
Qy 61 GluSerLysGlnLysAspTyrGluLysSerSerTrpAspSerGluSerLeuCysGluThr 80
```

```
Db 1743 GAATCCAAACAAAGAGACTATGAAGAAATTTCTGGGATTTCTGAGATCTCTGTGAGACT 1802
```

```
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
```

```
Db 1803 GTTTCACAGAGAGTGTGTGTTTACCCAAAGCTRCRCATCAAAAAGAAATAGATAAAATA 1862
```

```
Qy 101 AsnGlyLysLeuGluLysSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
```

```
Db 1863 AATGAAAATTAGAAGAGTCTCCTGATATGATGTTTCTGAAGGCTCCCTGCAGAAATG 1922
```

```
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
```

```
Db 1923 AAAGTTTCTATTCCAACTAAAGCCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAG 1982
```

```
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
```

```
Db 1983 COTCCGAGAGAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTGTTCCAAAT 2042
```

```
Qy 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
```

```
Db 2043 AAAGCCTTGGAATTCGAAGATGAAACAAACATTTGAGCAGATCAGATGTTCCCTTCAGAA 2102
```

```
Qy 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
```

```
Db 2103 TCAAAACAAAAGAGAGTTCAGAAAAATTTCTGGGATTTCTGAGAGTCTCCGAGACTGTT 2162
```

```
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
```

Db 2163 TCACAGAGGATGTGTGTACCCAGGCTACACATCAAAAGAAATGATAAATAAGT 2222
Qy 221 GlyIysLeuGluAspSerThrSerLeuSerIysIleLeuAspThrValHisSerCysGlu 240
Db 2223 GGAAATATTAGAGATTCACATAGCTATCAAAATCTTGGATACAGTTTCATCTTGTGAA 2282
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyIysMetGluGlnMet 260
Db 2283 AGACAGAGGAACTTCANAAAGATCACTGTGACACAGCTACAGGAAATGGAACAATG 2342
Qy 261 LysIysLysPheCysValLeuLysLysIysLeuSerGluAlaLysGluIleLysSerGln 280
Db 2343 AAAACAGAGTTTGTGTACTGAAAGAAATCTGTGAGAGCAAGAAATGAAATCAAG 2402
Qy 281 LeuGluAsnGlnLysValIysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGACCAAAAGATTAAATGGGCAAGAGCTCTGAGTGTGAGATTGACITTTAAAC 2462
Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2463 CAAGAAGAGAGAGAGAGAAATCCGATATATTTAAATGAAATAATTAGGGAAGAAATTA 2522
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluAla 340
Db 2523 GGAAGATCGAGAGCAGCATAGGAAGATTAGAGTGAACACACAACTTGAACAGCT 2582
Qy 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2583 CTCAGATACAGATATAGATTGAAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCAC 2642
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 2643 ACTCATGAAATGAAATATCTCTTACATGAAATTTGCATGTTGAAAGAGAAATTTGCC 2702
Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 2703 ATGCTAAACACTGAAATAGCCACACTGAAACACCAATACCAGAAAGAAATGAAATAC 2762
Qy 401 PheGluAspIleLysIleLysLeuLysAsnAlaGluLeuGlnMetThrIleLysLeu 420
Db 2763 TTTGAGGACATTAAAGATTAAAGAAAGAAATGCTGAACCTTCAGATCACCTTAAACCTG 2822
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLysValLeuIle 440
Db 2823 AAAGAGGATCATTAACTAAGAGGCACTCTCATATAGTGGCAGCTTAAGTCTGATA 2882
Qy 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
Db 2883 GCTGAGAACACATGCTCACTTCTTAATTTGAAGGAAACACAGACAAAGAAATACTAGAG 2942
Qy 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2943 GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAT 3002
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 3003 GTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTTGCAGAGAGATGCTTTGTGAA 3062
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 3063 AGAAAAATGAATGTTGATGTGAGTAGTACG 3092

RESULT 13

US-09-551-621-474
; Sequence 474, Application US/09551621
; Publication No. US20030104366A1
; GENERAL INFORMATION:
; APPLICANT: Yuqi, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C5
; CURRENT APPLICATION NUMBER: US/09/551,621
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 474
; LENGTH: 3865
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2448)...(2631)
; OTHER INFORMATION: 184 bp insert of B726P splice form
US-09-551-621-474
Alignment Scores:
Pred. No.: 1,72e-224 Length: 3865
Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.19% Indels: 0
DB: 10 Gaps: 0
US-09-451-739H-16 (1-512) x US-09-551-621-474 (1-3865)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
Db 1563 ATGAAAGTTTCTATTCCAACTAAGCCTTAGAATTTGATGACATCAAACTTTCAGAGCA 1622
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1623 GAGCTTCCCGAGAGGAGCATCTGCTTCGAGCTGCCATTGCAATGCAATGCAAAAGTCTGTCCA 1682
Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 1683 AATAAAGCCTTGGAAATTGAAGAATGAACAAACATTGAGAGCAGATGAGATCTCCCATCA 1742
Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80
Db 1743 GAATCAAAACAAAGAGACTATGAGAAAGTTCTTGGATTTCTGAGAGTCTCTGTGAGACT 1802
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
Db 1803 GTTTCACAGAGGATGTGTGTTTACCAAGGCTTCRCATCAAAAGAAATAGATAAAATA 1862
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLysAlaProCysArgMet 120
Db 1863 AATGGAAATTAGAGAGTCTCTGATAATGATGGTTTTCTGAGGCTCCCTGCAGAAATG 1922
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 1923 AAAGTTTCTATTCCAACTAAGCCTTAGAATTTGATGACATGCAAACTTTCAGAGCAGAG 1982
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 1983 CTTCCCGAGAGGAGCATCTGCTTCGAGCTGCCATTGAAATGAAAGTCTGTGTCCAAAT 2042
Qy 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2043 AAAGCCTTGGAAATTGAAGATGAACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAA 2102
Qy 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 2103 TCAAAACAAAGAAAGTTGAAGAAATTTCTTGGATTTCTGAGAGTCTCCGTGAGACTGTT 2162
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2163 TCACAGAGGATGTGTGTGTACCAAGGCTTACCATCAAAAGAAATGATTAATAGT 2222
Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
Db 2223 GGAAATTTAGAGATTCAACTAGCTATCAAAATCTTGATACATCTTGTGATCTTCTGTGAA 2282

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Oy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2283 AGACAAAGGGAACCTCAAAAGATCACTGTGAACAACGTACAGAAAATGGAAACAATG 2342
Oy 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluLysSerGln 280
Db 2343 AAAAGAAGTTTGTGTACTGAGAAAGAACTGTCAAGACAAAGAAATATAATCACAG 2402
Oy 281 LeuGluGlnLysValLysThrGluGlnLeuGlnCysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTGAGTGTGAGATTGACATTTAAAC 2462
Oy 301 GlnGluGluLysArgAsnAlaAspLeuLeuGlnLysLysLeuArgGluGluLeu 320
Db 2463 CAGAGAGACAGAGAGAGAAATGCCGATATTAATGAATAATTTAGGAGAAATTA 2522
Oy 321 GlyArgLeuGluGlnHisArgLysGluLeuGlnValLysGlnGlnLeuGlnAla 340
Db 2523 CGAAGAATCGAAGACGACATAGGAAGAGTTAGAGTGAACCAACCACTTGAAACAGGCT 2582
Oy 341 LeuArgGlnGlnAspLeuGluLysSerValGluSerLeuAsnGlnValSerHis 360
Db 2583 CTCAGATACAGATATAGATTTGAGAGTGTAGAAAGTATTTGAATCAGGTTCTCAC 2642
Oy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380
Db 2643 ACTCATGAAATGAAATATATCTCTTACATGAAATATGCAATTTGAAAGAAATGTC 2702
Oy 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 2703 ATGCTAAACCTGGAATAGCCACACTGAAACCAATACCAAGAAAGGAAATATAATAC 2762
Oy 401 PheGluAspLeuLysLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2763 TTGGAGACATTAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATGACCTTAAACTG 2822
Oy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlnGlnLeuLysValLeuLe 440
Db 2823 AAAGAGGAATCAATTAACATAAGGAGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 2882
Oy 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluLeuGlu 460
Db 2883 GCTGAGAACACATCTCTCACTTCTTAAATTTAGGAAAGAAACCAAGCAAGAAATACAGAG 2942
Oy 461 AlaGluLeuGluSerHisArgLeuAlaSerAlaValGlnAspHisAspGlnLe 480
Db 2943 GCAGAAATTTGAATCAACCATCTAGACTGCTTCTGCTGTACAGACCATGATCAATTT 3002
Oy 481 ValThrSerArgLysSerGlnGluProAlaPheHisLeuAlaGlyAspAlaCysLeuGln 500
Db 3003 GTGACATCAAGAAAGTCAGAACCTGCTTCCACATTCGAGGAGATGCTTTGTTTGCNA 3062
Oy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 3063 AGAAAAATGAATGTTGATGTGAGTAGTAGC 3092
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RESULT 14

US-10-007-805-474

; Sequence 474, Application US/10007805

; Publication No. US20020150581A1

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Durham, Margarita

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007.805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 3865
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-007-805-474
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Alignment Scores:

Pred. No.:	1,72e-224	Length:	3865
Score:	2578.00	Matches:	508
Percent Similarity:	99.61%	Conservative:	0
Best Local Similarity:	99.61%	Mismatches:	2
Query Match:	99.19%	Indels:	0
DB:	14	Gaps:	0

US-09-451-739H-16 (1-512) x US-10-007-805-474 (1-3865)

Oy	1	MetLysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAla	20
Db	1563	ATGAAGTTTCTATTCCAACTTAAGCCTTAGATTGATGGACATGCAAACTTTCAAGCA	1622
Oy	21	GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro	40
Db	1623	GAGCTCCCGAGAGCCATCTGCCCTCGAGCTGCCATTTGAATGCAAAAGCTGTGTCCA	1682
Oy	41	AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer	60
Db	1683	ATAAAGCTTGGAAATGAAGAAATGAACAACATTTGAGAGCAGATGAGATCTCCATCA	1742
Oy	61	GluSerLysGlnLysAspTyrGluGluSerTyrTrpAspSerGluSerLeuCysGluThr	80
Db	1743	GAATCCAAACAAGAGACTATGAAGAAGTTCTTGGATTCTGAGAGTCTCTGTGAGACT	1802
Oy	81	ValSerGluLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysIle	100
Db	1803	GTTTCACAGAGAGATGTGTGTTTACCCAGGCTRCATCAAAAGAAATAGATAAATA	1862
Oy	101	AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet	120
Db	1863	ATGGAAATTTAGAGAGTCTCTCTGATAATGATGTTTCTGAAGGCTCCCTGCAGAAATG	1922
Oy	121	LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu	140
Db	1923	AAAGTTTCTATTCCAACTTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAGCAGAG	1982
Oy	141	ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn	160
Db	1983	CTCCCGAGAGCCATCTGCCCTCGAGCTGCCATTTGAATGCAAAAGTCTGTTCCAAAT	2042
Oy	161	LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluMetPheProSerGlu	180
Db	2043	AAAGCCTTGGAAATGAAGAAATGAACAACATTTGAGAGCAGATCAGATGTTCCTTTCAAGAA	2102
Oy	181	SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal	200
Db	2103	TCAAAACAAGAGAGTTGAGAAATTTCTGGATTCTGAGAGTCTCCGTGAGACTGTT	2162
Oy	201	SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer	220
Db	2163	TCACAGAGGATGTGTGTGTACCAAGGCTACACATCAAAAGAAATGATAAATAAGT	2222
Oy	221	GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu	240
Db	2223	GGAAAAATTAAGATTAACACTAGCCCTATCAAAAATCTTGGATACAGATTCATTTCTGTGAA	2282
Oy	241	ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet	260

Db 2283 AGACGAAGGGAACCTTCAAAAGATCACTGTGAACAACGTACAGGAAAAATGGAAACAATG 2342
Qy LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280
Db 2343 AAAAAAGAGTTTCTGTACTGAAAGAAAGAACTGTGACAGCAAGAAAGAAATATAATCACAG 2402
Qy LeuGluAsnGlnLysValLysTTPGluGlnGluLysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGAACCAAAAGTTAAATGGGACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2462
Qy GlnGluGluGluLysArgAsnAlaAspLysLeuAsnGluLysLysLysLysLysLysLys 320
Db 2463 CAAGAAGAAGAGAGAGAGAAATGCCGATATATTAATGAATAATTTAGGGAAGAAATTA 2522
Qy GlyArgLysGluGlnGlnHisArgLysGluLysGluLysGlnGlnGlnGlnGlnGlnGln 340
Db 2523 GGAAGAATCGAAGAGAGCATAGAAAGAGTTGAAGTGAACCAACACACACACACAGGCT 2582
Qy LeuArgLysGlnAspLysLysLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2593 CTCAGATACAGATATAGATTGAGAGGTGACAAAGTAATTTGAATCAGGTTTCTCAC 2642
Qy ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLysLysLys 380
Db 2643 ACTCATGAAATGAAATATCTCTTACATGAAATTTGCATGTTGCAAAAAGGAAATTTGCC 2702
Qy MetLeuLysLeuGluLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 400
Db 2703 ATGCTTAAACTGGAAATAGCACACTGAAACCAATACACAGGAAAGGAAATATAATAC 2762
Qy PheGluAspLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 420
Db 2763 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCCATAAACTG 2822
Qy LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlnLysLysLysLysLysLysLys 440
Db 2823 AAAGAGGAATCATTAACATAAAGGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATA 2882
Qy AlaGluAsnThrMetLeuThrSerLysLysLysLysLysLysLysLysLysLysLysLysLys 460
Db 2883 GCTGAGACACAATGCTCCTCAATTAAGGAAACCAAGCAAAAGAAATACATAGAG 2942
Qy AlaGluLysGluSerHisProArgLeuAlaSerAlaValGlnAsnHisAspGlnLys 480
Db 2943 CGAGAAATTAATCATCACATCTAGACTGGCTTCTGCTGACAGACCATGATCAAT 3002
Qy ValThrSerArgLysSerGlnGluProAlaPheHisLysLysLysLysLysLysLysLysLys 500
Db 3003 GTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATTGACAGGAGATGCTTTGTCGA 3062
Qy ArgLysMetAsnValAspValSerThr 510
Db 3063 AGAAAAATGAATGTTGATGTGAGTAGTAGC 3092

RESULT 15

US-10-076-622-474
; Sequence 474, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF BREAST CANCER
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 3865
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-076-622-474

Alignment Scores:
Pred. No.: 1,72e-224 Length: 3865
Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.19% Indels: 0
DB: 15 Gaps: 0

US-09-451-739H-16 (1-512) x US-10-076-622-474 (1-3865)

Qy 1 MetLysValSerLysLeuProThrLysAlaLeuMetAspMetGlnThrPheLysAla 20
Db 1563 ATGAAAGTTTCTATTCCAACTAAGCCCTTAGAATGTATGGACATGCAAACTTCAAAGCA 1622
Qy 21 GluProGluLysProSerAlaPheGluProAlaLysGluMetGlnLysSerValPro 40
Db 1623 GAGCCTCCCGAAGAACCTATGCGCTTCGAGCTCGCATTTGAAATGCAAAAGTCTGTTCCA 1682
Qy 41 AsnLysAlaLeuGluLysAsnGluLysLeuArgAlaAspGluLysLeuProSer 60
Db 1683 AATTAAGCCTTGGATTTGAAGATGAACAACATTTGAGACAGATGAGATATCCCATCA 1742
Qy 61 GluSerLysGlnLysAspTyrGluLysSerTrpAspSerGluSerLysLeuCysGluThr 80
Db 1743 GAATCCAAACAAAGAGACTATGAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACT 1802
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLysLysLys 100
Db 1803 GTTTCACAGAGAGTGTGTGTTTACCAAGGCTCCCATCAAAAGAAATAGATAAATA 1862
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 1863 AATGGAATTTAGAAAGAGTCTCTGATATGATGTTTCTGAAAGCTCCCTGCAAGATG 1922
Qy 121 LysValSerLysProThrLysAlaLeuGluLysMetAspMetGlnThrPheLysAlaGlu 140
Db 1923 AAAGTTTCTATTCCAACTAAGCCTTAGAATTTGATGACATGCAAACTTCAAAGCAGAG 1982
Qy 141 ProProGluLysProSerAlaPheGluProAlaLysGluMetGlnLysSerValProSer 160
Db 1983 CCTCCGAGAGGACATCTGCTTCGAGCTGCAATTAAGTGAATGCAAAAGTCTGTTCCAAT 2042
Qy 161 LysAlaLeuGluLysLysGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2043 AAAGCCTTGGATTTGAAGATGAACAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAA 2102
Qy 181 SerLysGlnLysLysValGluLysAsnSerTrpAspSerGluSerLysLeuArgGluThrVal 200
Db 2103 TCAAAACAAAGAAAGTCTGAGAAATTTCTGGGATTTCTGAGAGTCTCCGTGAGACTGTT 2162
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysLysSer 220
Db 2163 TCACAGAGGATGTGTGTATCCCAAGGCTACACATCAAAAGAAATGATATAATAGT 2222
Qy 221 GlyLysLeuGluAspSerThrSerLysLysLysLysLysLysLysLysLysLysLysLys 240
Db 2223 GGAATTTAGAGATTTCACTAGCCTATCAAAATCTTGGATACAGTTCATCTTGTGAA 2282
Qy 241 ArgAlaArgGluLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 260
Db 2283 AGAGCAAGGAGAACTTCAAAAGATCTCTGTGACCAACGTCACAGGAAATGAAACAAATG 2342
Qy 261 LysLysLysPheCysValLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 280
Db 2343 AAAAAGAGTTTGTGTACTGAAAAAGAACTGTGAGAGCAAAAGAAATATAATACACAG 2402
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGAACCAAAAGTTAAATGGGAAACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2462
Qy 301 GlnGluLysLysArgAsnAlaAspLysLeuLysLysLysLysLysLysLysLysLysLys 320

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Db 2463 CAAGAAGAGAGAGAGAGAGATGCCGATATATTAATCAAAAAATTAGGGAAGAAATTA 2522
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
Db 2523 GGAAGAATCGAAGAGCAGCATAGGAAAGAGTTAGAGTGAACAACAACCTTGAACAGGCT 2582
Qy 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2583 CTCAGAATACAGATATAGAAATGAGAGTGTAGAAGTAAATTTGAATCAGGTTTCTCAC 2642
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 2643 ACTCATGAAATGAAATTTATCTCTTACATGAAATTTGCATGTTGAAAAAGGAAATTGCC 2702
Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGlnLysGluAsnLysTyr 400
Db 2703 ATGCTAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAGGAAATAAATAC 2762
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2763 TTTGAGGACATTAAAGATTTTAAAAAGAAAGAAATGCTGAACCTTCAGATGACCTAAAACTG 2822
Qy 421 LysGlnGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 2823 AAGAGGAATCATTAACATAAAGGGCATCTCAATATATAGTGGGAGCTTAAAGTTCTGATA 2882
Qy 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
Db 2883 GCTGGAACACAAATGCTCCTTCTTAATTTGAAGGAAAAACAAGACAAAGAAATACTAGAG 2942
Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2943 GCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGACCATGATCAAATT 3002
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 3003 GTGACATCAAGAAAAAGTCAGAAACCTGCTTCCACATTCGAGGAGATGCTTCTTGCAA 3062
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 3063 AGAAAAATGAATGTTGATGTGAGTAGTACG 3092
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Search completed: May 6, 2004, 18:38:46
Job time : 681 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 6, 2004, 13:51:33 ; Search time 110 Seconds
(without alignments)
2583.044 Million cell updates/sec

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Perfect score: 2599
Sequence: 1 MKVSIPTKALEMDMQTFKA.....IAGDACLQRXNVDSSTDI 512

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.coi
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXI=7

Database : Issued Patents NA:
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2: /cgm2_6/ptodata/2/ina/5B.COMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2578	99.2	3288	4	US-09-620-405B-490
2	2578	99.2	3288	4	US-09-834-759-490
3	2578	99.2	3665	4	US-09-620-405B-474
4	2578	99.2	3865	4	US-09-604-287A-474
5	2578	99.2	3865	4	US-09-834-759-474
6	2227.5	85.7	2307	4	US-09-620-405B-468
7	2227.5	85.7	2307	4	US-09-433-826B-468
8	2227.5	85.7	2307	4	US-09-604-287A-468
9	2227.5	85.7	2307	4	US-09-834-759-468
10	2224.5	85.6	3681	4	US-09-620-405B-463
11	2224.5	85.6	3681	4	US-09-433-826B-463
12	2224.5	85.6	3681	4	US-09-604-287A-463

13	2224.5	85.6	3681	4	US-09-834-759-463	Sequence 463, App
14	2125	81.8	1337	4	US-09-620-405B-467	Sequence 467, App
15	2125	81.8	1337	4	US-09-433-826B-467	Sequence 467, App
16	2125	81.8	1337	4	US-09-604-287A-467	Sequence 467, App
17	2125	81.8	1337	4	US-09-834-759-467	Sequence 467, App
18	1556.5	59.9	2232	4	US-09-620-405B-491	Sequence 491, App
19	1556.5	59.9	2232	4	US-09-834-759-491	Sequence 491, App
20	1532.5	59.0	1665	4	US-09-389-681-178	Sequence 178, App
21	1532.5	59.0	1665	4	US-09-620-405B-178	Sequence 178, App
22	1532.5	59.0	1665	4	US-09-339-338-178	Sequence 178, App
23	1532.5	59.0	1665	4	US-09-433-826B-178	Sequence 178, App
24	1532.5	59.0	1665	4	US-09-604-287A-178	Sequence 178, App
25	1532.5	59.0	1665	4	US-09-285-480-178	Sequence 178, App
26	1532.5	59.0	1665	4	US-09-834-759-178	Sequence 178, App
27	1384	53.3	1681	4	US-09-389-681-180	Sequence 180, App
28	1384	53.3	1681	4	US-09-620-405B-180	Sequence 180, App
29	1384	53.3	1681	4	US-09-339-338-180	Sequence 180, App
30	1384	53.3	1681	4	US-09-433-826B-180	Sequence 180, App
31	1384	53.3	1681	4	US-09-604-287A-180	Sequence 180, App
32	1384	53.3	1681	4	US-09-285-480-180	Sequence 180, App
33	1384	53.3	1681	4	US-09-834-759-180	Sequence 180, App
34	1032	39.7	1729	4	US-09-620-405B-466	Sequence 466, App
35	1032	39.7	1729	4	US-09-433-826B-466	Sequence 466, App
36	1032	39.7	1729	4	US-09-604-287A-466	Sequence 466, App
37	1032	39.7	1729	4	US-09-834-759-466	Sequence 466, App
38	889.5	34.2	1206	4	US-09-389-681-175	Sequence 175, App
39	889.5	34.2	1206	4	US-09-620-405B-175	Sequence 175, App
40	889.5	34.2	1206	4	US-09-339-338-175	Sequence 175, App
41	889.5	34.2	1206	4	US-09-433-826B-175	Sequence 175, App
42	889.5	34.2	1206	4	US-09-604-287A-175	Sequence 175, App
43	889.5	34.2	1206	4	US-09-285-480-175	Sequence 175, App
44	889.5	34.2	1206	4	US-09-834-759-175	Sequence 175, App
45	780.5	30.0	1233	4	US-09-620-405B-492	Sequence 492, App

ALIGNMENTS

RESULT 1

US-09-620-405B-490
; Sequence 490, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Repler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 21021.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 490
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-490

Alignment Scores:
Pred. No.: 2,23e-270 Length: 3288
Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.19% Indels: 0
DB: 4 Gaps: 0

US-09-451-739H-16 (1-512) x US-09-620-405B-490 (1-3288)

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Db 1471 GAATCCAAACAAAGGACTATGAAGAAAGTCTCTGGGATCTCTGAGACTCTCTGAGACT 1530
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLeuAspLysIle 100
Db 1531 GTTTCACAGAAGGATGTGTGTTTACCCAGGCTTCRCATCAAAAAGAAATAGATAAATA 1590
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Qy 141 ProProGluLysProSerAlaPheGluProLysLeuGluMetGlnLysSerValProAsn 160
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Qy 161 LysAlaLeuGluLysLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
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Qy 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 1831 TCAAAACAAAGAAAGGTTGAAGAAATCTTGGGATCTGAGAGTCTCCGTGAGAGCTGT 1890
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspValSer 220
Db 1891 TCACAGAAGGATGTGTGTATCCCAAGGCTACACATCAAAAAGAAATGATTAATAGT 1950
Qy 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240
Db 1951 GGAAATATAGAATCAACTAGCTATCAAAAATCTTGGATACAGTTCATCTTGTGAA 2010
Qy 241 ArgAlaArgGluGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2011 AGAGCAAGGGAACTTCAAAAGATCACTGTGTGAACCAAGTACAGGAAATGGAACAAATG 2070
Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280
Db 2071 AAAAAGATTTGTGTACTGAAAGAAAGAACTGTGAGAGCAAAAGAAATTAATCAG 2130
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuLysSerValArgLeuThrLeuAsn 300
Db 2131 TTAGAGAACCAAAAGCTTAATGGGAACCAAGAGCTCTGCAGTGTGAGATTTGACTTTAAAC 2190
Qy 301 GlnGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2191 CAGAAGAAAGAGAGAGAGAAATGCCGATATATTAAATGAAGAAATTAGGAAGAAATTA 2250
Qy 321 GlyArgIleGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
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Db 2311 CTCAGAAATCAAGATATAGAAATGAAGATGTAGAAGTAATTTGAATCAGTTTCTAC 2370
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysGluLysIleAla 380
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Qy 381 MetLeuLysLeuGluLysIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
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Db 2551 AAAGAGGATCATTAACATAAAGGCACTCTCAATATAGTGGCAGCTTTAAAGATTTCTGATA 2610
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Db 2611 GCTGAGAACACAACTCTCACTTCAATTTGAAGGAAAAACAAGACAAGAAATACTAGAG 2670
Qy 461 AlaGluLysGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2671 GAGAAATTTGAATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAAT 2730
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Qy 501 ArgLysMetAsnValAspValSerSerThr 510
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RESULT 3
US-09-620-405B-474
; Sequence 474, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCES: 210121.470C6
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 474
; LENGTH: 3865
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2448)...(2631)
; OTHER INFORMATION: 184 bp insert of B726P splice form
US-09-620-405B-474

Alignment Scores:
Pred. No.: 2,86e-270 Length: 3865
Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.19% Indels: 0
DB: 4 Gaps: 0

US-09-451-739H-16 (1-512) x US-09-620-405B-474 (1-3865)

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Db 1563 ATGAAAGTTTCTATTCTCAACTTAAGCCTTAGAATTGATGACATGCAAACTTTCAAAGCA 1622
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1623 GAGCCTCCGAGAGCCATCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTC 1682
Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLysLeuProSer 60
Db 1693 AATAAGCCTTGGAAATGAAGATGAACAACATTCAGAGCAGATGAGATACCTCCATCA 1742
Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80

Db 1743 GAATCCAAACAAAGGACTATGAGAAAGTTCTTGGGATTCGAGAGTCTCTGTGAGACT 1802
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Db 1803 GTTTCACAGAGGATGTGTGTATCCCAAGGCTRCRCATCAAAAAGAAATAGATAAATA 1862
Qy 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
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Db 2223 GGAATAATTAGAGATTCAACTAGCTATCAAAAATCTTGGATTCAGTACAGTTCAATCTTGAA 2282
Qy 241 ArgAlaArgGluLeuGlnLysAsnHisCysGluGlnPargThrGlyLysMetGluGlnMet 260
Db 2283 AGACRAAGGAACTTCAAAAGATCTCTGTGACACACTACAGGAAATGGAACAAATG 2342
Qy 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluLysSerGln 280
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Qy 281 LeuGluGlnLysValLysTrpGluGlnLeuCysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGAACCAAAAGTTAAATGGACCAAGAGCTCTGAGTGTGAGATTGACTTTAAAC 2462
Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2463 CAAGAAGAGAGAGAGAGAAATGCCATATATTAATGAAATAATTAGGGAAGATTA 2522
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGlnAla 340
Db 2523 GGAAGAATCGAAGAGCAGCATAGGAAGAGTTAGAGTGAACCAACAACTTTGAACAGGCT 2582
Qy 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2583 CTCAGATACAGATATAGATTGAAGAGTGTAGAAAGTAAATTTGAATCAGGTTCTCAC 2642
Qy 361 ThrHisGluAsnGluAsnTyrieuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380
Db 2643 ACTCATGAAATGAAATATCTCTTATGAAATTCATGATGAAATGCAAAAGAAATGGCC 2702
Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrieuGlnLysGluAsnLysTy 400
Db 2703 ATGCTTAAATCGAATAGCCACACTGAACCAATACCAAGGAAAGAAATATAATAC 2762
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Db 2763 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATCACCTTAAACTG 2822
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrieuSerGlyGlnLeuLysValLeu 440

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Db 2883 GCTGAGAACCAATGCTCACTTCTTAATTCAGAGGAAAAACACAGACAAAGAACTAGAG 2942
Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2943 GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAT 3002
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 3003 GTGACATCAAGAAAAAGTCAAGAACCTCTTTCCATTCGAGGAGATGCTTGTGTCGA 3062
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 3063 AGAAATGAATGTTGATGTGAGTAGTACG 3092

RESULT 4
US-09-604-287A-474
; Sequence 474, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudi
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604, 287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 474
; LENGTH: 3865
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2448)...(2631)
; OTHER INFORMATION: 184 bp insert of B726P splice form
US-09-604-287A-474

Alignment Scores:
Pred. No.: 2,869-270 Length: 3865
Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.13% Indels: 0
DB: 4 Gaps: 0

US-09-451-739H-16 (1-512) x US-09-604-287A-474 (1-3865)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
Db 1563 ATGAAAGTTTCTTATTCCAACTTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAGCA 1622
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1623 GAGCTTCCGAGAGGACATCTGCTTCGAGCTGCCATTGAATGAATGCAAAAGTCTGTCCA 1682
Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuAlaAspGluLeuProSer 60
Db 1683 AATAAGCCTTGAATTTGAAGAAATGAACAAACATTCAGAGCAGATGAGATATCCCATCA 1742
Qy 61 GluSerLysGlnLysAspTyrieuGluSerSerTrpAspSerGluSerLeuCysGluThr 80
Db 1743 GAATCCAAACAAAGGACATATGAAGAAATGCTTGGGATTCGAGAGTCTCTGTGAGACT 1802
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysIle 100

QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
DB 1863 AATGGAAATTTAGAGAGTCTCTGATATGATGTTTCTGAGGCTCCCTGCAGAATG 1922
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
DB 1923 AAGTTTCTATTCCAACTAAGCTTTAGAAATTTGATGGACATCAAACTTTCAACACAG 1982
QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
DB 1983 CTTCCCGAGAGGCACTGCTCTCGAGCTGCGATTTGAAATGCAAAAGTCTCTTCCAAAT 2042
QY 161 LysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
DB 2043 AAAGCCTTGGATTTGAAGATGAACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAA 2102
QY 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
DB 2103 TCACAAACAAAGAAAGTTGAGAAATTTCTTGGATTCTGAGAGTCTCCGTGAGACTGTT 2162
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
DB 2163 TCACAGAGGATGTTGTGTACCAAGGCTACATCAAAAGAAATGATGATAAATAAGT 2222
QY 221 GlyLysLeuGluAspSerThrSerLysLysIleLeuAspThrValHisSerCysGlu 240
DB 2223 GGAATATTAGAGATTCACATGACCTATCAAAATCTTGATACAGTTCATCTTGTGAA 2282
QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
DB 2283 AGAGCAAGGGAACCTTCAAAAGATCACTGTGAACAGCTACAGGAAATGGAAACAAATG 2342
QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280
DB 2343 AAAAGAAAGTTTGTGTACTGAAAGAAAGAACTGTCAAGCAAAAGAAATATAATCACAG 2402
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLysSerValArgLeuThrLeuAsn 300
DB 2403 TTAGAGAACCAAAAGTTAAATGGAAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2462
QY 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
DB 2463 CACAGAGAGAGAGAGAGAGAAATCCCGATATATTAATGAAGAAATTAGGAGAAATTA 2522
QY 321 GlyArgIleGluGlnHisArgLysGluLeuValLysGlnLysGlnLysGlnAla 340
DB 2523 CGAAGAAATCGAAGAGCAGCATAGAAAGAGTTAGAGTGAACAAACAACTTGAACAGGCT 2582
QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
DB 2583 CTCAGATACAGATATAGAAATTTGAAGAGTTAGAAAGTAAATTTGAATCAGGTTCTCAC 2642
QY 361 ThrHisGluAsnGluAsnTyLysLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
DB 2643 ACTCATGAAATGAAATTTATCTCTTACATGAAATTTGCATTTGAAAGAAAGAAATGTC 2702
QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrgLysGluAsnLysTyL 400
DB 2703 ATGCTAAACATGGAATAGCCACACTGAACACCAATACACAGAAAGAAATTAATATAC 2762
QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
DB 2763 TTTGAGGACATTAAAGATTTAAAGAAAGAAATGCTGAACCTTCAGATGACCTTAAACTG 2822
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrgLysGlnLeuLysValLeuIle 440
DB 2823 AAAGAGGAATCAATTAACATAAGGGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 2882
QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
DB 2883 GCTGAGAACACAACTGCTCATTCTTAATTTGAAGGAAACAAACAGACAAAGAAATACTAG 2942
QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480

DB 2943 GCAGAAATTTGAATCAACCATCTCTAGACTGGCTTCTGCTGTACAGACCATCAAAATT 3002
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
DB 3003 GTGACATCAAGAAAAAGTCAAGAACCTGCTTTTCCACATTCGAGGAGATCTGTTTTCGAA 3062
QY 501 ArgLysMetAsnValAspValSerSerThr 510
DB 3063 AGAAAAATGAATGTTGATGTAGTAGTAG 3092
RESULT 6
US-09-620-405B-468
; Sequence 468, Application US/09620405B
; Patent No. 5528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudi
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-468
Alignment Scores:
Pred. No.: 1,81e-232 Length: 2307
Score: 2227.50 Matches: 446
Percent Similarity: 87.65% Conservative: 1
Best Local Similarity: 87.45% Mismatches: 2
Query Match: 85.71% Indels: 62
DB: 4 Gaps: 1
US-09-451-739H-16 (1-512) x US-09-620-405B-468 (1-2307)
QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
DB 206 ATGAAAGTTTCTATTCCAACTTAAGCCCTTAGAATTTGACATGCAAACTTTCAAAGCA 265
QY 21 GluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
DB 266 GAGCTCCCGAGAGGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCA 325
QY 41 AsnLysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGluIleLeuProSer 60
DB 326 AATRAAGCCTTGGAAATGAAGAAATGAACAAACATTTGAGAGCAGATGAGATCTCCATCA 385
QY 61 GluSerLysGlnLysAspTyrgLysSerSerTrpAspSerGluSerLeuCysGluThr 80
DB 386 GAATCCAAACAAAGAGACTATGAAGAAAGTTTCTTGGATTCTGAGAGTCTCTGTGAGACT 445
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
DB 446 GTTTCACAGAGAGATGTTGTTTACCCAGGCTACACATCAAAAGAAATAGATAAATA 505
QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
DB 506 AATGGAATTTAGAGAGTCTCTGATATGATGTTTCTGAGTCTCCCTGCAGAATG 565
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
DB 566 AAAGTTTCTATTCCAACTAAGCCTTAGAATTTGATGGACATCAAAAGTCTTCAACAGCAG 625

141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
626 CCTCCGAGAGCCATCTGCTCGAGCCGCAATGAAATGAAAGTCTGTCCAAAT 695
161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
686 AAACCCCTTGAATTGAAGATGAACAAACATTTAGAGCAGATGATGTTCCCTTCAGAA 745
181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLysArgGluThrVal 200
746 TCAAAACAAAGAACGTTGAAGAAATTTCTTGGATTTCTGAGAGTCTCCGTGAGACTGTT 805
201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
806 TCACAGAGGATGTGTGTGTACCCAGGCTACACATCAAAAGAAATGGATAAAATAGT 865
221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240
866 GGAATAATTAGAAGATTCAACTAGCTATCAAAATCTTGGATACAGTTCACTTCTGGAA 925
241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
926 AGACCAAGGAACTTCAAAAGATCACCTGTGAACACGTACAGGAAATGGAACAAATG 985
261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluLysSerGln 280
986 AAAAAGAGTCTTGTACTGAAAGAACTGTGAGAGCAAAAGAAATAAATCAAG 1045
281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
1046 TTAGAGAACCAAAAGATTAAATGGACACAGCTCTGAGTGTGAGTT----- 1095
301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
1095 ----- 1095
321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGlnAla 340
1095 ----- 1095
341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
1096 -----TCTCAC 1101
361 ThrHisGluAsnGluAsnTrpLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
1102 ACTCATGAAATGAAATATCTCTTATGAAATTCATGATGAAATGCAATGAAAGAAATGCC 1161
381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTrpGlnGluLysGluAsnLysTrp 400
1162 ATGCTAAACCTGAAATAGCCACACTGAAACACCAATACCAAGAAAGAAATATAATAC 1221
401 PheGluAspIleLysIleLeuLysGlnLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
1222 TTTGAGGACATTATGATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTG 1281
421 LysGluGluSerLeuThrLysArgAlaSerGlnTrpSerGlyGlnLeuLysValLeuIle 440
1282 AAAGAGGAATCATTAACATAAGGCACTCTCAATATAGTGGCAGCTTAAAGTCTGATA 1341
441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluIleLeuGlu 460
1342 GGTGAGAACACAAATGCTCACTTCTTAATTTGAAGGAAACCAAGCAAAAGAAATACTAG 1401
461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
1402 GAGAAATTTGAATCATCACCATCTAGACTGGCTTCTGTGTACAGACATGATCAATATT 1461
481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
1462 GTGACATCAAGAAAGTCAAGAACTGCTTTCCACATTTGACAGGAGTCTGTTTGGCAA 1521
501 ArgLysMetAsnValAspValSerSerThr 510

1522 AGAAATGAATGTTGATGTGAGTAGTACG 1531
RESULT 7
US-09-433-826B-468
; Sequence 468, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqi
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-468
Alignment Scores:
Pred. No.: 1,81e-232 Length: 2307
Score: 2227.50 Matches: 446
Percent Similarity: 87.65% Conservative: 1
Best Local Similarity: 87.45% Mismatches: 2
Query Match: 85.71% Indels: 62
Gaps: 1
US-09-451-739H-16 (1-512) x US-09-433-826B-468 (1-2307)
QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
Db 206 ATGAAAGTTTCTATCCAACTAAAGCCTTAGAATGTAGTGGACATGCAAACTTTCAAAGCA 265
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 266 GAGCCTCCGAGAGCCATCTGCTCGAGCCTGCAATGAAATGCAAAAGTCTGTTCCTCA 325
QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 326 ATAAAGCCTTGGATTGAGATGACAAACATTTAGAGCAGATGAGATCTCCATCA 385
QY 61 GluSerLysGlnLysAspTrpGluGluSerSerTrpAspSerGluSerLysCysGlnThr 80
Db 386 GAATCAAAACAAAGGACTATGAAGAAATCTTGGATTTCTGAGAGTCTCTGTGAGACT 445
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
Db 446 GTTTCACAGAGATGTTGTTTACCCAGGCTACACATCAAAAGAAATAGATAATA 505
QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 506 AATGGAATAATTAGAGAGTCTCTGATAATGATGTTTCTGAGTCTCCCTGCGAAGT 565
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 566 AAAGTTTCTATTCCAACTAAGCCTTAGAATTTAGTGGACATGCAAACTTTCAAAGCAG 625
QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 626 CTTCCCGAGAGCCATCTGCTTCGAGCCTGCAATGAAATGAAATGCTGTCTCCAAAT 685
QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 686 AAAGCCTTGAATTTGAAGATGAACAAACATTTAGAGCAGATCAGATGTTCCCTTCAGAA 745
QY 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLysArgGluThrVal 200

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Db 746 TCAAAACAAAGAACGTTGAAGAAATTCCTGGATCTCAGAGTCTCCGTGAGACTGTT 805
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 806 TCACAGAGGATGTTGTGTACCCAGGCTACACATCAAAAGAAATGGATAAAATAGT 865
Qy 221 GlyLysLeuGluAspSerThrSerLysLysIleLeuAspThrValHisSerCysGlu 240
Db 866 GGAATAATTAGAAATCAACTAGCTTCAAAATCTTGATACAGTTCATTCTCTGTAA 925
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 926 AGACGAAGGAACTTCAAAAGATCACTGTGAACAGCTACAGAAATGGAAACAAATG 985
Qy 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluLysSerGln 280
Db 986 AAAAAGAGTTTGTGTACTGAAAAGAACTGTGAGAGCAAGAAAGAAATAAATCACAG 1045
Qy 281 LeuGluGlnLysValLysValLysGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 1046 TTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGCAGTGTGAGGTT----- 1095
Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 1095 ----- 1095
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340
Db 1095 ----- 1095
Qy 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 1096 -----TCTCAC 1101
Qy 361 ThrHisGluAsnGluAsnTyrIleLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 1102 ACTCATGAAATGAAATTAATCTCTTACATGAAATTTGCATGTTGAAAGAAATGCTCC 1161
Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 1162 ATGCTAAAACTGGAATAGCCACTGAACACCAATACAGGAAAGAAAGAAATAAATAC 1221
Qy 401 PheGluAspIleLysIleLysLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 1222 TTTGAGGACATTAGATTTAAAGAAAGAAATGCTGAACCTTCAGATGACCTTAAACTG 1281
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 1282 AARGAGGAATCAATTAACATAAGGCACTCTCAATTAATGCGCAGCTTAAAGTTCTGATA 1341
Qy 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluIleLeuGlu 460
Db 1342 GCTGAGAACACAATGCTCACTTCTAAATTAAGGAAAGAAACAAAGCAAGAAATACTAGAG 1401
Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisGlnIle 480
Db 1402 CGAGAAATGAATCAACATCTAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1461
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 1462 GTGACATCAAGAAAGTCAAGAACTGCTTTCCACATTCGAGGAGATGCTTGTGTGCAA 1521
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 1522 AGAAAAATCAATGTTGATGTAGTAGTAGTACG 1551
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RESULT 8

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US-09-604-287A-468
; Sequence 468, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
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; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-604-287A-468
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Alignment Scores:

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Prod. No.: 1,81e-232 Length: 2307
Score: 2227.50 Matches: 446
Percent Similarity: 87.65% Conservative: 1
Best Local Similarity: 87.45% Mismatches: 2
Query Match: 85.71% Indels: 62
DB: 4 Gaps: 1
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US-09-451-739H-16 (1-512) x US-09-604-287A-468 (1-2307)

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Qy 1 MetLysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAla 20
Db 206 ATGAAAGTTTCATTCCAACTAAAGCCTTAGAATTGATGGACATGCAAACTTTCAAGCA 265
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 266 GAGCCTCCGAGAGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTGCCA 325
Qy 41 AsnLysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGluIleuProSer 60
Db 326 AATAAAGCCTTCGAAATGAAGAAATGAACAAACATTGAGAGCAGATGAGATCTCCATCA 385
Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80
Db 386 GAATCCAAACAAAGGACTATGAGAAAGTTCTTGGATTCTGAGAGTCTCTGTGAGACT 445
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLysIle 100
Db 446 GTTTCACAGAGGATGTTGTGTTTACCCAGGCTCACATCAAAAGAAATAGATAAATA 505
Qy 101 AsnGlyLysLeuGluLysSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 506 AATGGAAATTAGAGAGTCTCTGTAATGATGTTTCTGAACTCTCCCTGCAGAAATG 565
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 566 AAAGTTTCTATTCCAACTTAAGCCTTAGAATTGATGGACATGCAAACTTTCAAGACAGAG 625
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 626 CTTCCGAGAGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTCCAAAT 685
Qy 161 LysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 686 AAAGCCTTGAATTAAGAAATGAACAAACATTGAGAGCAGATCGATGTTCCCTTCAGAA 745
Qy 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 746 TCAAAACAAAGAACCTTGAAGAAATTTCTGGATTCTGAGAGTCTCCGTGAGACTGTT 805
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 806 TCACAGAGGATGTTGTGTGTACCCAGGCTACACATCAAAAGAAATGATAAATAAAGT 865
Qy 221 GlyLysLeuGluAspSerThrSerLysLysIleLeuAspThrValHisSerCysGlu 240
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866	GGAAAAATTAGAAAGATTCAACTAGCCATCAAAAATCTTTGGATACAGTTCAATCTTTGTGAA	925
241	ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet	260
926	AGAGCAAGGGAACCTTCAAAAAGATCACTGTGTAACAACGTCACAGAAAAATGGAAACAATG	985
261	LysIlyLysPheCysValLeuLysLysLysLeuSerGlnAlaLysGluIleLysSerGln	280
986	AAAAAGAAGTTTGTGTACCGAAAAAGAACTGTCAAGCAAAAGAAATAAAATCACAG	1045
281	LeuGluAsnGlnLysValLysTTPGluGlnGluLeuCysSerValArgLeuThrLeuAsn	300
1046	TTAGAGAACCAAAAAAGTTAAATGGAAACAAGAGCTCTGCAGTGTGAGGTT	1095
301	GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu	320
1095	-----	1095
321	GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla	340
1095	-----	1095
341	LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis	360
1096	-----	1101
361	ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla	380
1102	ACTCATGAAATGAAATTTATCTCTACATGAAATTTGCATGTTTGAAGAAAGGAATTTGCC	1161
381	MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr	400
1162	ATGCTAAACCTGGAAATAGCCACACTGAAACCCAACTACCAAGGAAAGGAAATAAATAC	1221
401	PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu	420
1222	TTTGAGGACATTAAAGTTTAAAGAAAAAGAAATGCTGAACCTCAGATGACCCATAAAACCTG	1281
421	LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle	440
1282	AAAGAGGAATCATTTAACTAAAGGGCATCTCAATATAGTGGCGAGCTTAAAGTTCTCATATA	1341
441	AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu	460
1342	GCTGAGAACACAAATGCTTCACTTCTAAATTGAGGAAAAACAAGACAAAGAAATACCTAGAG	1401
461	AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle	480
1402	GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAATT	1461
481	ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln	500
1462	GTGACATCAAGAAAAGTCAGAACCTGCTTCCATCTGAGGAGATGCTTTGTTGCCAA	1521
501	ArgLysMetAsnValAspValSerSerThr	510
1522	AGAAAAATCAATGTTGTAGTGTGAGTAGTACG	1551

RESULT 9

US-09-834-759-468	Qy	201	SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer	220
; Sequence 468, Application US/09834759				
; Patent No. 6680197				
; GENERAL INFORMATION:				
; APPLICANT: Jjiang, Yugu				
; APPLICANT: Dillon, Davin C.				
; APPLICANT: Mitcham, Jennifer L.				
; APPLICANT: Xu, Jiangchun				
; APPLICANT: Harlocker, Susan L.				
; APPLICANT: Hepler, William T.				
; APPLICANT: Henderson, Robert A.				
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND				
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER				
	Db	806	TCACAGAAAGGATGTGTGTATCCCAAGGCTACATCAAAAGAAGAAATGGATAAAATAGT	865
	Qy	221	GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu	240
	Db	866	GGAAAATTAGAAGATTCAACTAGCCTATCAAAATCTTGGATACAGTTCATCTTGTGAA	925
	Qy	241	ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet	260
	Db	926	AGGCAAGGGAACCTTCAAAAGATCACTGTGAACAACGTACAGGAAAAATGGAACAAATG	985

QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLeuLysSerGln 280
Db 986 AAAAGAGAGTTTGTGTACTGAAAGAGAACTGTGAGAGCAAGAAAGAAATAAAATCACAG 1045
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuLysSerValArgLeuThrLeuAsn 300
Db 1046 TTAGAGAACCAAAAGTTAAATCGGAAACAGAGCTCTGAGGTGTAGGTT----- 1095
QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 1095 ----- 1095
QY 321 GlyArgIleGluGlnHisArgLysGluLeuValLysGlnGlnLeuGlnAla 340
Db 1095 ----- 1095
QY 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 1096 -----TCTCAC 1101
QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 1102 ACTCATGAAATGAAATATATCTTACATGAAATTCATGTTGAAAGGAAATTCGC 1161
QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 1162 ATGCTAAACTGGAATAGCCACACTGAACACCATACACGGAAGGAATATATAC 1221
QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuMetThrLeuLysLeu 420
Db 1222 TTTGAGGACATTAAGATTTTAAAGAGAAAGATGCTGAATCTCAGATGACCTTAAACTG 1281
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 1282 AAAGAGAAATCATTAATAAAGGSCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 1341
QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
Db 1342 GCTGAGAACACAAATGCTCACTTCTAAATTAAGGAAAGAAACAAAGAAAGAAATACTAGAG 1401
QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 1402 GCAGAAATTAATCACACCATCTAGAGTGGCTTCTGCTGTACAGACCATGATCAAT 1461
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 1462 GTGACATCAAGAAAGAGTCAAGAACCTGCTTCCACATTCGAGGAGATGCTTGTGTCAA 1521
QY 501 ArgLysMetAsnValAspValSerSerThr 510
Db 1522 AGAAAAATGAATGTTGATGTGAGTAGTACG 1551

RESULT 10

US-09-620-405B-463
; Sequence 463, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yufu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 463
; LENGTH: 3681
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-620-405B-463

Alignment Scores:

Pred. No.: 7,83e-232 Length: 3681
Score: 2224.50 Matches: 446
Percent Similarity: 87.45% Conservative: 0
Best Local Similarity: 87.45% Mismatches: 3
Query Match: 85.59% Indels: 62
DB: 4 Gaps: 1

US-09-451-739H-16 (1-512) x US-09-620-405B-463 (1-3681)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
Db 1563 ATGAAGTTTCTATTCACACTAAAGCTTAGAATTGATGGACATGCAAACTTTCAAGCA 1622
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1623 GAGCCTCCGAGAGACCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTC 1682
QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 1683 AATAAGCCTTGGAAATTGAAGATGAACAAACATTGAGACAGATGAGATCTCCCATCA 1742
QY 61 GluSerLysGlnLysAspTyrGluLysSerTrpAspSerGluSerLeuCysGluThr 80
Db 1743 GAATCCAAACAAAGGACTATGAAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAG 1802
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
Db 1803 GTTTCACAGAGAGGATGTGTGTTTACCACAGGCTRCRCATCAAAAGAAATAGATAAATA 1862
QY 101 AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 1863 AATGGAAATTAAGAGAGTCTCTGATAATGATGGTTTCTGAGAGGCTCCCTGAGAGAT 1922
QY 121 LysValSerIleProThrLysAlaLeuLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 1923 AAAGTTTCTATTCACACTAAAGCCTTAGAATTGATGACATGCAAACTTTCAAGCAGAG 1982
QY 141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 1983 CTCTCCGAGAGACCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTC 2042
QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2043 AAAGCCTTGGAAATTGAAGATGAACAAACATTGAGACAGATCAGATGTTCCCTTCAG 2102
QY 181 SerLysGlnLysValGluLysSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 2103 TCATAACAAAGAAAGAGTTGAAGAAATTTCTGGGATTTCTGAGAGTCTCCGTGAGACT 2162
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2163 TCACAGAGAGTGTGTGTGTACCCAGGCTACACATCAAAAGAAATGCAATAAATAAGT 2222
QY 221 GlyLysLeuGluAspSerThrSerLysIleLeuAspThrValHisSerCysGlu 240
Db 2223 GGAATTTAGAAGATTCACATGACCTATCAAAATCTTGGATACAGATTCATTTGTGAA 2282
QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2283 AGAGCAAGGGAACCTTCAAAAGATCACTGTGAACACCTACAGGAAATGGAACAAATG 2342
QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280
Db 2343 AAAAGAGAGTTTGTGTCTGTAAGAAAGAACTGTGAGAGCAAGAAATAAATACACAG 2402
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGAACCAAAAGTTAAATGGGAAACAGAGCTCTGCAGTGTGAGGTT----- 2452

QY 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2452 -----
QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340
Db 2452 -----
QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2453 -----TCTCAC 2458
QY 361 ThrHisGluAsnGluAsnTyrIleuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 2459 ACTCATGAAATGAAATATCTCTTACATGAAATTCATGTTGAAAGAAATGCTCC 2518
QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 2519 ATGCTTAAACTGGAATAGCACACTGAAACACCATACAGGAAGAAAGAAATTAATAC 2578
QY 401 PheGluAspIleLysIleLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2579 TTGAGGACATTAAGATTTAAGAAAGAAAGAAATGCTGAATTCAGATGACCTTAAACTG 2638
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 2639 AAGAGGAATCAATTAACATAAGGCACTCATATAGTGGCAGCTTAAAGTTCTGATA 2698
QY 441 AlaGluAsnThrMetLeuThrSerLysLysGluLysGlnAspLysGluIleLeuGlu 460
Db 2699 GCTGAGACACATGCTCACTTCTAAATTAAGGAAACAAAGCAAGAAATTAAGTACAG 2758
QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2759 CAGAAATTAAGATCAACATCTAGCTGGCTTCTGTACAGACATGATCAATTAAT 2818
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 2819 GTGACATCAAGAAAGTCAAGAACCTGCTTCCACATTCGAGGAGATGCTTGTTCGAA 2878
QY 501 ArgLysMetAsnValAspValSerThr 510
Db 2879 AGAAATTAAGTGTGATGTAGTAGTAGC 2908

RESULT 11

US-09-433-826B-463
; Sequence 463, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: DIAGNOSIS OF BREAST TUMORS AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 463
; LENGTH: 3681
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-463

Alignment Scores:
Pred. No.: 7,83E-232 Length: 3681
Score: 2224.50 Matches: 446
Percent Similarity: 87.45% Conservative: 0
Best Local Similarity: 87.45% Mismatches: 3
Query Match: 85.59% Indels: 62

DB: 4 1 Gaps: 1
US-09-451-739H-16 (1-512) x US-09-433-826B-463 (1-3681)
QY 1 MetLysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAla 20
Db 1563 ATGAAAGTTTCTATTCCAACTTAAAGCTTAGAATTGATGGACATGCAAACTTTCAAAGCA 1622
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1623 GAGCTCCCGAGAGCCATCTGCTTCGAGCTGCTGCAATGAAATCAAAAGTCTGTTCCA 1682
QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 1683 AATAAGCTTGGATTGAGAAATGAACAAACATTGAGAGCAGATGAGATATCTCCATCA 1742
QY 61 GluSerLysGlnLysAspTyrGluLysSerSerTrpAspSerGluSerLeuLysGluThr 80
Db 1743 GAATCCAAACAAAGGACTATGAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACT 1802
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
Db 1803 GTTTCACAGAGATGTGTGTTTACCAAGGCTTCCCATCAAAAGAAATAGATAAATA 1862
QY 101 AsnGlyLysLeuGluLysSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 1863 AATGGAATTTAGACAGTCTCTGATATGATGTTTCTGAGGCTCCCTGCGAATG 1922
QY 121 LysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAlaGlu 140
Db 1923 AAGTTTCTATTCCAACTTAAAGCTTAGAATTGATGGACATGCAAACTTTCAAAGCAG 1982
QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 1983 CTTCCCGAGAGCCATCTGCTTCGAGCTGCAATGAAATCAAAAGTCTCTTCCAAAT 2042
QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2043 AAGCTTGTGAATTTGAAGATGAACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAA 2102
QY 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 2103 TCAAAACAAAGAAAGTGTGAAGAAATTTCTGGGATTTCTGAGAGTCTCGTGAGACTGTT 2162
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2163 TCACAGAGGATGTGTGTGTACCAAGGCTTACATCAAAAGAAATGATGATTAATTAAT 2222
QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
Db 2223 GGAATTTAGAGATTTCACTAGCTTATCAAAATCTTGGATACAGTTCATTTCTGTGAA 2282
QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2283 AGAGCAAGGAACTTCAAAAGATCTGTGAACACGTCAGAGAAATGGAACAAATG 2342
QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280
Db 2343 AAAAGAAAGTTTGTGTACTGAAAGAAATCTCAGAGCAAAAGAAATATAATCACAG 2402
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLysCysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTGCAAGTGTGAGTT----- 2452
QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2452 -----
QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340
Db 2452 -----
QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360

Db 2453 -----TCTCAC 2458
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysGluLeuAla 380
Db 2459 ACTCATGAAATGAAATATCTCTTACATGAAATTTGCATGTTGAAAGGAAATGGCC 2518
Qy 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 2519 ATGCTAAATCTGGAATAGCCACACAGAACCAATACACAGGAAAGGAAATATAATAC 2578
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2579 TTTGAGGACATTAAGATTTTAAAGAAAGAAAGCTCAACTTCAGATGACCCCTTAAAGCTG 2638
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlnLeuLysValLeuIle 440
Db 2639 AAGAGAGAAATCAATTAATAAGGCGCATCTCAATATAGTGGGCGAGCTTAAAGTTCTGATA 2698
Qy 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGlnLysGlnAspLysGluLeuLeuGlu 460
Db 2699 GCTGAGAACCAATGCTCACTTCTTAATTTGAAGGAAACCAAGACAAAGAAATACTAGAG 2758
Qy 461 AlaGluLeuGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2759 GCAGAAATTTGAATCACACCATCTCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAAT 2818
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 2819 GTGACATCAAGAAAGCTCAAGACCTGCTTCCACATTCGAGGAGATGCTTGTGTCGAA 2878
Qy 501 ArgLysMetAsnValAspValSerThr 510
Db 2879 AGAAATGAAATGTGATGTGAGTAGTACG 2908

RESULT 12

US-09-604-287A-463
; Sequence 463, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 463
; LENGTH: 3681
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-463

Alignment Scores:
Pred. No.: 7,83e-232 .Length: 3681
Score: 2224.50 Matches: 446
Percent Similarity: 87.45% Conservative: 0
Best Local Similarity: 87.45% Mismatches: 3
Query Match: 85.59% Indels: 62
DB: 4 Gaps: 1

US-09-451-739H-16 (1-512) x US-09-604-287A-463 (1-3681)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
Db 1563 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAAGCA 1622

Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1623 GAGCCTCCGAGAGCCATCTGCTTCGAGCCTGCCAATGAAATGCAAAAGTCTGTCCA 1682
Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 1683 AATAAGCCTTGGAAATGAAAGATGAACAAACATTTAGAGCAGATGAGATCTCCCATCA 1742
Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLeuCysGluThr 80
Db 1743 GAATCCAAACAAAGGACTATGAAGAAAGTTCTTGGATTTCTGAGAGTCTCTGTGAGACT 1802
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
Db 1803 GTTTCCAGAGAGATGTGTGTTTACCACAGGCTRCRCATCAAAAGAAATAGATAAATA 1862
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 1863 AATGGAAATTTGAAGAGTCTCTCGATATGATGTTTCTGAAGGCTCCCTGCAGAAATG 1922
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 1923 AAAGTTTCTATTCCAACTTAAAGCCTTAGAATTTGATGACATGCAAACTTTCAAAGCAGAG 1982
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 1983 CTTCCCGAGAGCCATCTGCTTCGAGCCTGCCAATGAAATGCAAAAGTCTGTTCCTTCAAA 2042
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2043 AAAGCCTTGAATTTGAAGATGAACAAACATTTGAGAGCAGATCAGATGTTTCCCTTCAAA 2102
Qy 181 SerLysGlnLysValGluGluAsnSerTyrAspSerGluSerLeuArgGluThrVal 200
Db 2103 TCAAAACAAAGAAAGAGTTGAAGAAATTTCTTGGATTTCTGAGAGTCTCCGAGAGCTGTT 2162
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2163 TCACAGAGAGGATGTGTGTACCCAAAGGCTACACATCAAAAGAAATGGATTAATAAATAGT 2222
Qy 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240
Db 2223 GGAAATTTAGAGATTCACATAGCCTATCAAAATTTCTTGGATACAGTTCATCTTGTGAA 2282
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2283 AGAGCAGGAGACTTCAAAAGATCACCTGTGAACAACATCAGAGAAATGGAAACAAATG 2342
Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280
Db 2343 AAAAAAGAGTTTGTGTACTGAAAAAGAACTGTGAGAGCAAGAAAGAAATTAATATCAG 2402
Qy 281 LeuGluAsnGlnLysValLysTyrGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGAACCAAAAGTTAATTTGGAACAACAGAGCTCTGAGTGTGAGTGT----- 2452
Qy 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2452 ----- 2452
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGlnAla 340
Db 2452 ----- 2452
Qy 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2453 -----TCTCAC 2458
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 2459 ACTCATGAAATGAAATATTTCTTACATGAAATTTGCATGTTGAAAGGAAATTTGCC 2518
Qy 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400

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Db 2519 ATGCTAAACCTGGAAATAGCCACACTGAAACACCAATACCAAGAAAGGAAATTAATATAC 2578
Qy 401 PheGluAspIleLysIleLeuLysGluLysAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2579 TTTGAGGACATTAAAGATTTAAAGAAAGAAAGTGTGAACCTTCAGATGACCTAAAACGTG 2638
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuLe 440
Db 2639 AAAGAGGAATCATTAACATAAAGGCATCTCAATATAGTGGCAGCTTAAAGTCTGATA 2598
Qy 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGlnLysGlnAspLysGluLeuGlu 460
Db 2699 GCTGAGAACACAACTGCTCACTTCTAAATGAAGGAAACCAAGCAAAAGAAATACTAGAG 2758
Qy 461 AlaGluIleGluSerHisGlnProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2759 GCAGAAATGAATCACCATCTAGACTGCTTCTGCTGTACAGACCATGATCAAAAT 2818
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 2819 GTGACATCAAGAAAGTCAAGAACCTGCTTCCACATTCGAGGAGATGCTTGTGTCAA 2878
Qy 501 ArgLysMetAsnValAspValSerThr 510
Db 2879 AGAAAAATGAATGTTGATGTGAGTAGTACG 2908

RESULT 13
US-09-834-759-463
; Sequence 463, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepier, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 463
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-463

Alignment Scores:
Pred. No.: 7,83e-232 Length: 3681
Score: 2224.50 Matches: 446
Percent Similarity: 87.45% Conservative: 0
Best Local Similarity: 87.45% Mismatches: 3
Query Match: 85.59% Indels: 62
DB: 4 Gaps: 1

US-09-451-739H-16 (1-512) x US-09-834-759-463 (1-3681)
Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
Db 1563 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTCAGATGAGCATGCAAACTTTCAAGCA 1622
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1623 GAGCCTCCCGAGAGCCATCTGCTTCGAGCTGCTGATGAAATGCAAAAGTCTGTTCCA 1682
Qy 41 AsnLysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 1683 AATAAAGCCTTGAATTAAGAAATGAACAAACATTCGAGGAGCAGATGAGTACTCCCA 1742
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Qy 61 GluSerLysGlnLysAspTyrGluSerSerTrpAspSerGluSerLeuCysGluThr 80
Db 1743 GAATCCAAACAAAGAGACTATGAGAAAGATTTCTGGATTCTGAGAGTCTCTGTGAGACT 1802
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
Db 1803 GTTTCACAGAGGATGTGTGTTTACCCCAAGGCTRCRCATCAAAAAGAAATAGATAAATA 1862
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 1863 AATGGAAATTAAGAGAGTCTCTGATATGATGATGTTTCTGAAGGCTCCCTGCGCAATG 1922
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 1923 AAAGTTTCTATTCCAACTAAAGCCTTAGAATGTAGTCGACATGCAAACTTTCAAGCAGAG 1982
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 1983 CTTCCCGAGAGCCATCTGCTTCGAGGCTGCCATTGAAATGCAAAAGTCTGTTCCAAT 2042
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2043 AAAGCCTTGGAAATGAAGATGACAAACATTCAGAGCAGATCAGATGTTCCCTTCAGAA 2102
Qy 181 SerLysGlnLysValGluLysAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 2103 TCAAAACAAAGAAAGTGTGAAGAAATTTCTGGGATTCGAGAGTCTCGTGAGACTGTT 2162
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2163 TCACAGAGATGTGTGTGTTACCAAGCTCACATCAAAAGAAATGATTAATAAGT 2222
Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
Db 2223 GGAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAA 2282
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2283 AGAGCAAGGAGACTTCAAAAGATCTGTGTAACACAGTACAGGAAATGAACAATG 2342
Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280
Db 2343 AAAAGAAAGTTTGTCTACTGAAAAAGAAACTGTGAGAAAGCAAAAGAAATAAATCAGAG 2402
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnLeuCysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGACCAAAAGTAAATTAAGAAAGAAAGTCTGAGAGTCTGAGTGTGAGTT----- 2452
Qy 301 GlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2452 ----- 2452
Qy 321 GlyArgIleGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluAla 340
Db 2452 ----- 2452
Qy 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2453 -----TCTCAC 2458
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 2459 ACTCATGAAATGAAATTAATCTCTTACATGAAATTTGATGTTGAAAGGAAATTTGCC 2518
Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 2519 ATGCTAAACTGGAATAGCACACCTGAAACACCATACAGGAAAGGAAATAATAATAC 2578
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2579 TTTGAGGACATTAAAGATTTTAAAGAAAGAAAGATGCTGAACTTCAGATGCCCTTAAACTG 2638
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QY 421 LysGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuile 440
 Db 2639 AAGAGGAATCATTAATAAGGGGATCTCAATATAGTGGGACCTTAAGATCTGATA 2698
 QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluLeuGlu 460
 Db 2699 GCTGAGACACAAATGCTCACTTCTAATTTGAAGGAAAAACAAGACAAAAATACTAGAG 2758
 QY 461 AlaGluLeuGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnile 480
 Db 2759 GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAT 2818
 QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
 Db 2819 GTGACATCAAGAAAAAGTCAAGAACCTGCTTTCACATTCGAGGAGATGCTTTGTTCAA 2878
 QY 501 ArgLysMetAsnValAspValSerThr 510
 Db 2879 AGAAAAATGAATGTTGATGTGAGTAGCTAGC 2908
 RESULT 14
 US-09-620-405B-467
 ; Sequence 467, Application US/09620405B
 ; Patent No. 6528054
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Yuqu
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Hepler, William T.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
 ; FILE REFERENCE: 210121.470C8
 ; CURRENT APPLICATION NUMBER: US/09/620.405B
 ; CURRENT FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 495
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 467
 ; LENGTH: 1337
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-620-405B-467
 Alignment Scores:
 Pred. No.: 1,13e-221 Length: 1337
 Score: 2125.00 Matches: 416
 Percent Similarity: 99.76% Conservative: 0
 Best Local Similarity: 99.76% Mismatches: 1
 Query Match: 81.76% Indels: 0
 DB: Gaps: 0
 US-09-451-739H-16 (1-512) x US-09-620-405B-467 (1-1337)
 QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
 Db 78 ATGAAGATTTCTATTCCAACTTAAGCCCTTAAGATTTGATGGACATGCCAACTTTCAAAGCA 137
 QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
 Db 138 GAGCTCCCGAGAGCCATCTGCTTCGAGCTGCTTGAATGCAAAAGTCTGTTCCA 197
 QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer 60
 Db 198 AATAAAGCCCTTGAATTTGAAGAAATGAACAAACATTTGAGAGCAGATGAGATCTCCCATCA 257
 QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuLysGluThr 80
 Db 258 GAATCCAAACAAAGGACTATGAAAGAGTCTTGGGATTTCTGAGACTCTGTTGAGACT 317
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysIle 100
 Db 318 GTTTCACAGAGGATGTGTTTTCACCAAGGCTGGCCTCAAAAGAAATAGATAAATA 377

QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
 Db 378 AATGGAATTTAGAGAGTCTCTCTGATAATGATGGTTTCTGAAGGCTCCCTGCAAGATG 437
 QY 121 LysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAlaGlu 140
 Db 438 AAGTTTCTATTCCAACTTAAGCCTTAAGATTTGATGGACATGCACAACTTTCAAAGCAGAG 497
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
 Db 498 CTTCCCGAGAGCCATCTGCTTCGAGCCTGCAATTTGAATTCGCAAAAGTCTGTTCACAAAT 557
 QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
 Db 558 AAGCCTTGAATTTGAAGAAATGAACAACTTGAAGAGCAGATCAGATGTTCCCTTCAGAA 617
 QY 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
 Db 618 TCAAAACAAAGAGGTTGAAGAAATTTCTGGATTTCTGAGAGTCTCCGTGAGACTGTT 677
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
 Db 678 TCACAGAGGATGTGTGTACCCAGGCTACACATCAAAAGAAATGGTAAATAAAGT 737
 QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
 Db 738 GGAATTTAGAGATTTCACTAGCTATCAAAATCTTGGATACAGTTCAATCTTGTGAA 797
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
 Db 798 AGAGCAAGGAACTTCAAAAGATCACTGTGAACACAGTACAGAGAAATGGAAACAATG 857
 QY 261 LysLysLysPheCysValLeuLysLysLeuSerGluAlaLysGluIleLysSerGln 280
 Db 858 AAAAGAGATTTTGTGTACTGAAAGAAACTGTGACAGAGCAAAAGAAATAAATACAG 917
 QY 281 LeuGluAsnGlnLysValLysValLysValLysValLysValLysValLysValLysVal 300
 Db 918 TTAGAGAACCAAAAGATTTAAATGGAAACAGAGCTCTGAGTGTGAGATTCACTTTAAAC 977
 QY 301 GlnGluGluGluLysArgCysAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
 Db 978 CAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1037
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnLysGlnLysGlnAla 340
 Db 1038 GGAAGAAATCGAAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1097
 QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
 Db 1098 CTCAGAAATCAAGATATAGATTTGAGAGTGTAGAACTAATTTGAATCAGGTTTCTCAC 1157
 QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380
 Db 1158 ACTCATGAAATGAAATATCTCTTACATGAAATTTGCATGTTGAAAGAGAAATGCC 1217
 QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
 Db 1218 ATGCTAAAATCGAATATGCCACTGTGAACCCAAATACCAAGAGAGAGAGAGAGAGAG 1277
 QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThr 417
 Db 1278 TTTGAGGACATTAAGATTTTAAAGAGAAAGAAATGCTGAATTCAGATGACC 1328

RESULT 15
 US-09-433-826B-467
 ; Sequence 467, Application US/09433826B
 ; Patent No. 6579973
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Yuqu
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.

APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433.826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 467
; LENGTH: 1337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-467

Alignment Scores:
Pred. No.: 1,13e-221 Length: 1337
Score: 2125.00 Matches: 416
Percent Similarity: 99.76% Conservative: 0
Best Local Similarity: 99.76% Mismatches: 1
Query Match: 81.76% Indels: 0
DB: 4 Gaps: 0

US-09-451-739H-16 (1-512) x US-09-433-826B-467 (1-1337)

QY	1	MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla	20
DB	78	ATGAAGTTTCTATTCACACTTAAGCCTTAGAATTGATGACATGCCAACTTTCAGACA	137
QY	21	GluProGluLysProSerAlaPheGluProLalleGluMetGlnLysSerValPro	40
DB	138	GAGCTCCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCCAAAGTCTGTTC	197
QY	41	AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLleLeuProSer	60
DB	198	ATAAAGCCTTGAATTGAGATGACAAACATGAGAGCAGATGAGATCTCCCATCA	257
QY	61	GluSerLysGlnLysAspTyrGluGluSerTrpAspSerGluSerLeuGluThr	80
DB	258	GAATCCAAACAAAGGACTATCAAGAAAGTTCTTGGGATCTGAGAGTCTCTGTGAGACT	317
QY	81	ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLleAspLysLle	100
DB	318	GTTCACAGAGGATGTGTGTTTCCCAAGGCTGCCATCAAAAGAAATAGATAAATA	377
QY	101	AsnGlyLysLeuGluGluSerProAsnAspGlyPheLeuLysAlaProCysArgMet	120
DB	378	ATGGAAATTAAGAGAGTCTCTCTGATATGATGATGTTTCTGAAGGCTCCCTGCAGATG	437
QY	121	LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu	140
DB	438	AAAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGGACATGCCAACTTTCAGACAG	497
QY	141	ProProGluLysProSerAlaPheGluProAlalleGluMetGlnLysSerValProAsn	160
DB	498	CTCCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCCAAAGTCTGTTC	557
QY	161	LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu	180
DB	558	AAAGCCTTGAATTGAAGATGAACAAACATTCGAGAGCAGATCAGATGTTCCCTTCAGAA	617
QY	181	SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal	200
DB	618	TCAAAACAAAGAGTTGAGAAATTTCTTGGGATCTCGAGAGTCTCCGTGAGACTGTT	677
QY	201	SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysLleSer	220
DB	678	TCACAGAGGATGTGTGTGTACCAAGGCTACACATCAAAAGAAATGGATAAATAAGT	737
QY	221	GlyLysLeuGluAspSerThrSerLeuSerLysLleLeuAspThrValHisSerCysGlu	240
DB	738	GGAAATTTAGAGATTCAACTAGCCCTATCAAAATCTTGATACAGTTCATCTTGTGAA	797

QY	241	ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet	260
DB	798	AGAGCAGGGAGACTTCAAAAAGATCACTGTGACACACGTACAGGAAAAATGGAAACAAATG	857
QY	261	LysLysLysPheCysValLeuLysLysLysSerGluLalalysGluLleLysSerGln	280
DB	858	AAAAAGAAAGTTTCTGTACTGAAAAAGAAACTGTGCAGACGCAAAAGAAATAAAATCAG	917
QY	281	LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn	300
DB	918	TTAGAGAACCAAAAAGTTTAAATGGGACACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC	977
QY	301	GlnGluGluLysArgArgAsnAlaAspLleLeuAsnGluLysLleArgGluGluLeu	320
DB	978	CAAGAAGAAGACAGAGAGAAATGCCGATATATTTAAATGAAAAAATTAGGGAGAAATTA	1037
QY	321	GlyArgLleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluAla	340
DB	1038	GGAGAAATCGAAGACGACATAGGAAGAGTTTGAAGTGAACACACAACTTGAACAGGCT	1097
QY	341	LeuArgLleGlnAspLleGluLysSerValGluSerAsnLeuAsnGlnValSerHis	360
DB	1098	CTCAGAATACAGATATAGAAATTTGAAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCAC	1157
QY	361	ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLleAla	380
DB	1158	ACTCATGAAAAATGAAAAATTTATCTTTACATGAAAAATTCATGTTGAAAAAGAAATTGCC	1217
QY	381	MetLeuLysLeuGluLleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr	400
DB	1218	ATGCTTAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAAAGAAAAATAATAC	1277
QY	401	PheGluAspLleLysLleLeuLysAsnAlaGluLeuGlnMetThr	417
DB	1278	TTTGAGGACATTAAGATTTTAAAGAAAAAGAAATGCTGAACCTTCAGATGACC	1328

Search completed: May 6, 2004, 17:03:37
Job time : 138 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	2599	100.0	2030	4	AH28489	Ah28489 Nucleotid
2	2589	99.6	4047	7	ABT33372	ABT33372 Human tum
3	2589	99.6	4458	6	ABT07694	Ereast ca
4	2589	99.6	4458	7	ABT33371	Human tum
5	2589	99.6	4458	7	ACC50246	Ereast ca
6	2578	99.2	3288	7	ACS47421	Human cDN
7	2578	99.2	3288	6	ABS64022	Human bre
8	2578	99.2	3288	7	ABT33234	Human tum

Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;
 WPI; 2001-441706/47.
 P-PSDB; AAB84703.
 Isolated cancer associated nucleic acid molecule identified by SPREX
 (serological identification of antigens by recombinant expression
 cloning) technique, useful in nucleic acid based therapies to treat
 cancer.
 Claim 1; Page 49-50; 62pp; English.
 The present sequence encodes a human cancer associated antigen. The
 sequence was identified using probes derived from the INGI gene. The INGI
 gene is a tumour suppressor candidate gene. The cancer associated antigen
 polynucleotides and polypeptides are useful for screening for the
 possible presence of a pathological condition in a subject such as
 cancer. The cancer associated antigen polypeptides are useful for
 producing vaccines
 Sequence 2030 BP; 827 A; 334 C; 397 G; 460 T; 0 U; 12 Other;
 Alignment Scores:
 Pred. No.: 1,2e-196 Length: 2030
 Score: 2599.00 Matches: 512
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-451-739H-16 (1-512) x AAH28489 (1-2030)
 QY 1 MetLysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAla 20
 DB 42 ATGAAGGTTCTATTCCAACTTAAGCCCTTAAGATTGATGGACATGCCAACTTCARAGCA 101
 QY 21 GluProGluLysProSerAlaPheGluProAlaLeuMetGlnLysSerValPro 40
 DB 102 GAGCCTCCGAGAGCCATCTGCCCTTCAGCCTGCCATTGAATGCAAACTCTGTCCA 161
 QY 41 AsnLysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGluLeuLeuProSer 60
 DB 162 AATAAGCCTTGAATTAAGAAATGAACAACATTGAGACGATGATGACTCCATCA 221
 QY 61 GluSerLysGlnLysAspTyroGluSerSerTTPAspSerGluSerLysCysGluThr 80
 DB 222 GAATCCAAACAAAGAGCTATGAAGAAAGTTCTTGGGATCTGAGAGTCTCTGTGAGACT 281
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysTle 100
 DB 282 GTTTCACAGAGGATGTGTTTACCCAGGCTACACATCAAAAGAAATAGATAATA 341
 QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
 DB 342 AATGGAAATTTAGAGAGTCTCTGATATGATGTTTCTGAAGGCTCCCTCGAGAAATG 401
 QY 121 LysValSerIleProThrLysAlaLeuLeuMetAspMetGlnThrPheLysAlaGlu 140
 DB 402 AAGATTCTATTCCAACTTAAGCCCTTAGAATTGATGGACATCAAACTTTCAAGACAG 461
 QY 141 ProProGluLysProSerAlaPheGluProAlaLeuMetGlnLysSerValProAsn 160
 DB 462 CTTCCCGAGAGCCATCTGCCCTTCGAGCTGCCATTGAATGCAAAAGTCTGTTCCAAAT 521
 QY 161 LysAlaLeuGluLeuLysAsnGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
 DB 522 AAAGCCTTGAATTAAGAAATGAACAACATTGAGACGATGATGATGTTCCCTTCAGAA 581
 QY 181 SerLysGlnLysValGluGluAsnSerTTPAspSerGluSerLeuArgGluThrVal 200
 DB 582 TCAPACAAAGAGGTTGAGAAATTTCTGGGATTTGAGAGTCTCGTGAGACTGTT 641
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysSer 220

DB 642 TCACAGAGGAGTGTGTGTACCCAGGCTACATCAATAAAGAAATGGATTAATAGT 701
 QY 221 GlyLysLeuGluAspSerThrSerLysSerLysLeuAspThrValHisSerCysGlu 240
 DB 702 GGAAATTTAGAGATTCAACTAGCTATCAAAATCTTGGATACAGTTCATTCTGTGAA 761
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
 DB 762 AGAGCAGGGAACCTTCAAAAGATCTGTGACACAGCTACAGGAAATATGGAACAATG 821
 QY 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluLysSerGln 280
 DB 822 AAAAGAGAGTTTGTGTACTCAAAAGAAATCTGTCAGAGCAAAAGAAATATAATCAAG 881
 QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
 DB 882 TTAGAGAACCAAAAGTTTAAATGGACACAGAGCTCTGACGTGAGATTCACCTTAAAC 941
 QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
 DB 942 CAAAGAGAGAGAGAGAGAAATGCCGATATATTAAATGAAAAAATAGGGAAGATTA 1001
 QY 321 GlyArgIleGluGlnHisArgLysGluLeuGluValLysGlnLeuGluAla 340
 DB 1002 CGAAGATCGAAGACAGCAGCAGTAGAAGAGTAGAAGTGAACCAACACTTGAACAGCT 1061
 QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
 DB 1062 CTCAGATACAGATATAGATTTGAAGAGTGTAGAAAGTAATTTGAATCAGGTTCTCAC 1121
 QY 361 ThrHisGluAsnGluAsnTyroLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380
 DB 1122 ACTCATGAAATGAAATTTATCTTACATGAAATTCATGTTGAAAAGGAAATTCGCC 1181
 QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyroGlnGluLysGluAsnLysTyr 400
 DB 1182 ATGCTAAACTGGAATAGCCACACTGAAACACCAATACCAGGAAAGGAAATAAATAC 1241
 QY 401 PheGluAspIleLysIleLeuLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
 DB 1242 TTTGAGCATTAAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATGACCTAAACCTG 1301
 QY 421 LysGluLysSerLeuThrLysArgAlaSerGlnTyroSerGlyGlnLysValLeuIle 440
 DB 1302 AAAGAGAAATCAATTAATAAGGGCACTCAATATATAGTGGCAGCTTAAAGTCTGATA 1361
 QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGlnAspLysGluLeuGlu 460
 DB 1362 GCTGAGAACACAAATGCTCACTTCTAAATTAAGGAAAGAAACAAAGACAAAGAAATCTAGAG 1421
 QY 461 AlaGluIleGluSerHisIleProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
 DB 1422 GCAGAAATTAATCACCACCTCTAGACCTGCTTCTGCTGTACAGACCATGATCAAT 1481
 QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
 DB 1482 GTGACATCAAGAAAAAGTCAAGAACCTGCTTCCCATTCAGAGGATGCTGTTTTCGAA 1541
 QY 501 ArgLysMetAsnValAspValSerSerThrAspIle 512
 DB 1542 AGAAAAATGAATGTTGATGTAGTAGTACCGATATA 1577

RESULT 2
 ABT33272
 ID ABT33272 standard; DNA; 4047 BP.
 XX
 AC ABT33272;
 XX
 DT 15-MAY-2003 (first entry)
 XX
 DE Human tumour-related DNA sequence - SEQ ID No 566.
 XX

KW Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;
XW tumour; breast cancer; cancer; immune response stimulation.
XX Homo sapiens.
XX WO200283956-A1.
XX 24-OCT-2002.
XX 15-APR-2002; 2002WO-US012378.
XX 13-APR-2001; 2001US-00834759.
XX 07-DEC-2001; 2001US-00007805.
XX 13-FEB-2002; 2002US-00076622.
XX (CORI-) CORIXA CORP.
XX Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;
PI Mitcham JL, Xu J, Harlocker SL, Repler WT, Henderson RA, Fanger GR;
PI Vedvick TS, McNeill PD, Durham M;
XX WPI; 2003-103376/09.
XX New polypeptide and polynucleotide useful for stimulating and/or
PT expanding T cells specific for a tumor protein and treating breast
PT cancer.
XX Example 12; Page 346-347; 375pp; English.
XX The invention comprises a method of stimulating and/or expanding T cells
CC specific for a tumor protein. The invention further comprises human
CC nucleic acids and proteins that are associated with tumours (e.g. breast
CC cancer). The method and sequences of the invention are useful for
CC stimulating and/or expanding T cells specific for a tumor protein,
CC detecting the presence of cancer, stimulating an immune response in a
CC patient and treating breast cancer. The present DNA sequence represents a
CC human tumour-related DNA sequence
XX
SQ Sequence 4047 BP; 1563 A; 716 C; 850 G; 918 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,66e-195 Length: 4047
Score: 2589.00 Matches: 510
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.62% Indels: 0
DB: 7 Gaps: 0

US-09-451-739H-16 (1-512) x ABT33272 (1-4047)

QY 1 MetLysValSerIleProThrLysAlaLeuGluMetMetGlnThrPheLysAla 20
Db 2053 ATGAAAGTTTCTATTCCAACTTAAGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCA 2112
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 2113 GAGCTCCGAGAGCCATCTGCTTCGAGCCTGCCATTGAATGCAAAAGTCTGTCCA 2172
QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLysLeuProSer 60
Db 2173 AATAAGCCTTGGAAATTCAGAAATGAACAAACATTGAGAGCAGATGAGATCTCCCATCA 2232
QY 61 GluSerLysGlnLysAspTyrGluLysSerTyrPheSerGlnSerGluLysLeuThr 80
Db 2233 GAATCCCAACAAAGAGCTATGAAGAAGTTCTTGGGATTCGAGAGTCTCTGTGAGACT 2292
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysAspLysIle 100
Db 2293 GTTTTCAGAGAGGATGTGTGTTTACCACCAAGCTACACATCAAAAGAAATAGATAAATA 2352
QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 2353 AATGAAATTTAGAGAGAGTCTCTCTGAATATGATGGTTTCTGAGAGGCTCCCTGCGAATG 2412

QY 121 LysValSerIleProThrLysAlaLeuGluMetMetGlnThrPheLysAlaGlu 140
Db 2413 AAAAGTTTCTATTCCAACTTAAGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAG 2472
QY 141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 2473 CTTCCCGAGAGCCATCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCTCAAT 2532
QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2533 AAAGCCTTGGAAATTCAGAAATGAACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAA 2592
QY 181 SerLysGlnLysValGluGluAsnSerTyrPheSerGlnSerLeuArgGluThrVal 200
Db 2593 TCAAAACAAAGAGGTTGAGAAATTTCTTGGATTCTTGAGAGTCTCCGTGAGACTGTT 2652
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2653 TCACAGAGGATGTGTGTACCAAGGCTACACATCAAAAGAAATGGAATAAATAAGT 2712
QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
Db 2713 GGAATTTAGAGATTCACTAGCCTATCAAAATCTTGGATACAGTTCATCTTGTGAA 2772
QY 241 ArgAlaArgGluLysGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2773 AGAGCAAGGAACTTCAAAAGATCACTGTGAACACGTACAGGAAAAATGGAACAAATG 2832
QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280
Db 2833 AAAAGAGTTTCTGTTACTGAAAAGAACTGTGAGAACAAAGAAATATAATCACAG 2892
QY 281 LeuGluAsnGlnLysValLysTyrGluGlnGluLysCysSerValArgLeuThrLeuAsn 300
Db 2893 TTACAGAACCAAAAGTTAAATGGAAACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2952
QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2953 CAAGAAGAGAGAGAGAGAAATGCCGATATTAATGAATAAATTAGGAGAAATTA 3012
QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluAla 340
Db 3013 GGAAGATCGAAGAGCAGCATAGGAAAGAGTTAGAACTGAAACAACTTGAACAGCT 3072
QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 3073 CTCGAATACAGATATAGAAATTCAGAGTGTAGAAAGTAAATTTGAATCAGTTTCTCAC 3132
QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLysLeu 380
Db 3133 ACTCATGAATGAATTAATCTCTTACATGAATTTGCAATGTTGAAAAAGAAATGTC 3192
QY 381 MetLeuLysLeuGluLysAlaThrLeuLysHisGlnTyrGlnGlnLysGluAsnLysTyr 400
Db 3193 ATGCTAAACTGGAATAGCCACACTGAAACACCAATACCAAGAAAGGAAATAAATAC 3252
QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 3253 TTTGAGGACATTAGATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTG 3312
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuLys 440
Db 3313 AAAGAGGAATCATTAACCTAAAGGAGCATCTCAATATATAGTGGGAGCTTAAAGTTCTGATA 3372
QY 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluLysLeuGlu 460
Db 3373 GCTGAGAACACATGCTCCTTCTAAATTTGAAGAAACAAACAGCAAGAAATATACTAGAG 3432
QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 3433 GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGCTGTACAGAGCATTGATCAAT 3492

QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
 Db 3493 GTGACATCAAGAAAAAGTCAAGACCTGCTTCCACATTCGAGGAGATGCTGTTTGCAA 3552
 QY 501 ArgLysMetAsnValAspValSerSerThr 510
 Db 3553 AGAAAAATGAATGTTGATGTAGTAGTACG 3582

RESULT 3

ABT07694

ID ABT07694 standard; DNA; 4458 BP.

XX AC ABT07694;

XX DT 14-NOV-2002 (first entry)

XX DE Breast cancer-associated gene sequence 2.

XX KW Gene; ds; breast cancer; breast cancer-associated gene sequence;

XX KW drug development; pharmacogenetics; biosensor development.

XX OS Unidentified.

XX XX

XX PN W0200259377-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-05002242.

XX PR 24-JAN-2001; 2001US-0263965P.

XX PR 02-FEB-2001; 2001US-0265928P.

XX PR 09-APR-2001; 2001US-00829472.

XX PR 03-APR-2001; 2001US-0282698P.

XX PR 04-MAY-2001; 2001US-0288590P.

XX PR 29-MAY-2001; 2001US-0294443P.

XX XX

XX PA (BOSB-) EOS BIOTECHNOLOGY INC.

XX XX

XX PI Mack DH, Gish KC, Afar D;

XX XX

XX DR WFI; 2002-583738/62.

XX DR N-PSDB; ABJ05537.

XX XX

XX PT Detecting a breast cancer-associated transcript in a patient's cell,

XX PT useful for diagnosing breast cancer, comprises contacting a biological

XX PT sample with a polynucleotide that selectively hybridizes with breast

XX PT cancer nucleic acids.

XX XX

XX PS Claim 9; Page 347-348; 414pp; English.

XX XX

XX CC The invention comprises a method of detecting a breast cancer-associated

XX CC transcript in a cell from a patient. The method of the invention involves

XX CC contacting a biological sample from the patient with a nucleotide that

XX CC hybridizes to one of the 69 breast cancer-associated gene sequences shown

XX CC in the specification. The method of the invention is useful in the

XX CC diagnosis or prognosis of breast cancer, and for detecting genes that are

XX CC up or down-regulated in breast cancer cells. Genes identified by the

XX CC method of the invention can be used in diagnostic purposes and also as

XX CC targets for screening for therapeutic compounds that modulate breast

XX CC cancer (e.g. hormones or antibodies). Identification of genes that are

XX CC over or under expressed in breast cancer can additionally provide high-

XX CC resolution, high-sensitivity datasets which can be used in the areas of

XX CC diagnostics, therapeutics, drug development, pharmacogenetics, protein

XX CC structure and biosensor development. DNA sequences ABT07693 - ABT07761

XX CC represent the 69 breast cancer-associated gene sequences of the invention

XX XX

XX SQ Sequence 4458 BP; 1698 A; 812 C; 931 G; 1017 T; 0 U; 0 Other;

XX XX

XX Alignment Scores:

XX Pred. No.: 1.86e-195 Length: 4458

XX Score: 2589.00 Matches: 510

XX Percent Similarity: 100.00% Conservativity: 0

XX Best Local Similarity: 100.00% Mismatches: 0

Query Match:

DB: 99.62% Indels: 0

Gaps: 6

US-09-451-739H-16 (1-512) x ABT07694 (1-4458)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
 Db 2128 ATGAAAGTTTCTATTCCAACTTAAAGCCTTGAATTTGATGGACATGCAAACTTTTCAAGCA 2187
 QY 21 GluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
 Db 2188 GAGCCTCCCGAAGGCCATCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCOA 2247
 QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
 Db 2248 AATAAAGCCTTGGAAATGAAGATGAACAACATTGAGACGATGAGATATCCCATCA 2307
 QY 61 GluSerLysGlnLysAspTyrGluLysSerSerTrpAspSerGluSerLeuCysGluThr 80
 Db 2308 GAATCCAAACAAAGGACTATGAAGAAAGTTCTTGGGATTCGAGAGTCTCTGTGAGACT 2367
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
 Db 2368 GTTTCACAGAAGGATGTGTGTTTACCAGGCTACACATCAAAAGAAATAGATAAATA 2427
 QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
 Db 2428 AATGGAATAATTAGAAGAGTCTCTCTGATATGATGCTTTTCTGAAGGCTCCCTCGAGAATG 2487
 QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
 Db 2488 AAAGTTTCTATTCCAACTTAAAGCCTTGAATTTGATGGACATGCAAACTTTTCAAGCAGAG 2547
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
 Db 2548 CCTCCGGAAGGCCATCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAAT 2607
 QY 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
 Db 2608 AAAGCCTTGGAAATGAAGATGAACAACATTGAGACGATGAGATGTTCCTTCAGAA 2667
 QY 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
 Db 2668 TCAAAACAAAGAGGTTTGAAGAAATTTCTTGGGATTCGAGAGTCTCCGTGAGACTGTT 2727
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
 Db 2728 TCACAGAAGGATGTGTGTACCCAGGCTACACATCAAAAGAAATGGATTAATAGT 2787
 QY 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240
 Db 2788 GGAATAATTAGAAGATTTCAACTAGCCTATCAAAAATCTTGGATACAGTTTCAATTTGTGAA 2847
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
 Db 2848 AGAGCAAGGGAATTCAAAAGATCACTGTGACACAGGTACAGAAAATGGACAAATG 2907
 QY 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysSerGluIleLysSerGln 280
 Db 2908 AAAAAGAGATTTTGTGTACTGAAAAGAAACTGTCTCAGAGCAAAAGAAATAAATCACAG 2967
 QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
 Db 2968 TTAGAGAACCCAAAAGTTTAATGGACACAGAGCTCTGCACTGTGAGATGACTTTAAAC 3027
 QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGlnLysIleArgGluGluLeu 320
 Db 3028 CAAGAAGAGAGAGAGAGAAATGCCGATATTAATGAAAATAATTTAGGAGAAATTA 3087
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGlnAla 340
 Db 3088 GGAAGAAATCGAGAGAGCAGCAGTATGAGAAAGAGTTAGAACTGAAACAACTTGGACAGGCT 3147

QY 341 LeuArgileGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
 Db 3148 CTGAGATACAGATATAGAAATTTGAAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCAC 3207
 QY 361 ThrHisGluAsnGlnAsnIleLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
 Db 3208 ACTCATGAAATGAAATATATCTTACATGAAATTTGATTTGAAAGGAAATTTGCC 3267
 QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
 Db 3268 ATGCTAAATCTGGAATAGCCACCTGAAACCAATACCGAGAAAGGAAATTAATATAC 3327
 QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
 Db 3328 TTTGAGGACATTAAATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTG 3387
 QY 421 LysGluGluSerLeuThrLysAlaSerGlnTyrSerGlnLysValLeuIle 440
 Db 3388 AAGAGGAAATCATTAATTAAGGGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 3447
 QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
 Db 3448 GCTGAGAACACAATGCTCACTTCTAAATTTGAAGGAAACCAAGACAAAGAAATACTAGAG 3507
 QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
 Db 3508 GCGAAATTTGATCACCACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAAT 3567
 QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
 Db 3568 GTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTCGAGGAGATGCTTTGTTCGAA 3627
 QY 501 ArgLysMetAsnValAspValSerSerThr 510
 Db 3628 AGAAAAATGATGTTGATGAGTAGTAGC 3657
 RESULT 4
 ABT33271
 ID ABT33271 standard; DNA; 4458 BP.
 AC ABT33271;
 XX
 DT 15-MAY-2003 (first entry)
 XX
 DE Human tumour-related DNA sequence - SEQ ID No 564.
 XX
 KW Human; ss; vaccine; gene therapy; T cell stimulation; T cell expansion;
 KW tumour; breast cancer; cancer; immune response stimulation; PCR; primer.
 XX
 OS Homo sapiens.
 XX
 PN W0200283956-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 15-APR-2002; 2002WO-US012378.
 XX
 PR 13-APR-2001; 2001US-00834759.
 PR 07-DEC-2001; 2001US-00007805.
 PR 13-FEB-2002; 2002US-00076522.
 XX
 XX (CORI-) CORIXA CORP.
 PA
 XX Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;
 PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;
 PI Vedvick TS, McNeill PD, Durham M,
 XX WPI; 2003-103376/09.
 DR
 XX New polypeptide and polynucleotide useful for stimulating and/or
 PT expanding T cells specific for a tumor protein and treating breast
 PT cancer.

PS Example 9; Page 340-341; 375pp; English.

CC The invention comprises a method of stimulating and/or expanding T cells
 CC specific for a tumour protein. The invention further comprises human
 CC nucleic acids and proteins that are associated with tumours (e.g. breast
 CC cancer). The method and sequences of the invention are useful for
 CC stimulating and/or expanding T cells specific for a tumour protein,
 CC detecting the presence of cancer, stimulating an immune response in a
 CC patient and treating breast cancer. The present DNA sequence represents a
 CC human tumour-related PCR primer
 XX

SQ Sequence 4458 BP; 1698 A; 812 C; 931 G; 1017 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1-866-195 Length: 4458
 Score: 2589.00 Matches: 510
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.62% Indels: 0
 DB: 7 Gaps: 0

US-09-451-739H-16 (1-512) x ABT33271 (1-4458)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
 Db 2128 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCCAACTTTTCAAGCA 2187
 QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
 Db 2188 GAGCCTCCCGAGAGACCCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCTCA 2247
 QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
 Db 2248 AATAAGGCTTGTGAATTTGAAGATGAACAAACATTTGAGAGCAGATGAGATCTCCCTCA 2307
 QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80
 Db 2308 GAATCCAAACAAAGAGCTATGAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACT 2367
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
 Db 2368 GTTTCACAGAGAGATGTGTGTTTACCCAAAGGCTACACATCAAAAGAAATAGATAAAATA 2427
 QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
 Db 2428 AATGGAAATTTAGAGAGTCTCTGATAATGATGTTTCTGGAAGGCTCCCTGCAGAAATG 2487
 QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
 Db 2488 AAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCAAACTTTTCAAGCAGAG 2547
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
 Db 2548 CCTCCCGAGAGACCCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCTCAAT 2607
 QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
 Db 2608 AAGCCTTGTGAATTTGAAGATGAACAAACATTTGAGAGCAGATCAGATGTTTCCCTTCGAA 2667
 QY 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
 Db 2668 TCAAAAACAAAGAGAGTTGAAGAAATTTCTGGGATTTCTGAGAGTCTCCCTGAGACTGTT 2727
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
 Db 2728 TCACAGAGAGATGTGTGTACCCAGGCTACACATCAAAAGAAATGGAATAAATTAAGT 2787
 QY 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240
 Db 2788 GGAAATTTAGAGATTTCACTAGCCTATCAAAATTTTGGATACAGTTTCACTTCTTGTGAA 2847
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260

Db 2848 AGACGAGGGAAGCTTCAAAAGATCACTGTGAACACGCTACAGGAAAATGGACAAATG 2907
 Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLeuLysSerGln 280
 Db 2908 AAAAAGAGTTTGTGTACTGAAAGAAAGAACTGTCAAGACGAAAGAAATATAATCAAG 2967
 Qy 281 LeuGluAsnGlnLysValLysTTPGluGlnGluLeuLysCysValArgLeuThrLeuAsn 300
 Db 2968 TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 3027
 Qy 301 GluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluLeu 320
 Db 3028 CAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3087
 Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluAla 340
 Db 3088 GGAAGATCAAGAGCAGCAGTAGCAAGAGAGTTAGAGTGAACAACAACACTTGAACAGGCT 3147
 Qy 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
 Db 3148 CTGAGATACAGATATAGATTTGAAGAGTGTAGAAAGTATTTGAATCAGATTCTTCAC 3207
 Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
 Db 3208 ACTCATGAAATGAAATATCTCTTACATGAAATTCATGTTGAAAAGGAAATTCGCC 3267
 Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
 Db 3268 ATGCTAAATCGAATAGCCACCTGAAACACCATACCCAGAAAGGAAAGAAATTAATAC 3327
 Qy 401 PheGluAspIleLysLysLysLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
 Db 3328 TTTGAGGACATTAAAGATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTG 3387
 Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
 Db 3388 AAGAGGAATCATTAATAAGGGCATCTCAATATAGTGGCCACTTAAGTCTGATA 3447
 Qy 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluIleLeuGlu 460
 Db 3448 GCTGAGAACACAATGCTCACTTCTTAATTTGAAGGAAACACAGACAAAGAAATACTAGAG 3507
 Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
 Db 3508 GCAGAAATTTGAATCAACACCTCTAGACTGGCTTCTGCTGTACAGACCATGATCAAT 3567
 Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
 Db 3568 GTGACATCAAGAAAGAGTCAGAAACCTGCTTTCCACATTCGAGGAGATGCTTGTTCGAA 3627
 Qy 501 ArgLysMetAsnValAspValSerSerThr 510
 Db 3628 AGAAATGAATGTTGATGTGACTAGTACG 3657
 RESULT 5
 ACCS0246
 ID ACCS0246 standard; cDNA; 4458 BP.
 AC ACCS0246;
 XX ACCS0246;
 XX ACCS0246;
 DT 12-JUN-2003 (first entry)
 DE Breast cancer associated cDNA sequence SEQ ID NO:333.
 XX Human; breast cancer; cytostatic; gene therapy; gene; ss.
 KW Homo sapiens.
 OS Homo sapiens.
 XX WO2003004989-A2.
 XX 16-JAN-2003.
 PD 21-JUN-2002; 2002WO-US019669.
 PF

XX 21-JUN-2001; 2001US-0299887P.
 PR 27-JUN-2001; 2001US-0301572P.
 PR 18-JUL-2001; 2001US-0306501P.
 PR 25-SEP-2001; 2001US-0325002P.
 PR 05-MAR-2002; 2002US-0362585P.
 PR 14-MAY-2002; 2002US-0380391P.
 XX (MILL-) MILLENIUM PHARM INC.
 PA
 XX Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S,
 PI Mericms M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
 PI East RC, Hortobagyi GN, Fuzsai L, Meric F, Sahin A, Mills GB;
 XX WPI; 2003-210381/20.
 DR P-PSDB; ABR47548.
 XX
 PT Breast cancer diagnosis or treatment by comparing the level of expression
 PT of a marker in a patient sample with that in the control non-breast
 PT cancer sample.
 XX
 PS Claim 1; SEQ ID NO 333; 128pp; English.
 CC The present invention describes a method for assessing whether a patient
 CC is afflicted with breast cancer. The method comprises comparing the level
 CC of expression of a marker (gene/polypeptide see ACCS0076 to ACCS0334 and
 CC ABR47385 to ABR47632) in a patient sample and the normal level of
 CC expression of the marker in a control non-breast cancer sample, where a
 CC significant increase in the level of expression of the marker in the
 CC patient sample and the normal level is an indication that the patient is
 CC afflicted with breast cancer. The breast cancer associated sequences from
 CC the present invention have cytostatic activities and can be used in gene
 CC therapy. The method is useful for diagnosing and treating breast cancer.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences
 XX
 SQ Sequence 4458 BP; 1698 A; 812 C; 931 G; 1017 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,86e-195 Length: 4458
 Score: 2589.00 Matches: 510
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.62% Indels: 0
 DB: 7 Gaps: 0
 US-09-451-739H-16 (1-512) x ACCS0246 (1-4458)
 Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
 Db 2128 ATGAAAGTTTCTATTCCACTTAAGCCTTAGAATTGATGACATGCAAACTTTCAAGCA 2187
 Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
 Db 2188 GAGCCTCCCGAAGAGCCATCTGCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTCCA 2247
 Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
 Db 2248 AATAAGCCTTGGAAATGAAGAATGAACAACATTCAGACGACATGATCTCCCATCA 2307
 Qy 61 GluSerLysGlnLysAspTyrGluLysSerSerThrAspSerGluSerLeuGluThr 80
 Db 2308 GAATCAACAAAGAGGACTATGAAGAAGTTCTGGGATTCTGAGAGTCTCTGTGAGACT 2367
 Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
 Db 2368 GTTTCACAGAAGGATGTGTGTTTACCCAGGCTACACATCAAAAGAAATAGATAAATA 2427
 Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspClyPheLeuLysAlaProCysArgMet 120
 Db 2428 AATGGAATAATTAGAAGAGTCTCTGTAATGATGTTTCTGGAAGGCTCCCTCGAGATG 2487

121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
 2488 AAGTTTCTATTCAACTAAGGCTTAGAATTGATGACATGCAAACTTTCAAGCAGAG 2547
 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
 2548 CCTCCGAGAGCCATCTGCTTCGAGCCGCCATTGAAATGCAAAAGTCTGTTCAAAT 2607
 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
 2608 AAGCCCTTGGAAATTGAAGATGAACAAACATTGAGAGCAGATGATGTTCCCTTCAGAA 2667
 181 SerLysGlnLysLysValGluGluLysSerTrpAspSerGluSerLeuArgGluThrVal 200
 2668 TCAAAACAAAAGAGGTGAAGAAATTCCTGGGATTCAGAGCTCCCGTGAGACGTT 2727
 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
 2728 TCACAGAAGGATGTGTGTGATCCCAAGGCTACACATCAAAAGAAATGGATAAATAAGT 2787
 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240
 2788 GGAATATTAGAAGATTCACATAGGCTATCAAAATCTTGGATACAGTTCATCTTGTGAA 2847
 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
 2848 AGACGAGGAGACTTCAAAAGATCACTGTGAACACCTACAGAAAAATGGACAAATG 2907
 261 LysLysLysPheCysValLeuLysLysLysLysSerGluAlaLysGluLysLysSerGln 280
 2908 AAAAAGAAAGTTTGTGTACTGAAAAAGAACTGTGAGAGCAAGAAAGAAATAAATCAAG 2967
 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
 2968 TTAGAGAACCAAAAGATTAAATGGGACACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 3027
 301 GlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysLysLysLysLysLys 320
 3028 CAAGAAGAAGAGAGAGAGAAATGCCGATATATTAATGAAAAATTTAGGGAAGAATTA 3087
 321 GlyArgIleGluGlnHisArgLysGluLeuValLysGlnLeuGluGlnAla 340
 3088 GGAAGAATCGAAGAGCAGATAGGAAGAGTTAGAAAGTGAACACAACTTGAACAGGCT 3147
 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
 3148 CTCAGAAATCAAGATATAGATTGAAGAGCTGTAGAAAGTAATTTCAATCAGGCTTTCTCAC 3207
 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysLysLysLys 380
 3208 ACTCATGAAATGAAATTTATCTCTTACATGAAATTTGATGTTGAAAAGGAAATTCGC 3267
 381 MetLeuLysLeuGluLysAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
 3268 ATGCTAAACTGGAAATAGCCACCTGAAACACCAATACAGGAAAGGAAATTAATATAC 3327
 401 PheGluAspIleLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 420
 3328 TTTGAGGACATTAAAGATTAAAGAAAGAAATGCTGGAATCTCAGATGACCTTAAACATG 3387
 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
 3388 AAAGAGGAATCATTAATAAGAGGATCTCATATATAGTGGCAGCTTAAAGTTCTGATA 3447
 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysLysLysLysLys 460
 3448 GCTGAGAACCAATGCTCACTTCTAAATTAAGGAAAGAAACAGACAAAGAAATATCTAGAG 3507
 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
 3508 GCAGAAATTGAATCAACCACTCTAGACTGCTTCTGCTGTACAGACCATGATCAATTT 3567
 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500

3568 GTGACATCAGAAAAAGTCAAGAACCTGCTTCCACATTGAGAGATGCTTGTTCGAA 3627
 501 ArgLysMetAsnValAspValSerSerThr 510
 3628 AGAAAAATGAATGTGTGATGTGAGTAGTACG 3657
 RESULT 6
 AAS47421
 ID AAS47421 standard; cDNA; 3288 BP.
 AC AAS47421;
 XX 18-DEC-2001 (first entry)
 DT
 XX Human cDNA encoding breast cancer protein B726P fusion protein #1.
 DE
 XX Human; ss; breast cancer protein; tumour; cancer; cytostatic;
 KW gene therapy.
 XX Homo sapiens.
 OS
 PN WO200179286-A2.
 XX 25-OCT-2001.
 PD
 XX 12-APR-2001; 2001WO-US012164.
 PF
 XX 17-APR-2000; 2000US-00551621.
 PR 08-JUN-2000; 2000US-00590751.
 PR 22-JUN-2000; 2000US-00604287.
 PR 20-JUL-2000; 2000US-00620405.
 XX
 PA (CORI-) CORIXA CORP.
 PI Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
 XX WPI; 2001-611721/70.
 DR P-PSDB; AAU33357.
 XX
 PT Breast Tumor Proteins and nucleic acids useful for the prevention,
 PT diagnosis and treatment of breast cancer.
 PS Claim 37; Page 290-291; 297pp; English.
 XX The invention relates to isolated breast tumour proteins and nucleic
 CC acids that encode them, including immunogenic fragments of the proteins.
 CC Also included are expression vectors expressing the proteins, transformed
 CC cells and antibodies raised against the proteins or an antigen presenting
 CC cell expressing the protein. The proteins and nucleic acids may be used
 CC in the prevention, diagnosis and treatment of diseases associated with
 CC inappropriate breast tumour protein expression, i.e. breast tumours and
 CC breast cancer e.g. by gene therapy. The nucleic acids and their
 CC complements may also be used as DNA probes in diagnostic assays to detect
 CC and quantitate the presence of similar nucleic acids in samples, and
 CC therefore which patients may be in need of restorative therapy. The
 CC proteins, nucleic acids and antibodies may be used in assays to identify
 CC modulators (e.g. antagonists) of breast tumour protein expression and
 CC activity. The antibodies and antagonists may also be used to down
 CC regulate expression and activity. The antibodies may also be used as
 CC diagnostic agents for detecting the presence of the proteins in samples
 CC (e.g. by enzyme linked immunosorbent assay (ELISA)) and in other immuno-
 CC purification diagnostic techniques. The present sequence is a cDNA from a
 CC breast tumour cDNA library isolated by subtractive hybridisation against
 CC a normal breast cDNA library and encodes a breast tumour protein of the
 CC invention
 XX
 SQ Sequence 3288 BP; 1293 A; 564 C; 664 G; 761 T; 0 U; 6 Other;
 Alignment Scores:
 Pred. No.: 9.71e-195 Length: 3288
 Score: 2578.00 Matches: 508
 Percent Similarity: 99.61% Conservative: 0

Best Local Similarity: 99.61% Mismatches: 2		
Query Match: 99.19% Indels: 0		
DB: 4 Gaps: 0		
US-09-451-739H-16 (1-512) x AAS47421 (1-3288)		
QY	1	MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
DB	1291	ATGAAGATTTCATTCCAACTAAGCCTTAGAATTGATGGACATGCCAACTTTCAAGCA 1350
QY	21	GluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
DB	1351	GAGCCTCCCGAAGAGCCATCTCCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTC 1410
QY	41	AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
DB	1411	AATTAAGCCTTGGAAATGAAGAAATGAACAACATTGAGAGCAGATGATCTCCCATCA 1470
QY	61	GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80
DB	1471	GAATCCAAACAAAGAGACTATGAAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACT 1530
QY	81	ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
DB	1531	GTTTCACAGAGGATGTGTGTTTACCCAGGCTRCRCATCAAAAGAAATAGATAAATA 1590
QY	101	AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
DB	1591	AATGGAAATTAGAAGAGTCTCTGATAATGATGGTTTCTGAAGCTCCCTGAGAAATG 1650
QY	121	LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
DB	1651	AAAGTTTCTATTCCAACTTAAGCCTTAGAATTGATGGACATGCCAACTTTCAAGCAGAG 1710
QY	141	ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
DB	1711	CCTCCCGAAGAGCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAAT 1770
QY	161	LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
DB	1771	AAAGCCTTGGAAATGAAGATGAACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAA 1830
QY	181	SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
DB	1831	TCAAAACAAAGAGAGTGTGAAGAAATCTTGGGATTTCTGAGAGTCTCCGTGAGACTGTT 1890
QY	201	SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
DB	1891	TCACAGAGGATGTGTGTGTACCCAGGCTACACATCAAAAGAAATGATGATTAATAAGT 1950
QY	221	GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
DB	1951	GGAAAAATTAGAAGATTCAACTAGCCTATCAAAAAATCTTGGATACAGTTCATTCTTGAA 2010
QY	241	ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
DB	2011	AGAGCAAGGGAATCTCAAAAAATCACTGTGAAACACGTACAGGAAAAATGGNACAAATG 2070
QY	261	LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280
DB	2071	AAAAAGAGTTTGTGTACTGAAAGAAAGAACTGTGAGAGCAAAAGAAATAAATACAG 2130
QY	281	LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
DB	2131	TTAGAGAACCAAAAGATTAAATGGGAACAAGAGCTCTGCAAGTGTGAGATTTGATTAAC 2190
QY	301	GlnGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
DB	2191	CAAGAGAGAGAGAGAGAAATGCCGATATATTAAATGAAAAAATTAGGAGAAATTA 2250
QY	321	GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
DB	2251	GGAAAGATCGAAGAGCAGCATAGGAAGAGTTAGAGTGAACAACTTGACAGAGGCT 2310
RESULT 7		
ABS64022		
ID	ABS64022 standard; DNA; 3288 BP.	
XX	ABS64022;	
XX	15-NOV-2002 (first entry)	
XX	Human breast tumour polynucleotide #471.	
DE	Human; breast tumour protein; gene; ds; breast cancer; cytostatic;	
KW	vaccine.	
XX	Homo sapiens.	
OS	US2002085998-A1.	
XX	04-JUL-2002.	
XX	13-APR-2001; 2001US-00834759.	
XX	28-DEC-1998; 98US-00222575.	
XX	02-APR-1999; 99US-00285480.	
XX	23-JUN-1999; 99US-00339338.	
XX	02-SEP-1999; 99US-00389681.	
XX	03-NOV-1999; 99US-00433826.	
XX	17-APR-2000; 2000US-00551621.	
XX	08-JUN-2000; 2000US-00590751.	
XX	22-JUN-2000; 2000US-00604287.	
XX	20-JUL-2000; 2000US-00620405.	
XX	(CORI-) CORIXA CORP.	
XX	Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;	
XX	Henderson RA;	

XX Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;
 KW tumour; breast cancer; cancer; immune response stimulation.
 XX Homo sapiens.
 XX W0200283956-A1.
 XX 24-OCT-2002.
 XX 15-APR-2002; 2002WO-US012378.
 XX 13-APR-2001; 2001US-00834759.
 PR 07-DEC-2001; 2001US-00007805.
 PR 13-FEB-2002; 2002US-00076622.
 XX (CORI-) CORIXA CORP.
 XX Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;
 PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;
 PI Vedvick TS, McNeill PD, Durham M;
 XX WI; 2003-103376/09.
 XX New polypeptide and polynucleotide useful for stimulating and/or
 PT expanding T cells specific for a tumor protein and treating breast
 PT cancer.
 XX Disclosure; Page 307-308; 375pp; English.
 XX The invention comprises a method of stimulating and/or expanding T cells
 CC specific for a tumor protein. The invention further comprises human
 CC nucleic acids and proteins that are associated with tumours (e.g. breast
 CC cancer). The method and sequences of the invention are useful for
 CC stimulating and/or expanding T cells specific for a tumour protein,
 CC detecting the presence of cancer, stimulating an immune response in a
 CC patient and treating breast cancer. The present DNA sequence represents a
 CC human tumour-related DNA sequence
 XX
 SQ Sequence 3288 BP; 1293 A; 564 C; 664 G; 761 T; 0 U; 6 Other;

Alignment Scores:
 Pred. No.: 9,71e-195 Length: 3288
 Score: 2578.00 Matches: 508
 Percent Similarity: 99.61% Conservative: 0
 Best Local Similarity: 99.61% Mismatches: 2
 Query Match: 99.19% Indels: 0
 DB: 7 Gaps: 0

US-09-451-739H-16 (1-512) x ABT33234 (1-3288)

QY 1 MetLysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAla 20
 DB 1291 ATGAAGTTTCTATTCACAACTTAAGCCCTTAGATTGATGGACATGCCAACTTTCAGGCA 1350
 QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
 DB 1351 GAGCTCCCGAGAAGCCATCTGCCCTCGAGCCCTGCAATGAAATGCAAAAGCTCTGTCCA 1410
 QY 41 AsnLysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGluIleLeuProSer 60
 DB 1411 AATAAGCCCTTGAATTGAAGATGAACAAACATTGAGAGCAGATGAGATCTCCATCA 1470
 QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLysCysGluThr 80
 DB 1471 GAATCCAAACAAAGGACATATGAAGAAAGTCTCTGGATTCTGAGAGTCTCTGTGAGACT 1530
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
 DB 1531 GTTTCAGAGGATGTGTGTTTACCAAGGCTTCRCATCAAAAGAAATAGATATAATA 1590
 QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120

DB 1591 AATGGAATAATTAGAAGTCTCTGTATATGATGTTTCTGAAGGCTCCCTGCAGATG 1650
 QY 121 LysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAlaGlu 140
 DB 1651 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGCATCAAACTTTTCAAGCAGAG 1710
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
 DB 1711 CTTCCCGAGAAGCCATCTGCCCTTCGAGCCCTGCCATTAATGCAAAAGTCTGTCTCCAAT 1770
 QY 161 LysAlaLeuGluLysAsnGluInThrLeuArgAlaAspGlnMetPheProSerGlu 180
 DB 1771 AAGCCTTGGATTGAAGATGAACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAA 1830
 QY 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
 DB 1831 TCAAAACAAAGAGAGTGTGAAGAAATTTCTGGATTCTGAGAGTCTCCGTGAGACTGTT 1890
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
 DB 1891 TCACAGAGAGNTGTGTGTGTACCAAGCTTACACATCAAAAGAAATGGATAAAATAAGT 1950
 QY 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240
 DB 1951 CGAAAATTTAGAAGATTCAACTAGCCTATCAAAATCTTGGATTACAGTTCAATCTTGTGAA 2010
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
 DB 2011 AAGCAGAGGAACTTCAAAAGATCACTGTGAACACAGTACAGGAAATGGAAACAAATG 2070
 QY 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluIleLysSerGln 280
 DB 2071 AAAAAGAAAGTTTGTGTACTGAAAAGAAACTGTGCAGAGCAAAAGAAATAAATTCACAG 2130
 QY 281 LeuGluAsnGlnLysValLysTrpGluGlnLysCysSerValArgLeuThrLeuAsn 300
 DB 2131 TTAGAGAACCAAAAGTTTAATTTGGACACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2190
 QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
 DB 2191 CAAGAAGAAGAGAGAGAGAAATGCCGATATATTAATGAAATAATTTAGGGAAGAAATTA 2250
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
 DB 2251 GGAAGAATCGAAGACAGCATTAGGAAGAGTTAGAGTGAACAACTTTGAACAGGCT 2310
 QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
 DB 2311 CTCAGAAATCAAGATATAGAAATTTGAAGAGTGTAGAAGATAATTTGAATCAGGTTTCTCAC 2370
 QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
 DB 2371 ACTCATGAAAATGAAAATTTATCTCTTACATGAAAATTTGCATGTTGAAAAGGAAATTC 2430
 QY 381 MetLysLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
 DB 2431 ATGCTAAACTGGAAATAGCCACACTGAAACACCAATACCAGAAAAGAAAATAAATAC 2490
 QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
 DB 2491 TTTGAGGACATTAAGATTTTAAAGAAAAGATGCTGAACTTCAGATGACCCCTAAACTG 2550
 QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLysValLeuIle 440
 DB 2551 AAAGAGGAATCATTAACCTAAAGGGCATCTCAATATAGTGGGCGAGCTTAAAGTCTTGATA 2610
 QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
 DB 2611 GCTGAGAACCAATGCTCACTTCTTAATTTGAAGAAAACCAAGCAAAAGAAATACTAGAG 2670
 QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
 DB 2671 GCAGAAATTCATGATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAAT 2730

Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 2731 GTGACATCAAGAAAGTCAAGAACCTGCTTCCACATTCAGAGAGATGCTTGTTCGAA 2790

Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 2791 AGAAAAATGAATGTGTGAGTAGTACG 2820

RESULT 9
ID AAS47411 standard; cDNA; 3865 BP.
AC AAS47411;
XX

DT 18-DEC-2001 (first entry)
XX
DE Human cDNA encoding breast cancer protein B726P alternative splice form.
XX

XX Human; ss; breast cancer protein; tumour; cancer; cytostatic;
KW gene therapy.
XX

OS Homo sapiens.
XX
XX WO200179286-A2.
XX

XX 25-OCT-2001.
XX
XX 12-APR-2001; 2001WO-US012164.
XX

XX 17-APR-2000; 2000US-00551621.
PR 08-JUN-2000; 2000US-00590751.
PR 22-JUN-2000; 2000US-00604287.
PR 20-JUL-2000; 2000US-00620405.
XX

XX (CORI-) CORIXA CORP.
PA
XX

XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
PI WPI; 2001-611721/70.
XX P-PSDB; AAU33351.
DR

XX Breast Tumor Proteins and nucleic acids useful for the prevention,
PT diagnosis and treatment of breast cancer.
XX

PS Claim 1; Page 280-281; 297pp; English.
XX

XX The invention relates to isolated breast tumour proteins and nucleic
CC acids that encode them, including immunogenic fragments of the proteins.
CC Also included are expression vectors expressing the proteins, transformed
CC cells and antibodies raised against the proteins or an antigen presenting
CC cell expressing the protein. The proteins and nucleic acids may be used
CC in the prevention, diagnosis and treatment of diseases associated with
CC inappropriate breast tumour protein expression, i.e. breast tumours and
CC breast cancer e.g. by gene therapy. The nucleic acids and their
CC complements may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC proteins, nucleic acids and antibodies may be used in assays to identify
CC modulators (e.g. antagonists) of breast tumour protein expression and
CC activity. The antibodies and antagonists may also be used to down
CC regulate expression and activity. The antibodies may also be used as
CC diagnostic agents for detecting the presence of the proteins in samples
CC (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immuno-
CC purification diagnostic techniques. The present sequence is a cDNA from a
CC breast tumour cDNA library isolated by subtractive hybridisation against
CC a normal breast cDNA library and encodes a breast tumour protein of the
CC invention. The present sequence is also a splice variant
XX

SQ Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;
XX

Alignment Scores: 1.17e-194 Length: 3865
Pred. No.:

Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.99% Indels: 0
DB: 4 Gaps: 0

US-09-451-739H-16 (1-512) x AAS47411 (1-3865)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAla 20
Db 1563 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATGTATGGACATGCAAACTTTCAAGCA 1622
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1623 GAGCCTCCGAGAGCCATCTGCCTTCGAGCCTGCCTTGAATGAAATCAAAAGTCTCTTCCA 1682
Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 1683 ATAAAGCCTTGGATTTGAGATGAAACAACATTTGAGAGCAGATGAGATATCCCATCA 1742
Qy 61 GluSerLysGlnLysAspTyrGluLysSerSerTrpAspSerGluSerLeuGluThr 80
Db 1743 GAATCCAAACAAAGGACTATGAGAAAGTTCTTGGATTCTTGAGAGTCTCTGTGAGACT 1802
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
Db 1803 GTTTCACAGAGGATGTGTGTTTACCCAGGCTTCRCATCAAAAGAAATAGATAAATA 1862
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 1863 AATGGAAATTTAGAGAGTCTCTGATAATGATGGTTTCTGAGGCTCCCTGCAAGATG 1922
Qy 121 LysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAlaGlu 140
Db 1923 AAAAGTTTCTATTCCAACTAAAGCCTTAGAATGTATGGACATGCAAACTTTCAAGCAGAG 1982
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 1983 CTTCCCGAGAGGCACTCTGCCTTCGAGCCTGCCATTGAAATCAAAAGTCTGTTCCAAT 2042
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2043 AAAAGCCTTGGATTTGAAGATGAACAAACATTTGAGAGCAGATCAGATGTCTCCTTCAGAA 2102
Qy 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 2103 TCAAAACAAAGAAAGTGTGAAGAAATTTCTGGATTCTTGAGAGTCTCGGTGAGACTGT 2162
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2163 TCACAGAGGATGTGTGTACCAAGGCTACACATCAAAAGAAATGGATATAAATAGT 2222
Qy 221 GlyLysLeuGluAspSerThrSerLysLysIleLeuAspThrValHisSerCysGlu 240
Db 2223 GGAATTTAGAGATTTCACTAGCCTATCAAAATCTTGATACAGTTCATTCTTGTA 2282
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluArgThrGlyLysMetGluGlnMet 260
Db 2283 AGAGCAAGGGAACCTTCAAAAGATCACTGTGAACAACTGACAGGAAAAATGGAAACAAATG 2342
Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280
Db 2343 AAAAAGAGTTTTGTGTACTGAAAAGAAACTGTCAAGAACCAAAAGAAATAAATCACAG 2402
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGAACCAAAAGTTAAATGGGAAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2462
Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2463 CAAGAGAGAGAGAGAGAGAAATGCCGATATATTAATGAAAAAATTAGGAGAAATTA 2522
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340

Db 2523 GGAGAAATCGAAGCAGCAGTAGAAGAGATTGAGTGAACACAACTTGAACAGGCT 2582
 Qy LeuArgilleGlnAspilleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
 Db 2593 CTCAGAATACAGATATAGATTGAGAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCAC 2642
 Qy ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380
 Db 2643 ACTCATGAATAATGAATAATATCTCTTACATGAAATTCATGTTGTGAAAAGGAATTCGCC 2702
 Qy MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyrGlnGlnLysGluAsnLysTyr 400
 Db 2703 ATGTCTAAACCTGGAATATAGCCACTGAACACCAATATACCAGGAAAAGGAATAATATAC 2762
 Qy PheGluAspilleLysLysLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
 Db 2763 TTTGAGGACATTAGATTTTAAAGAAAAGAAAGTGTGACTTCAGATGACCTTAAACTG 2822
 Qy LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuLeu 440
 Db 2823 AAAGAGGAATCAITTAACCTAAAGGGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 2882
 Qy AlaGluAsnThrMetLeuThrSerLysLeuLysGlnAspLysGluLysLeuGlu 460
 Db 2883 GCTGAGAACACATGCTCACTTCTTAATTCAGAGAAAACACAGACAAAGAAATACTAGAG 2942
 Qy AlaGluLeuGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisGlnLeu 480
 Db 2943 GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAAT 3002
 Qy ValThrSerArgLysSerGlnGluProAlaPheHisLeuAlaGlyAspAlaCysLeuGln 500
 Db 3003 CTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATTCAGAGAGATGCTTTTGCAA 3062
 Qy ArgLysMetAsnValAspValSerSerThr 510
 Db 3063 AGAAAAATGAATGATGTAGTAGTAGC 3092
 RESULT 10
 ID ABS64012 standard; cDNA; 3865 BP.
 XX
 AC ABS64012;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human breast tumour polynucleotide #464.
 XX
 KW Human; breast tumour protein; gene; ss; breast cancer; cytostatic;
 KW vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2002085998-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 13-APR-2001; 2001US-00834759.
 XX
 PR 28-DEC-1998; 98US-00222575.
 PR 02-APR-1999; 98US-00285480.
 PR 23-JUN-1999; 99US-00339338.
 PR 02-SEP-1999; 99US-00389681.
 PR 03-NOV-1999; 99US-00433826.
 PR 17-APR-2000; 2000US-00551621.
 PR 08-JUN-2000; 2000US-00590751.
 PR 22-JUN-2000; 2000US-00604287.
 PR 20-JUL-2000; 2000US-00620405.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
 PI

PI Henderson RA;
 XX WPI; 2002-635657/68.
 DR P-PSDB; ABG78918.
 XX
 PT Novel breast cancer polynucleotides and polypeptides encoded by the
 PT polynucleotides, useful for detecting the presence of breast cancer in a
 PT patient, and in pharmaceutical compositions, for treating breast cancer.
 XX
 XX Claim 1; Page 207-208; 247pp; English.
 XX
 CC The invention relates to an isolated breast tumour polynucleotide and the
 CC polypeptide it encodes. The polynucleotide and polypeptide are useful for
 CC detecting the presence of breast cancer in a patient, and in
 CC pharmaceutical compositions for treating breast cancer. The sequences are
 CC useful for stimulating an immune response in a patient and can therefore
 CC be used in production of vaccines. The sequences are also useful for
 CC detecting the presence of a cancer in a patient, by obtaining a
 CC biological sample from the patient, contacting the biological sample with
 CC a composition of the invention and detecting the amount of polynucleotide
 CC that hybridizes to the sample. This sequence represents a human breast
 CC tumour polynucleotide of the invention
 XX
 SQ Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;

Alignment Scores:
 Pred. No.: 1,17e-194 Length: 3865
 Score: 2578.00 Matches: 508
 Percent Similarity: 99.61% Conservative: 0
 Best Local Similarity: 99.61% Mismatches: 2
 Query Match: 99.19% Indels: 0
 DB: 6 Gaps: 0
 US-09-451-739H-16 (1-512) x ABS64012 (1-3865)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
 Db 1563 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAAGCA 1622
 Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
 Db 1623 GAGCCTCCCGAGAGAGCCATCTGCTTCGAGCGTCCATTGAATGCAAAAGTCTGTTCCTCA 1682
 Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuProSer 60
 Db 1683 AATAAGCCTTGGAAATTGAAGAAATGAACAAACATTGAGAGCAGATGAGATCTCCCATCA 1742
 Qy 61 GluSerLysGlnLysAspTyrGluLysSerSerTrpAspSerGluSerLeuLysGluThr 80
 Db 1743 GAATCCAAACAAAAGGACATATGAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACT 1802
 Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysTle 100
 Db 1803 GTTTCAGAGAGGATGTGTGTTTACCAAGGCTRCRCATCAAAAGAAANTAGATAAATA 1862
 Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
 Db 1863 AATGGAAAATTAAGAGAGTCTCTGATAATGATGTTTCTTCAAGGCTCCCTGCAGAGT 1922
 Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
 Db 1923 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAAGCAGAG 1982
 Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
 Db 1983 CTTCCCGAGAGAGCATCTGCTTCGAGCGTCCATTGAATGCAAAAGTCTGTTCCTCAAAAT 2042
 Qy 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
 Db 2043 AAAGCCTTGGAAATTGAAGAAATGAACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAA 2102
 Qy 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200

Db	2103	TCAAAACAAAGAAAGTGGTGAAGAAAATCTTGGATCTCAGAGCTCCCGTGAGACTGTT	2162	XX	Human tumour-related DNA sequence - SEQ ID No 474.
Qy	201	SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer	220	XX	Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;
Db	2163	TCACAGAGGATGTGTGTGTACCAAGGCTACACATCAAAAGAAATGGATAAAATAGT	2222	KW	tumour; breast cancer; cancer; immune response stimulation.
Qy	221	GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu	240	OS	Homo sapiens.
Db	2223	GGAAAATTGAAGATTCACTAGCTATCAAAAATCTTGGATACAGTTCTTCTGTGAA	2282	PN	WO200283956-A1.
Qy	241	ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet	260	PD	24-OCT-2002.
Db	2283	AGACCAAGGAACCTTCAAAAGATCACTGTGAACAACGTACAGAAAAATGGAAACAATG	2342	XX	15-APR-2002; 2002WO-US012378.
Qy	261	LysLysLysPheCysValLeuLysLysLysLeuSerCysGluAlaLysGluLysSerGln	280	PR	13-APR-2001; 2001US-00834759.
Db	2343	AAAAAGAGTTTCTGTACTGAAAGAAAGAACTGTCAAGACAAAGAAATATAATCACAG	2402	PR	07-DEC-2001; 2001US-00007805.
Qy	281	LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn	300	XX	13-FEB-2002; 2002US-00076622.
Db	2403	TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAAC	2462	PA	(CORI-) CORIXA CORP.
Qy	301	GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGlnLysIleArgGluGluLeu	320	XX	Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;
Db	2463	CAAGAAGAAGAGAGAGAGAAATGCCGATATATTAAATGAAAAATTTGGGAAGAAATTA	2522	PI	Mitcham JL, Xu J, Harlock SL, Hepler WT, Henderson RA, Fanger GR;
Qy	321	GlyArgIleGluGlnGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla	340	PI	Vedvick JS, McNeill PD, Durham M;
Db	2523	CGAAGATCGAAGAGCAGCATAGGAAGAGTTAGAGTGAACACAACTTGAACAGGCT	2582	XX	WPI; 2003-103376/09.
Qy	341	LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis	360	XX	New polypeptide and polynucleotide useful for stimulating and/or
Db	2583	CTCAGATACACAGATATAGAAATGAAGAGTGTAGAAAGTATTTGAATCAGGTTCTCAC	2642	PT	expanding T cells specific for a tumor protein and treating breast
Qy	361	ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla	380	CC	cancer.
Db	2643	ACTCATGAATGAAATATCTCTTACATGAAATTCGATGTTGAAAGGAATTTGCC	2702	CC	Example 1; Page 296-297; 375pp; English.
Qy	381	MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr	400	CC	The invention comprises a method of stimulating and/or expanding T cells
Db	2703	ATGCTAAACTGGAATAGCCACACTGAACACCAATACCAGGAAGAAAGGAAATAAATAC	2762	CC	specific for a tumour protein. The invention further comprises human
Qy	401	PheGluAspIleLysIleLeuLysAsnAlaGluLeuGlnMetThrLeuLysLeu	420	CC	nucleic acids and proteins that are associated with tumours (e.g. breast
Db	2763	TTTGAGGACATTAGATTTTAAAGAAAGAAATGCTGAACCTCAGATGACCTTAAACTG	2822	CC	cancer). The method and sequences of the invention are useful for
Qy	421	LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle	440	CC	stimulating and/or expanding T cells specific for a tumour protein,
Db	2823	AAAGAGGAATCATTAACTAAAGGGCATCTCAATATAGTGGGAGCTTAAAGTCTGATA	2882	CC	detecting the presence of cancer, stimulating an immune response in a
Qy	441	AlaGluAsnThrMetLeuThrSerLysLysGluLysGlnAspLysGluIleLeuGlu	460	CC	patient and treating breast cancer. The present DNA sequence represents a
Db	2883	GCTGAGAACACAACTCTCACTTCTAAATTTGAAGAAACAAAGCAAGAAAGAAATCTAGAG	2942	CC	human tumour-related DNA sequence
Qy	461	AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle	480	XX	Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;
Db	2943	GCAGAAATGTATCATCACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAATT	3002	XX	Alignment Scores:
Qy	481	ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln	500	XX	Pred. No.: 1-17e-194 Length: 3865
Db	3003	GTGACATCAAGAAAAAGTCAAGAACTGCTTTCCACATTCGAGGAGATGCTTTGTTCGA	3062	XX	Score: 2578.00 Matches: 508
Qy	501	ArgLysMetAsnValAspValSerThr	510	XX	Percent Similarity: 99.61% Conservative: 0
Db	3063	AGAAAAATGAATGTTGATGTGAGTAGTAGC	3092	XX	Best Local Similarity: 99.61% Mismatches: 2
RESULT 11				XX	Query Match: 7 Gaps: 0
ID	ABT33224			XX	US-09-451-739H-16 (1-512) x ABT33224 (1-3865)
XX	ABT33224			Qy	1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
AC	ABT33224;			Db	1563 ATGAAAGTTTCTATTCCTCAACTAAGCCTTAGAATTCATGACATGCAAACTTTCAAGCA 1622
XX	15-MAY-2003 (first entry)			Qy	21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
DT				Db	1623 GAGCTCCCGAGAAGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTCCA 1682
				Qy	41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
				Db	1683 AATAAAGCCTTGGAAATGGAAGATGAACAAACATTGAGAGCAGATGAGATATCCCATCA 1742
				Qy	61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLeuCysGluThr 80
				Db	1743 GAATCCAAACAAAGGACATATGAAGAAAGTCTTGGGATTCCTGTGAGACTCTGTGAGACT 1802
				Qy	81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
				Db	1803 GTTTCACAGAGGATGTGTCTTTACCCAGGCTTCRCATCAAAAGAAATAGATAAATA 1862

101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
1863 AATGGAATAATTAGAGAGTCTCTGATAATATGATGGTTTCTGAAGGCTCCCTGCGAAGT 1922
121 LysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAlaGlu 140
1923 AAGTTTCTATTCCATTAAAGCTTTAGAAATTTGATGACATGCAAACTTTCAAGCAGAG 1982
141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
1983 CCTCCCGAGAGGCAATCTGCTCTCGAGCTGCCATTGCAATGCATAAGTCTGTTCACAT 2042
161 LysAlaLeuGluLysLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
2043 AAGCCCTTGAATTTGAAGATGAACAAACATTCAGAGCAGATCAGATGTTCCCTTCAGAA 2102
181 SerLysGlnLysLysValGluGluAsnSerTyrAspSerGluSerLeuArgGluThrVal 200
2103 TCAAAACAAAGAAGAGTTGAAGAAATCTTGGATTCTGAGAGTCTCGTGAGACTGTT 2162
201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
2163 TCACAGAGGATGTGTGTACCAAGGCTACACATCAAAAGAAATGGAATGATTAATAGT 2222
221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
2223 GGAATAATTAGAGATTCAACTAGCTATCAAAATCTTGATACAGTTCAATCTCTGTGAA 2282
241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
2283 AGACCAAGGGAACCTTCAAAAGATCACTGTGAACAGCTACGGAAGAAATGGAACAAATG 2342
261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysLysSerGln 280
2343 AAAAGAAGTTTGTGTACTGAAAGAACTGTGAGAACCAAGAAATTAATACAG 2402
281 LeuGluAsnGlnLysValLysTyrGluGlnLeuCysSerValArgLeuThrLeuAsn 300
2403 TTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGAGTGTGAGATTGACTTTAAAC 2462
301 GlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
2463 CAAGAGNAGAGAGAGAGAGAAATGCCGATATATTAATGAAATAATAGGAAAGATTA 2522
321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnLysGluGlnAla 340
2523 GGAAGAATCGAAGAGCAGCATAGAAAGAGTTAGAGTGAACAACTTGAACAGGCT 2582
341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
2583 CTCAGATACAGATATAGATTTAGAGTGTAGAAAGTAAATTGAATCAGGTTCTCTAC 2642
361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
2643 ACTCATGAAATGAAATATCTCTTACATGAAATTTGCATGTTGAAAGAGAAATGTC 2702
381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
2703 ATGCTAAACTGGAATAGACCACTGAAACCAACATACAGGAAAGAGAAATTAATAC 2762
401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
2763 TTTGAGGACATTAGATTAAAGAAAGAAATGCTGAATCTCAGATGACCCCTAAACTG 2822
421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
2823 AAAGAGGAATCATTAACATAAAGGCACTCTCAATATAGTGGCAGCTTAAAGTTCTGATA 2882
441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
2883 GCTGAGACACAACTCTCACTTCTAAATTGAAGGAAACCAAGCAAGAAATACTAGAG 2942
461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480

2943 GCAGAAATTGAATCACACCATCTCTAGACTGGCTTCGTGTACAGCCATGATCAAT 3002
481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
3003 GTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATTGCAGGAGATGCTTTGTCGA 3062
501 ArgLysMetAsnValAspValSerSerThr 510
3063 AGAAAAATGAATGTTGATGAGTAGTAG 3092
RESULT 12
ADE44426
ID ADE44426 standard; cDNA; 3865 BP.
XX ADE44426;
AC ADE44426;
XX 29-JAN-2004 (first entry)
XX Human cDNA associated with breast cancer #464.
KW human; ss; gene; breast tumour; cancer; vaccine; T cell stimulator;
T cell expander.
XX Homo sapiens.
OS Homo sapiens.
XX US2003104366-A1.
XX 05-JUN-2003.
XX 17-APR-2000; 2000US-00551621.
XX 28-DEC-1998; 98US-00222575.
XX 02-APR-1999; 99US-00285480.
XX 23-JUN-1999; 99US-00339338.
XX 02-SEP-1999; 99US-00389681.
XX 03-NOV-1999; 99US-00433826.
XX (JIAN/) JIANG Y.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (XUJ/) XU J.
PA (HASL/) HARLOCKER S L.
XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL;
PI WPI; 2004-020270/02.
XX P-PSDB; ADE44427.
XX Novel isolated polypeptide comprising immunogenic portion of breast tumor protein or its variant, useful for formulating vaccines for inhibiting cancer development in a patient.
XX Claim 5; SEQ ID NO 474; 217pp; English.
XX The invention relates to an isolated polypeptide comprising at least an immunogenic portion of a breast tumour protein. The polynucleotide, its polypeptide, its antibody, a pharmaceutical composition comprising the fusion protein or the polynucleotide encoding it, a vaccine comprising the fusion protein or the polynucleotide encoding it, an isolated T cell population comprising T cells specific for a breast tumour protein, and a method for removing tumour cells from a biological sample is useful for inhibiting the development of a cancer in a patient. The polypeptide is useful for stimulating and/or expanding T cells specific for a breast tumour protein. Stimulating and/or expanding T cells specific for a breast tumour protein is useful for inhibiting the development of a cancer in a patient. The method additionally involves the step of cloning at least one proliferated cell and then administering the cloned T cells to the patient. The present sequence represents a cDNA associated with breast cancer.
XX Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;

Alignment Scores:

Pred. No.: 1.17e-194 Length: 3865
 Score: 2578.00 Matches: 508
 Percent Similarity: 99.61% Conservative: 0
 Best Local Similarity: 99.61% Mismatches: 2
 Query Match: 99.19% Indels: 0
 DB: 10 Gaps: 0

US-09-451-739H-16 (1-512) x ADE44426 (1-3865)

Qy	1	MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla	20
Db	1563	ATGAAGTTCTATTCCAACTTAAAGCCTTAGAATTGATGACATGCCAACTTTCAAAGCA	1622
Qy	21	GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro	40
Db	1623	GAGCTCCCGAGAGCCTATCGCTTCGAGCTGCCATTGAATGCAAAAGTCTGTTC	1682
Qy	41	AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer	60
Db	1683	AATRAAGCCTTGAATTTGAAGATGAACAAACATTGAGAGCAGATGAGATCTCCCATCA	1742
Qy	61	GluSerLysGlnLysAspTyrGluLysSerTrpAspSerGluSerLeuCysGluThr	80
Db	1743	GAATCCAAACAAAGGACTATGAAGAAAGTTCTTGGGATCTGAGAGTCTCTGGAGACT	1802
Qy	81	ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle	100
Db	1803	GTTCACAGAGGATGTGTGTTATCCCAAGGCTRCRCATCAAAAGAAATAGATAAAATA	1862
Qy	101	AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet	120
Db	1863	AATGAAATATAGAGAGTCTCCGTATATGATGTTTCTGAAGGCTCCCTGAGAGTG	1922
Qy	121	LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu	140
Db	1923	AAAGTTCTATTCCAACTTAAGCCTTAGAATTGATGGACATGCAACTTTCCAAAGCAGAG	1982
Qy	141	ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn	160
Db	1983	CCTCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGAATGAAATGCCAAAGTCTGTCCAAAT	2042
Qy	161	LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu	180
Db	2043	AAAGCCTTGAATTTGAAGATGAACAAACATTGAGAGCAGATCATGATGTTCCCTTCAGAA	2102
Qy	181	SerLysGlnLysValGluLysAsnSerTrpAspSerGluSerLeuArgGluThrVal	200
Db	2103	TCAAACAAAGAAAGSGTTGAAGAAATTTCTGGGATTTCTGAGAGTCTCCGTGAGACTGT	2162
Qy	201	SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer	220
Db	2163	TCACAGAGGATGTGTGTGTATCCCAAGGCTACACATCAAAAGAAATGATGAATAAATAGT	2222
Qy	221	GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu	240
Db	2223	GGAAATTTAGAGATTCAACTAGCCTATCAAAATCTTTGGATACAGTTCACTCTGTGAA	2282
Qy	241	ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet	260
Db	2283	AGAGCAAGGAACTTCAAAAGATCATCTGTGAACACGTCACAGGAAATGGAACAAATG	2342
Qy	261	LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln	280
Db	2343	AAAAAGAGTTTGTCTACTGAAAGAAAGAACTGTGAGAGCAAGAAAGAAATAAATACAG	2402
Qy	281	LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn	300
Db	2403	TTAGAGAACCAAAAGCTTAAATGGGAACCAAGAGCTCTGCAGTGTGAGATTGCTTTAAAC	2462
Qy	301	GlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu	320
Db	2463	CAAGAGAGAGAGAGAGAGAGATGCCGATATATTAAATGAAATTAAGGAGAGATTA	2522

Qy	321	GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnLeuGluGlnAla	340
Db	2523	GGAGATTCGAAGAGCAGCATAGGAAGAGTTAGAGTGAACACCAACTTTGAACAGCT	2582
Qy	341	LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis	360
Db	2583	CTCAGATACAGATATAGAATTGAAGAGTGTAGAAAATTAATTTGAATTCAGTTTCTCAC	2642
Qy	361	ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla	380
Db	2643	ACTCAAGAAATGAATAATTAATCTCTTACATGAATAATTCATCTTGAAGAAAGAAATTC	2702
Qy	381	MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr	400
Db	2703	ATGCTAAATTCGAAATAGCCACACTGAAACACCAATACCAGGAAAGAAATAAATATAC	2762
Qy	401	PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu	420
Db	2763	TTTGAGGACATTAAAGATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTG	2822
Qy	421	LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle	440
Db	2823	AAAGAGGAATCATTAACATAAAGGCGCATCTCAATATAGTGGCGAGCTTAAAGTTCTGATA	2882
Qy	441	AlaGluAsnThrMetLeuThrSerLysLysLysGlyLysGlnAspLysGluIleLeuGlu	460
Db	2883	GCTGAGAACACAAATGCTCACTTCTAAATTTGAAGGAAACCAAGACAAAGAAATATACAG	2942
Qy	461	AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle	480
Db	2943	GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGTGTACAAGACCATGATCAAAAT	3002
Qy	481	ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln	500
Db	3003	GTGACATCAAGAAAGTCAAGAACCTGCTTTCCACATTCAGAGAGATGCTTGTTCGAA	3062
Qy	501	ArgLysMetAsnValAspValSerSerThr	510
Db	3063	AGAAATTAAGTTGATGTGAGTAGTAGC	3092

RESULT 13

ABT33258
 ID ABT33258 standard; DNA; 3045 BP.

XX AC ABT33258;

XX AC 15-MAY-2003 (first entry)

XX DE Human tumour-related DNA sequence - SEQ ID No 548.

XX DE Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;
 tumour; breast cancer; cancer; immune response stimulation.

XX OS Homo sapiens.

XX OS WO200283956-A1.

XX PN 24-OCT-2002.

XX PF 15-APR-2002; 2002WO-US012378.

XX PR 13-APR-2001; 2001US-00834759.

XX PR 07-DEC-2001; 2001US-00007805.

XX PR 13-FEB-2002; 2002US-00076522.

XX PA (CORI-) CORIXA CORP.

XX PI Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;

XX PI Mitcham JL, Xu J, Harlocker SL, M, Hepler WT, Henderson RA, Fanger GR;

XX PI Vedwick TS, McNeill PD, Durham

XX DR WPI; 2003-103376/09.

XX New polypeptide and polynucleotide useful for stimulating and/or
PT expanding T cells specific for a tumor protein and treating breast
PT cancer.
XX Example 8; Page 329-330; 375pp; English.
XX The invention comprises a method of stimulating and/or expanding T cells
CC specific for a tumor protein. The invention further comprises human
CC nucleic acids and proteins that are associated with tumours (e.g. breast
CC cancer). The method and sequences of the invention are useful for
CC stimulating and/or expanding T cells specific for a tumour protein,
CC detecting the presence of cancer, stimulating an immune response in a
CC patient and treating breast cancer. The present DNA sequence represents a
CC human tumour-related DNA sequence.
XX
SQ Sequence 3045 BP; 1222 A; 521 C; 613 G; 689 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.28e-194 Length: 3045
Score: 2576.00 Matches: 507
Percent Similarity: 99.61% Conservative: 1
Best Local Similarity: 99.41% Mismatches: 2
Query Match: 99.12% Indels: 0
DB: 7 Gaps: 0

US-09-451-739H-16 (1-512) x ABT33258 (1-3045)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetMetMetGlnThrPheLysAla 20
Db 1045 ATGAAAGTTTCTATTCAAACTAAAGCCCTTAGAATGTGATGACATGCAAACTTTCAAGCA 1104
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1105 GAGCCTCCGAGAGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCTCA 1164
Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 1165 AATAAGCCTTGGAAATTCAGAAATCAACAAACATTTGAGAGCAGATGATCTCCCATCA 1224
Qy 61 GluSerLysGlnLysAspTyrGluLysSerThrTaspSerGluSerLeuLysGluThr 80
Db 1225 GAATCCAAACAAAGAGATATGAGAAAGTTCTTGGGATTCCTGAGATCTCTGTGAGACT 1284
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
Db 1285 GTTTCACAGAGAGATGTGTGTTTACCCAAAGCTGGCCATCAAAAGAAATAGATAAATA 1344
Qy 101 AsnGlyLysLeuGluLysSerProAspAsnAspGlyPheLysAlaProCysArgMet 120
Db 1345 AATGGAAATTTAGAGAGTCTCTGATATGATGTTTCTGAGATCTCTGTGAGACT 1404
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetMetMetGlnThrPheLysAlaGlu 140
Db 1405 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAGCAGAG 1464
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 1465 CCTCCGAGAGCCATCTCCCTCGAGCTGCAATGAAATGCAAAAGTCTGTTCCTCAAT 1524
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 1525 AAAGCCTTGGAAATTTGAGAAATGACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAA 1584
Qy 181 SerLysGlnLysValGluGluLeuSerThrTaspSerGluSerLeuArgGluThrVal 200
Db 1585 TCAAAACAAAGAACCTTGAAGAAATTTCTGGATTCCTGAGATCTCCGTGAGACTGTT 1644
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 1645 TCACAGAGAGATGTGTGTACCCAAAGGCTACACATCAAAAGAAATGATTAATAAGT 1704
Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240

Db 1705 GGAAATTAGAGATTCACTAGCTTATCAAAATCTTGATACAGTTCACTTTGTGAA 1764
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 1765 AGAGCAAGGGAATCTTCAAAAGATCACTGTGCAACAGCTACAGGAAATATGGAAACAATG 1824
Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280
Db 1825 AAAAAGAGTTTGTGTGATCTGAAAGAAAGAACTCTCAGAGCAAAAGAAATAAATACACAG 1884
Qy 281 LeuGluAsnGlnLysValLysTyrGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 1885 TTAGAGAACCAAAAGTTAAATGGGAACAAGACTCTGCAGTGTGAGATTGATCTTAAAC 1944
Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 1945 CAAGAAGAAGAGAAGAGAAATGCCGATATATTAAATGAAAAAATTAGGGAAGAAATTA 2004
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
Db 2005 GGAAGATCGAAGAGAGCAGCATAGGAAAGAGTTAGAGTGAACCAACAACTTGACAGGCT 2064
Qy 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2065 CTCAGATACAGATATAGAAATTCAGAGTGTAGAAAGTAAATTAATCAGTTTCTCAC 2124
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 2125 ACTCATGAAATGAAATTAATCTCTTACATGAAATTTGCATGTTGAAAAAGGAAATTGCC 2184
Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 2185 ATGCTTAAACCTGGAATAGCCACACTGAAACCAACCAATACCAAGGAAAGGAAATAAATAC 2244
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2245 TTTGAGGACATTAAGATTTTAAAGAAAAAGAAATGCTGAATTCAGATGACCTTAAACTG 2304
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 2305 AAAGAGGATCAATTAACATAAAGGCGCATCTCATATAGTGGCAGCTTAAAGTCTGATA 2364
Qy 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluLeuGlu 460
Db 2365 GCTGAGAACACAACTGCTCACTTCTTAAATTTGAAGGAAAAAACAAGACAAAGAAATACAG 2424
Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2425 GCAGAAATTTGAATTCACACCATCTAGACTGGCTTCTGTGTACAAGACCATGATCAAT 2484
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 2485 GTGACATCAAGAAATAAGCTCAGAACCTGCTTCCACATTCAGAGAGATGCTTGTTCGAA 2544
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 2545 AGAAAAATGAATTTGATGTGAGTAGTACG 2574

RESULT 14

AAS47405

ID AAS47405 standard; cDNA; 3681 BP.

XX AC AAS47405;

XX AC AAS47405;

XX 18-DEC-2001 (first entry)

XX 18-DEC-2001 (first entry)

DE Human cDNA cloneB726P-spliced_seq_B726P encoding a breast cancer protein.

XX Human; ss; breast cancer protein; tumour; cancer; cytostatic;

XX gene therapy.

XX Homo sapiens.

OS

XX W0200179286-A2.
 XX XX
 XX PD 25-OCT-2001.
 XX XX
 XX 12-APR-2001; 2001WO-US012164.
 XX PF
 XX 17-APR-2000; 2000US-00551621.
 PR 08-JUN-2000; 2000US-00590751.
 PR 22-JUN-2000; 2000US-00604287.
 PR 20-JUL-2000; 2000US-00620405.
 XX XX
 PA (CORI-) CORIXA CORP.
 XX XX
 XX JIang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
 XX P-PSDB; AAU33346.
 DR WPI; 2001-611721/70.
 DR P-PSDB; AAU33346.
 XX XX
 PT Breast Tumor Proteins and nucleic acids useful for the prevention,
 PT diagnosis and treatment of breast cancer.
 XX XX
 PS Claim 1; Page 271-272; 297pp; English.
 XX XX
 CC The invention relates to isolated breast tumour proteins and nucleic
 CC acids that encode them, including immunogenic fragments of the proteins.
 CC Also included are expression vectors expressing the proteins, transfected
 CC cells and antibodies raised against the proteins or an antigen presenting
 CC cell expressing the protein. The proteins and nucleic acids may be used
 CC in the prevention, diagnosis and treatment of diseases associated with
 CC inappropriate breast tumour protein expression, i.e. breast tumours and
 CC breast cancer e.g. by gene therapy. The nucleic acids and their
 CC complements may also be used as DNA probes in diagnostic assays to detect
 CC and quantitate the presence of similar nucleic acids in samples. The
 CC therefore which patients may be in need of restorative therapy. The
 CC proteins, nucleic acids and antibodies may be used in assays to identify
 CC modulators (e.g. antagonists) of breast tumour protein expression and
 CC activity. The antibodies and antagonists may also be used to down
 CC regulate expression and activity. The antibodies may also be used as
 CC diagnostic agents for detecting the presence of the proteins in samples
 CC (e.g. by enzyme linked immunosorbent assay (ELISA)) and in other immuno-
 CC purification diagnostic techniques. The present sequence is a cDNA from a
 CC breast tumour cDNA library isolated by subtractive hybridisation against
 CC a normal breast cDNA library and encodes a breast tumour protein of the
 CC invention. The present sequence is also a splice variant
 XX SQ
 SQ Sequence 3681 BP; 1412 A; 680 C; 758 G; 826 T; 0 U; 5 Other;

Alignment Scores:
 Pred. No.: 3,88e-167 Length: 3681
 Score: 2230.50 Matches: 447
 Percent Similarity: 87.65% Conservative: 0
 Best Local Similarity: 87.65% Mismatches: 2
 Query Match: 85.82% Indels: 62
 DB: 4 Gaps: 1

US-09-451-739H-16 (1-512) x AAS47405 (1-3681)
 QY 1 MetLysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAla 20
 Db 1563 ATGAAGTTTCTATTCCAACTTAAAGCCCTTGAAGTTGATGGACATGCAAACTTTCAAAGCA 1622
 QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
 Db 1623 GAGCCTCCCGAGAGCCATCTGCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTCCA 1682
 QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
 Db 1683 AATAAGCCTTGGAAATTGAAGAAATGAACAAACATTGAGAGCAGATGATACCTCCCATCA 1742
 QY 61 GluSerLysGlnLysAspTyrGluGluSerSerIleAspSerGluSerLeuLysGluThr 80
 Db 1743 GAATCCAAACAAAGGACTATGAGAAAGTTCTTGGGATTTCTGAGATCTCTGTGAGACT 1802

QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
 Db 1803 GTTTCACAGAGGATGTGTGTTTACCCAGGCTRCRCATCAAAAGAAATAGATAAATA 1862
 QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
 Db 1863 AATGGAAATTTAGAAGAGTCTCTCTGATAATGATGATGTTTCTGAAGGCTCCCTGCAGAAATG 1922
 QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
 Db 1923 AAAGTTTCTATTCCAACTTAAAGCCTTAGAATTTAGATGACATGCAAACTTTCAAGACGAG 1982
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
 Db 1983 CCTCCGAGAGCCATCTGCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCTCAAT 2042
 QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
 Db 2043 AAAGCCTTGGAAATTTGAAGATGAACAAACATTTGAGCAGATCAGATGTTTCCCTTCAGAA 2102
 QY 181 SerLysGlnLysLysValGluGluAsnSerIleAspSerGluSerLeuArgGluThrVal 200
 Db 2103 TCNAACAAAGAAAGTTGAAGAAATTTCTTGGGATTTCTGAGAGTCTCCGTGAGACTGTT 2162
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
 Db 2163 TCACAGAGGATGTGTGTGTACCAAGCTACACATCAAAAGAAATGGATAAAATTAAGT 2222
 QY 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240
 Db 2223 GGAAATTTAGAGATTCACCTAGCTATCAAAATCTTGGATACAGTTCATTCCTTGTGAA 2282
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
 Db 2283 AGAGCAAGGAACTTCAAAAGATCACTGTGAACACGTACAGAAATAATGGAAACAATG 2342
 QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280
 Db 2343 AAAAAGAGATTTTGTGTACTGAAAAGAAATCTCAGAGCAAAAGAAATAAATCAACAG 2402
 QY 281 LeuGluAsnGlnLysValIleTyrGluGlnGluLysCysSerValArgLeuThrLeuAsn 300
 Db 2403 TTAGAGAACCAAAAGTTAAATGGGAACACAGAGCTCTGCAGTGTGAGGTT 2452
 QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
 Db 2452 ----- 2452
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGlnAla 340
 Db 2452 ----- 2452
 QY 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
 Db 2453 -----TCTCAC 2458
 QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
 Db 2459 ACTCATGAAATGAAATTAATCTTACATGAAATTCATGTTGAAAGGAAATTCGCC 2518
 QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
 Db 2519 ATGCTAAAACCTGGAATAGCCACTGAAACACCAATACCAAGGAAAGGAAATAAATATAC 2578
 QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
 Db 2579 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAATTCAGATCCCTCAAACTG 2638
 QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
 Db 2639 AAAGAGGAATCATTAACATAAGGGGATCTCAATATAGTGGGACGCTTAAAGTCTTGATA 2698

QY 441 AlaGluAsnThrVetLeuThrSerLysLeuLysGluLysGlnAspLysGluLysLeuGlu 460
 Db 2699 GCTGAGAACACATGCTCACTTCTAAATGAAGGAAAAAACAAGACAAAGAAATCTAGAG 2759
 QY 461 AlaGluLeuGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
 Db 2759 GCAGAAATGATCATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAT 2818
 QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
 Db 2819 GTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATTCGAGGATGCTTTGTTGCAA 2878
 QY 501 ArgLysMetAsnValAspValSerThr 510
 Db 2879 AGAAAAATGATGTTGATGTGAGTAGTAG 2908
 RESULT 15
 AAF17980
 ID AAF17980 standard; cDNA; 2307 BP.
 XX
 AC AAF17980;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Human breast cancer associated B72P splice sequence #5.
 XX
 KW Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200060076-A2.
 XX
 PD 12-OCT-2000.
 XX
 PF 15-FEB-2000; 2000WO-US005308.
 XX
 PR 02-APR-1999; 99US-00285480.
 PR 23-JUN-1999; 99US-00339338.
 PR 02-SEP-1999; 99US-00389681.
 PR 03-NOV-1999; 99US-00433826.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Yuqiu J, Dillon DC, Mitcham JL, Xu J, Harlocker SL;
 XX
 DR WPI; 2001-122627/13.
 XX
 PT An isolated polypeptide useful for the treatment and diagnosis of tumors
 PT e.g. breast cancer comprises at least an immunogenic portion of a breast
 PT tumor protein.
 XX
 PS Claim 6; Page 229-230; 238pp; English.
 XX
 CC The present invention provides the coding sequences and some protein
 CC sequences of proteins associated with breast cancer in humans. These
 CC sequences can be used in the diagnosis and treatment of cancers,
 CC particularly breast tumours
 XX
 SQ Sequence 2307 BP; 919 A; 409 C; 439 G; 540 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. NO.: 3.9e-167 Length: 2307
 Score: 2227.50 Matches: 446
 Percent Similarity: 87.65% Conservative: 1
 Best Local Similarity: 87.45% Mismatches: 2
 Query Match: 85.71% Indels: 62
 DB: 4 Gaps: 1
 US-09-451-739H-16 (1-512) x AAF17980 (1-2307)
 QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
 Db 206 ATGAAGTTTCTATTCCACTAAGCCTTAGAATTGATGACATGCACAACTTTCAGCA 265

QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
 Db 266 GAGCCTCCCGAAGGCATCTGCCCTTCGAGCCTGCCATTTGAATGAAAAGTCTGTCCA 325
 QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLysLeuProSer 60
 Db 326 AATAAGCCITGGAATTGAAGATGAACAAACATTGAGAGCAGATGAGATCTCCCATCA 385
 QY 61 GluSerLysGlnLysAspThrGluLysSerSerTrpAspSerGlnSerLysLeuGluThr 80
 Db 386 GAATCCAAACAAAGACATATGAAGAAAGTTCTTGGATCTGAGAGTCTCTGTGAGACT 445
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLysIle 100
 Db 446 GTTTCACAGAGGATGTGTGTTTACCACAGGCTACACATCAAAAAGAAATAGATAAATA 505
 QY 101 AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
 Db 506 AATGGAATATTAGAAGAGTCTCTGATAATGATGGTTTCTTGAAGTCTCCCTGCAGAA 565
 QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
 Db 566 AAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAG 625
 QY 141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
 Db 626 CTTCCCGAAGGCATCTGCCCTTCGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAAT 685
 QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
 Db 686 AAGCCTTGAATGAAGAATGAACAAACATTGAGAGCAGATCGATGTTCCTTCAGAA 745
 QY 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGlnSerLeuArgGluThrVal 200
 Db 746 TCAAAACAAAAGACGTTGAAGAAATCTTGGGATCTTCAGAGTCTCCGTGAGACTGTT 805
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
 Db 806 TCACAGAGGATGTGTGTGTACCCAGGCTACACATCAAAAAGAAATGGATAAATAAGT 865
 QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
 Db 866 GGAAATATTAGAAGATTCACTAGCTATCAAAATCTTGATACAGTTCACTTCTTGTGAA 925
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
 Db 926 AGACCAAGGGAACTTCAAAAAGATCACTGTGAACACGTCAGAGAAATATGGACAAATG 985
 QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280
 Db 986 AAAAAGAGTTTGTGTACTGMAAAGAAACTGTCAAGACAAAAGAAATAAAATCACAG 1045
 QY 281 LeuGluAsnGlnLysValLysTrpGluGlnLeuCysSerValArgLeuThrLeuAsn 300
 Db 1046 TTAGAACCAAAAAGTTAAATGGAAACAAGAGCTCTGCAGTGTGAGGTT----- 1095
 QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
 Db 1095 ----- 1095
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
 Db 1095 ----- 1095
 QY 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
 Db 1096 -----TCTCAC 1101
 QY 361 ThrHisGluAsnGluAsnThrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
 Db 1102 ACTCATGAAATGAAATTAATCTCTTACATGAAATTCATGTTGAAAAAGGAAATGGCC 1161


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QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 1162 ATGCTAAAACTGGAAATAGCCACACTGAACACCAATACCAGGAAAGGAAATATAATAC 1221

QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGlnLeuGlnMetThrLeuLysLeu 420
Db 1222 TTTGAGGACATTAAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATGACCCCTAAACTG 1281

QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 1282 AAAGAGGAATCATTAACCTAAAGGGCATCTCAATATAGTGGCAGCTTAAAGTTCIGATA 1341

QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGlnGlnAspLysGluIleLeuGlu 460
Db 1342 GCTGAGAACACATGCTCACTTCTAAATTGAAGGAAACAAAGACAAAGAAATACTAGAG 1401

QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 1402 GCAGAAATTGAATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAATTT 1461

QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 1462 GTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTCAGGAGATGCTTGTGTCAG 1521

QY 501 ArgLysMetAsnValAspValSerSerThr 510
Db 1522 AGAAAAATGATGTTGATGTGAGTAGTACG 1551

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Search completed: May 6, 2004, 14:16:21
Job time : 623 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 6, 2004, 11:51:33 ; Search time 6047 Seconds
(without alignments)

3669.858 Million cell updates/sec

Title: US-09-451-739H-16

Perfect score: 2599
Sequence: 1 MKVSIPTKALELMDMOTFFA.....IAGDACLRQMNVDVSSDTI 512

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb.btg.*
3: gb.in.*
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23: em.pat.*
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35: em.htg.rodi.*
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39: em.tgo.hum.*
40: em.tgo.mus.*
41: em.tgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	2589	99.6	4458	6	AX829110	Sequence
3	2589	99.6	4458	9	AF269087	Homo sapi
4	2578	99.2	3288	6	AR283467	Sequence
5	2578	99.2	3288	6	AX303170	Sequence
6	2578	99.2	3288	6	AR283457	Sequence
7	2578	99.2	3288	6	AR351426	Sequence
8	2578	99.2	3288	6	AX303154	Sequence
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 DEFINITION Sequence 15 from Patent WO0147959.
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 ACCESSION
 VERSION AX367056.1 GI:18855278
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 ORGANISM
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and
 Chen,Y.T.
 TITLE Isolated nucleic acid molecules encoding cancer associated
 antigens, the antigens per se, and uses thereof
 JOURNAL Patent: WO 0147959-A 15 05-JUL-2001;
 LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL
 SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation
 (US)
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 VERSION AX829110.1 GI:39838904

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 Sequence 3 from Patent WO02059377.
 AX829110
 ACCESSION
 VERSION AX829110.1 GI:39838904

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Mack, D.H., Gish, K.C. and Afar, D.
TITLE Methods of diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer
JOURNAL Patent: WO 02059377-A 3 01-AUG-2002;
EOS Biotechnology, Inc. (US)
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DEFINITION Homo sapiens breast cancer antigen NY-BR-1 mRNA, complete cds.
ACCESSION AF269087
VERSION AF269087.1 GI:13469728
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 4458)
AUTHORS Jager, D., Stockert, E., Gure, A.O., Scanlan, M.J., Karbach, J., Jager, E., Knuth, A., Old, L.J. and Chen, Y.T.

TITLE Identification of a tissue-specific putative transcription factor in breast tissue by serological screening of a breast cancer library

JOURNAL Cancer Res. 61 (5), 2055-2061 (2001)

MEDLINE 21174979

PUBMED 11280766

REFERENCE 2 (bases 1 to 4458)

AUTHORS Jaeger,D., Stockert,E., Guere,A.O., Scanlan,M.J., Karbach,J.,

Jaeger,E., Kuth,A., Old,L.J. and Chen,Y.T.

TITLE Direct Submission

JOURNAL Submitted (18-MAY-2000) Pathology, Cornell Medical Center, 1300

York Avenue, New York, NY 10021, USA

FEATURES Location/Qualifiers

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ORIGIN

Alignment Scores:

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Query Match: 99.62% Indels: 0
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 Db 3508 GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGCTGTACACAGACCATGATCAAAT 3567
 QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaClyAspAlaCysLeuGln 500
 Db 3568 GTGACATCAAGAAAGTCAAGAACCTGCTTTCCACATTCAGAGATGCTTTGTTGCAA 3627
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 Db 3628 AGAAAAATGAATGTTGATGTGAGTAGTACG 3657

RESULT 4
 AR283467 LOCUS AR283467 3288 bp DNA linear PAT 10-APR-2003
 DEFINITION Sequence 490 from patent US 6528054.
 ACCESSION AR283467
 VERSION AR283467.1 GI:29720294
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 3288)
 REFERENCE Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.
 TITL Composition and methods for the therapy and diagnosis of breast cancer
 JOURNAL Patent: US 6528054-A 490 04-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..3288
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,69e-163 Length: 3288
 Score: 2578.00 Matches: 508
 Percent Similarity: 99.61% Conservative: 0
 Best Local Similarity: 99.61% Mismatches: 2
 Query Match: 99.19% Indels: 0
 DB: 6 Gaps: 0

US-09-451-739H-16 (1-512) x AR283467 (1-3288)

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 Db 1411 AATAAGCTTTGGAATTTGAGAAATGAAACAAACATTGAGACGATGAGATCTCCCATCA 1470
 QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTTPAspSerGluSerLeuCysGluThr 80
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 QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
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QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
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 QY 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
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Db 2731 GTGACATCAAGAAAAGTCAAGAACCTGCTTCCACATTGCAGGAGATGCTGTTTGCAA 2790
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RESULT 5
AX303170
LOCUS AX303170 3288 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 490 from Patent WO0179286.
ACCESSION AX303170
VERSION AX303170.1 GI:17383660
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0179286-A 490 25-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1..3288
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.69e-163 Length: 3288
Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.19% Indels: 0
DB: 6 Gaps: 0
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Db 1351 GAGCCTCCCGAAGCCATCTGCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCTCA 1410
Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 1411 AATAAGCCTTGAATTTGAAGAATGAACAAACATTGAGAGCAGATGAGATATCTCCCATCA 1470
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Db 1531 GTTTCACAGAGGATGTGTGTTTACCAGGCTRCRCATCAAAAAGAAATAGATAAATA 1590
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Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
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Db 1711 CCTCCGAGAAGCCATCTGCCTTCGAGCCTGCCATTGAATGAAGTCTGTGTTTCCAAAT 1770

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Qy 341 LeuArgIleGluAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
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Db 2791 AGAAAAATGAATGTTGATGTGAGTAGTACG 2820

RESULT 6
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LOCUS AR283457 3865 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 474 from patent US 6528054.
ACCESSION AR283457
VERSION AR283457.1 GI:29720284
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3865)
AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and Hepler, W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: US 6528054-A 474 04-MAR-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
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Alignment Scores:
Pred. No.: 2e-163 Length: 3865
Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.19% Indels: 0
DB: 6 Gaps: 0
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DB 1923 AAGATTCTATTCCAACTAAAGCCTTGAATGATGACATGCAAACTTTCAAGCAGAG 1982
QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
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LOCUS AR351426 3865 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 474 from patent US 6586572.
ACCESSION AR351426
VERSION AR351426.1 GI:33753105
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3865)
 Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and
 Hepler, W.T.
 TITLE Compositions and methods for the therapy and diagnosis of breast
 JOURNAL Cancer
 PATENT US 6586572-A 474 01-JUL-2003;
 LOCATION/Qualifiers
 FEATURES 1. 3865
 SOURCE /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 2e-163 Length: 3865
 Score: 2578.00 Matches: 508
 Percent Similarity: 99.61% Conservative: 0
 Best Local Similarity: 99.61% Mismatches: 2
 Query Match: 99.19% Indels: 0
 DB: 6 Gaps: 0

US-09-451-739H-16 (1-512) x AR351426 (1-3865)

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QY 121 LysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAlaGlu 140
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QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
 DB 2823 AAAGAGCATCATTAATACTAAAAGGCGCATCTCAATATAGTGGCGAGCTTAAAGTTCTGATA 2882

QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluLeuGlu 460
 DB 2883 GCTGAGACACAAATGCTCACTTCTAAATTTGAAGAAACCAAGACAAAGAAATACTAGAG 2942

QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
 DB 2943 GCAGAAATTTGAATTCACACCATCTAGACTGGCTTCTGCTGTATCAAGACCATGATCAAT 3002

QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
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QY 501 ArgLysMetAsnValAspValSerSerThr 510
 DB 3063 AGAAATATGAATGTGTGATGTAGTAGTACG 3092

RESULT 8
 AX303154 3865 bp DNA linear PAT 30-NOV-2001
 LOCUS Sequence 474 from Patent WO0179286.
 DEFINITION AX303154
 ACCESSION AX303154
 VERSION AX303154.1 GI:17383650
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and
 Hepler, W.T.
 TITLE Compositions and methods for the therapy and diagnosis of breast
 JOURNAL Cancer
 PATENT WO 0179286-A 474 25-OCT-2001;
 CORIXA CORPORATION (US)
 FEATURES Location/Qualifiers
 1. 3865
 source

/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 2e-163 Length: 3865
Score: 2578.00 Matches: 508
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Query Match: 99.19% Indels: 0
DB: 6 Gaps: 0

US-09-451-739H-16 (1-512) x AX303154 (1-3865)

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DB 3063 AGAAATGAATGTTGATGAGTAGTAGC 3092
RESULT 9
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LOCUS
DEFINITION Sequence 468 from patent US 6528054.
ACCESSION AR283456
VERSION AR283456.1 GI:29720283
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE Unclassified.
1 (bases 1 to 2307)
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL cancer
Patent: US 6528054-A 468 04-MAR-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
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Score: 87.65% Conservative: 1
Best Local Similarity: 87.45% Mismatches: 2

Query Match: 85.71% Indels: 62
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DB 386 GAATCCCAACAAAGAGGACTATGAAGAAAGTTCTTGGGATCTCGAGAGTCTCTGTGAGACT 445
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DB 446 GTTTCACAGAGGATGTGTGTTTACCAGGCTACACATCAAAAGAAATAGATAAATA 505
QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
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QY 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
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DB 1522 AGAAAAATGAATGTTGATGTGAGTAGTACG 1551
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LOCUS AR344224
DEFINITION Sequence 468 from patent US 6579973.
ACCESSION AR344224
VERSION AR344224.1 GI:33740124
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2307)
AUTHORS Yudiu, J., Dillon, D.C., Mitcham, J.L., Xu, J. and Harlocker, S.L.
TITLE Compositions for the treatment and diagnosis of breast cancer and methods for their use
JOURNAL Patent: US 6579973-A 468 17-JUN-2003;
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Location/Qualifiers
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Alignment Scores:
Pred. No.: 3,29e-140 Length: 2307
Score: 2227.50 Matches: 446
Percent Similarity: 87.65% Conservative: 1
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Query Match: 85.71% Indels: 62
DB: 6 Gaps: 1
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 LOCUS Sequence 468 from patent US 6586572.
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 ACCESSION AR351425
 VERSION AR351425.1 GI:33753104
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 2307)
 AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.
 TITLE Compositions and methods for the therapy and diagnosis of breast cancer
 JOURNAL Patent: US 6586572-A 468 01-JUL-2003;
 FEATURES Location/Qualifiers
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 /organism="unknown"
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 Pred. No.: 3.29e-140 Matches: 446
 Score: 2227.50
 Percent Similarity: 87.65% Conservative: 1
 Best Local Similarity: 87.45% Mismatches: 2
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QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 1096 -----TCTCAC 1101
QY 361 ThrHisGluAsnGluAsnTrpLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380
Db 1102 ACTCATGAAATGAAATATCTCTACATGAAATTTGCATGTTTCAAAAGAAATTCCTCC 1161
QY 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTrpGlnGluLysGluAsnLysTrp 400
Db 1162 ATGCTAAAAGTGAATAGCCACACTGAAACCAATACAGAAAGAAAGAAATTAATAC 1221
QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 1222 TTTGAGGACATTAAAGATTTTAAAGAAAGAAATGCTGAACCTCAGATGACCTTAAACTG 1281
QY 421 LysGluGlnSerLeuThrLysArgAlaSerGlnTrpSerGlyGlnLeuLysValLeuIle 440
Db 1282 AAAGAGGAATCATTAATAAGGGGATCTCAATATAGTGGCAGCTTAAAGTCTTGATA 1341
QY 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluLeuGlu 460

Db 1342 GCTGAGACACAAATGCTCACTTCTAAATTTGAAGAAAAAACAAGACAAATACTAGAG 1401
QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
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QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 1462 GTGACATCAAGAAAAAGTCAAGAACCTCTTCCACATTCAGGAGATGCTTGTTCGAA 1521
QY 501 ArgLysMetAsnValAspValSerSerThr 510
Db 1522 AGAAAAATGAATGTTGATGTGAGTAGTAG 1551
RESULT 12
LOCUS AX282975 2307 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 24 from Patent WO0175171.
ACCESSION AX282975
VERSION AX282975.1 GI:15609908
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Houghton, R.L., Dillion, D.C., Molesh, D.A., Xu, J., Zehentner, B. and
AUTHORS Persing, D.H.
TITLE Methods, compositions and kits for the detection and monitoring of
breast cancer
JOURNAL Patent: WO 0175171-A 24 11-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. .2307
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.: 3 298-140 Length: 2307
Score: 2227.50 Matches: 446
Percent Similarity: 87.65% Conservative: 1
Best Local Similarity: 87.45% Mismatches: 2
Query Match: 85.71% Indels: 62
DB: 6 Gaps: 1

US-09-451-739H-16 (1-512) x AX282975 (1-2307)

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QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 266 GAGCCTCCCGAGAGAGCCATCTGCCTTCGAGCTGCCATTTGAATGCAAAAGTCTGTTC 325
QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 326 AATAAGCCTTGGAAATGAAGAAATGAACAAACATTTGAGAGCAGATGAGATCTCCCATCA 385
QY 61 GluSerLysGlnLysAspTrpGluGluSerSerTrpAspSerGluSerLysGluThr 80
Db 386 GAATCCAAACAAAGAGACTATGAGAAAGTTCTTGGATCTCTGAGAGTCTCTGTGAGACT 445
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuLysIle 100
Db 446 GTTTCACAGAGGATGTGTGTTTACCAAGGCTTACACATCAAAAGAAATAGATAAATA 505
QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 506 AATGAAAAATTAGAAGAGTCTCTCTGATATGATGTTTCTGAGTCTCTCCCTGCAAGATG 565

481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
1462 GTGACATCAAGAAAGTCAAGAACTGCTTTCCACATTGCAGGAGATGCTTTGTCAA 1521

501 ArgLysMetAsnValAspValSerThr 510
1522 AGAAAAATGAATGTTGATGTGAGTAGTACG 1551

RESULT 13
AX303148 2307 bp DNA linear PAT 30-NOV-2001
LOCUS AX303148
DEFINITION Sequence 468 from Patent WO0179286.
ACCESSION AX303148
VERSION AX303148.1 GI:17383649
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and
Hepler, W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer
JOURNAL Patent: WO 0179286-A 468 25-OCT-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..2307
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Alignment Scores: 3.29e-140 Length: 2307
Pred. No.: 2227.50 Matches: 446
Score: 87.65% Conservative: 1
Percent Similarity: 87.45% Mismatches: 2
Best Local Similarity: 85.71% Indels: 62
Query Match: 6 Gaps: 1
DB:

US-09-451-739H-16 (1-512) x AX303148 (1-2307)

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Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 266 GAGCTCCCGAAGAGCCATCTGCTCGAGCCCTGCCATTGAAATGCAAAAGTCTGTCCA 325

Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer 60
Db 326 AATAAGCCTTGGAAATGAAGAATGAACAACTTGAGAGCAGATGAGATATCCCATCA 385

Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLeuCysGluThr 80
Db 386 GAATCCAAACAAAGGACTATGAAGAAAGTTCTTGGGATTCGAGAGTCTCTGTGAGACT 445

Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysIle 100
Db 446 GTTTCACAGAGGATGTGTGTTTACCACAGGCTACACATCAAAAGAAATAGATAAAATA 505

Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 506 AATCGAAATATAGAAGAGTCTCTCGATATGATGATGATGATGATGATGATGATGATG 565

Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
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Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnThrPheLysAla 160

Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 566 AAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAG 625

Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 626 CTTCCGAGAGAGCCATCTGCTTCAGAGCTGCTGATGAAATGCAAAAGTCTGTTCCTCAAT 685

Qy 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 686 AAGGCTTGGAAATGAAGATGAACAACTTGAGAGCAGATCAGATGTTCCCTTCAGAA 745

Qy 181 SerLysGlnLysValGluGluAsnSerTyrAspSerGluSerLeuArgGluThrVal 200
Db 746 TCAAAACAAAGAGAGCTTGAAGAAATTTCTTGGGATTCGTGAGTCTCCGTGAGACTGTT 805

Qy 201 SerGlnLysAsnValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 806 TCAAGAGAGGATGTGTGCTCCAGGCTACATCAAAAGAAATGATGAATAAATAGT 865

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Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
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Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280
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Db 1046 TTAGAGAACCAAAAGTTTAAATGGGAACAGAGCTCTGCAGTGTGAGGT----- 1095

Qy 301 GlnGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 1095 ----- 1095

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Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 1162 ATGCTAAACTGGAAATAGCCACCTGAAACACCAATACAGGAAAGGAAATTAATATAC 1221

Qy 401 PheGluAspIleLysIleLysLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 1222 TTTGAGGACATTAAAGATTTAAAGAAAGAAAGATGCTGAACCTCAGATGACCCCTAAACATG 1281

Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 1282 AAGAGAAATCAATTAATAAGGGCATCTCAATATAGTGGGAGCTTAAAGTCTTGATA 1341

Qy 441 AlaGluAsnThrMetLeuThrSerLysLysGluLysGlnAspLysGluIleLeuGlu 460
Db 1342 GCTGAGAACCAATGCTCACTCTAAATTAAGGAAACAAAGCAAGAAATATCTAGAG 1401

Qy 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 1402 GCAGAAATTAATCACCACTCTAGACTGGCTTCGTGTACAGACCATCATCAAT 1461

Db 626 CTTCCCGAGAGGCATCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAAT 685
Qy 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 686 AAAGCCTTGGAAATTTGAAGATGAACAAACATTCAGAGCAGATCAGATGTTCCCTTCAGAA 745
Qy 181 SerLysGlnLysValGluGlnAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 746 TCAAAACAAAGAACGTTTGAAGAAATTTCTGGATTTGAGAGTCTCCGTGAGACTGTT 805
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 806 TCACAGAGCATGTGTGTGTACCCAGGCTACACATCAAAAGAAATGATAAATAAGT 865
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Db 1095 ----- 1095
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Qy 361 ThrHisGluAsnGluAsnTrpLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 1102 ACTCATGAATGAATATCTCTCATGAAATTTGCATGTTGAAAGAAATTTGCC 1161
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Db 1162 ATGCTAAACTGGAATATGACCACTGAAACACCAATACCAAGGAAAGGAAATATAATAC 1221
Qy 401 PheGluAspIleLysIleLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 1222 TTTGAGGACATTAGATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTG 1281
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Db 1342 GCTGAGACACAAATGCTCACTTCTAAATGGAAGAAAGAAACAGCAAAAGAAATTAAGAG 1401
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Db 1402 GCAGAAATTAATCACCACCTCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAAT 1461
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 1462 GTGACATCAAGAAAGTCAAGAACTGCTTTCCACATTCGAGGAGATGCTGTTGTGCAA 1521
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 1522 AGAAATGAATGATGTTGATGTGAGTAGTAGC 1551

RESULT 14
AR283451
LOCUS
DEFINITION
SEQUENCE
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
ORIGIN

AR283451
Sequence 463 from patent US 6528054.
AR283451
AR283451.1 GI:29720278
Unknown.
Unclisified.
1 (bases 1 to 3681)
Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and
Hepler,W.T.
Compositions and methods for the therapy and diagnosis of breast
cancer
Patent: US 6528054-A 463 04-MAR-2003;
Location/Qualifiers
1..3681
/organism="unknown"
/mol_type="genomic DNA"

Alignment Scores:
Pred. No.: 8,51e-140 Length: 3681
Score: 2224.50 Matches: 446
Percent Similarity: 87.45% Conservative: 0
Best Local Similarity: 87.45% Mismatches: 3
Query Match: 85.59% Indels: 62
DB: 6 Gaps: 1

US-09-451-739H-16 (1-512) x AR283451 (1-3681)
Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
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Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1623 GAGCTCCCGAGAGCCATCTGCCTTCGAGCTGCCATTGAATGCAAAAGTCTGTTCCTCA 1682
Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLysLeuProSer 60
Db 1683 AATAAGCCTTGGAAATTTGAAGAAATGAACAAACATTTGAGAGCAGATGAGATATCTCCATCA 1742
Qy 61 GluSerLysGlnLysAspTrpGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80
Db 1743 GAATCCAAACAAAGAGACTATGAGAAAGTCTTGGGATTTCTGAGAGTCTCTGTGAGACT 1802
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysAspLysIle 100
Db 1803 GTTTCACAGAGGATGTGTGTTTACCCAGGCTRCRCATCAAAAGAAATAGATAAAATA 1862
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 1863 AATGGAAATTTAGAGAGTCTCTGATATATGATGTTTCTGAAGGCTCCCTGCGAATG 1922
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 1923 AAAGTTTCTATTCCAACTAAAGCCCTTAGAATTTGATGGACATGCAAACTTTCAAGACAG 1982
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
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Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
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Qy 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
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201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
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 Qy GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
 Db GGAAAAATTAGAGATTCACTAGCTATCAAAATCTTGATACAGTTCATTCTGTGAA 2282
 Qy ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
 Db AGAGCAAGGAACTTCAAAAGATCACTGTGAACACAGTACAGAAAAATGGAAACAATG 2342
 Qy LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysGluLysSerGln 280
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 LOCUS AR344219 3681 bp DNA linear PAT 17-AUG-2003
 DEFINITION Sequence 463 from patent US 6579973.
 ACCESSION AR344219
 VERSION AR344219.1 GI:33740119
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source

Unclassified.

1 (bases 1 to 3681)
 Yudin,J.; Dillon,D.C.; Mitcham,J.L.; Xu,J. and Harlocker,S.L.
 Compositions for the treatment and diagnosis of breast cancer and
 methods for their use
 Patent: US 6579973-A 463 17-JUN-2003;
 Location/Qualifiers
 1..3681
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 8.51e-140 Length: 3681
 Score: 2224.50 Matches: 446
 Percent Similarity: 87.45% Conservative: 0
 Best Local Similarity: 87.45% Mismatches: 3
 Query Match: 85.59% Indels: 62
 DB: 6 Gaps: 1

US-09-451-739H-16 (1-512) x AR344219 (1-3681)

Qy 1 MetLysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAla 20
 Db 1563 ATGAAAGTTTCTATTCCAACCTAAAGCCTTAGAATTGATGGACATGCAAACTTCAAGCA 1622
 Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
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 Db 1743 GAATCAAAACAAAGAGACTATGAAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACT 1802
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 Db 1803 GTTTCAAGAGAGATGTGTGTTTACCAGGCTCCATCAAAAGAAATAGATAAATA 1862
 Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
 Db 1863 AATGAAATTTAGAAAGATCTCCTGATAATGATGTTTCTGAGGCTCCCTGCAAGATG 1922
 Qy 121 LysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAlaGlu 140
 Db 1923 AAAGTTTCTATTCCAACCTAAAGCCTTAGAATTGATGGACATGCAAACTTCAAGCAGAG 1982
 Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
 Db 1983 CCTCCCGAGAGCCATCTGCTTCGAGCTGCTGAAATGCAAAAGTCTGTTCCTCAAAAT 2042
 Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
 Db 2043 AAAGCCTTGGAAATGAAGAAATGAACAACATTTGAGAGCAGATCAGATGTTCCCTTCAGNA 2102
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 Db 2103 TCAAAACAAAGAAAGTTCGAAGAAATTTCTGGGATTTCTGAGAGTCTCCGTGAGACTGTT 2162
 Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
 Db 2163 TCACAGAGGATGTGTGTGTACCCAGGCTACACATCAAAAGAAATGATGATAAATAAGT 2222
 Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
 Db 2223 GGAATATTAGAGATTCACTAGCCTATCAAAATCTTGATACAGTTCATTCTTGTGAA 2282
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 Db 2283 AGAGCAAGGGAATTTCAAAAGATCACTGTGAACACGTCACGGAAGAAATGGAAACAATG 2342

QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280
Db 2343 AAAAAGAGTTTGTGTACTGAAAAAGAACTGTCTAGAGCAAGAAAGAAATAAAATCACAG 2402
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Db 2403 TTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGCAGTGTGAGTT----- 2452
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Db 2452 ----- 2452
QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
Db 2452 ----- 2452
QY 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2453 -----TCTCAC 2458
QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 2459 ACTCATGAAATGAAATTTATCTCTTACATGAAATTTGCATGTTGAAAAGGAAATGGC 2518
QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 2519 ATGCTAAACTGGAAATAGCCACACTGAACACCCATACCAGGAAAGGAAATATATAC 2578
QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2579 TTTGAGGACATTAAGATTTTAAAGAAAGAAAGATGCTGAACCTTCAGATGACCCCTAAAACTG 2638
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 2639 AAAGAGGAATCATTTACTTAAAGGGCATCTCAATATAGTGGGAGGCTTAAAGTTCTGATA 2698
QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
Db 2699 GCTGAGAACACAAATGCTCACTTCTAAATTCAGGAAAAACAAGACAAAGAAATACTAGAG 2758
QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2759 GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTCTGTACAGACCATGATCAAT 2818
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 2819 GTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATTCAGGAGATGCTTGTGTCAA 2878
QY 501 ArgLysMetAsnValAspValSerThr 510
Db 2879 AGAAAAATGAATGTTGATGTGAGTAGTACG 2908

Search completed: May 6, 2004, 15:57:13
Job time : 6078 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 06:27:28 ; Search time 2575.23 Seconds
(without alignments)
8952.060 Million cell updates/sec

Title: US-09-451-739H-8
Perfect score: 772
Sequence: 1 aaagcttctcggcggcagc.....cagagcgagactccatctta 772

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estm:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hcc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_hcc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pla:*
 - 20: em_gss_prt:*
 - 21: em_gss_fun:*
 - 22: em_gss_lam:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_pri:*
 - 28: gb_gss1:*
 - 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	276	35.8	794	12	BM976892 UI-CF-EN1
C 2	274.4	35.5	729	13	BU622930 UI-H-FLI-
C 3	268	34.7	673	10	BF057660 7A51e08.x
C 4	265	34.3	761	12	BM042700 60361e058

5	260.8	33.8	503	28	AQ877998	HS_2160_A
6	258.2	33.4	822	12	BG249643	602319736
C 7	255	33.0	592	28	AQ351424	AQ351424
C 8	255	33.0	701	13	BU615970	UI-H-DF0-
9	254.2	32.9	458	28	B80438	CIT-HSP-204
10	253.4	32.8	613	28	AQ074754	CIT-HSP-2
C 11	253	32.8	689	29	AG158054	Pan trogl
12	252.8	32.7	731	28	AQ315280	RPC111-10
C 13	252.4	32.7	587	13	EX486697	DKFZp886A
C 14	252.2	32.7	662	29	AG144106	Pan trogl
15	252.2	32.7	1073	28	BZ601227	WHAD89TR
16	252	32.6	349	13	BU963522	AGENCOURT
17	251.6	32.6	1201	13	EX461522	EX461522
18	251.4	32.6	515	28	AQ019249	CIT-HSP-2
C 19	251.2	32.5	447	10	AW276817	XP66405.x
C 20	251.2	32.5	716	13	BU617628	UI-H-DF0-
C 21	250.6	32.5	517	9	AL046409	DKFZp434N
22	250.4	32.4	807	28	BZ606304	WHABT51TR
C 23	250	32.4	498	28	AQ540219	RPC1-11-3
C 24	250	32.4	669	29	AG155696	Pan trogl
C 25	250	32.4	706	14	CA416075	UI-H-PE0-
C 26	249.8	32.4	396	13	EX478578	DKFZp686C
27	249.8	32.4	591	9	AL704268	DKFZp686O
C 28	249.8	32.4	773	12	BI087460	BI087460 602851090
29	249.8	32.4	877	28	AQ740209	HS_5505_A
C 30	249.6	32.3	448	9	A1471481	A1471481 ta20907.x
C 31	249.6	32.3	562	14	CA388905	CA388905 c803f11.x
C 32	249.6	32.3	564	13	BU860291	AGENCOURT
C 33	249.6	32.3	566	13	BU957747	AGENCOURT
C 34	249.6	32.3	650	29	AG116352	AG115352 Pan trogl
C 35	249.4	32.3	455	28	BH367084	BH367084 UP_485-10
36	249.2	32.3	444	28	B89781	BM9781 CIT-HSP-217
C 37	249	32.3	865	13	EX431638	EX431638 BX431638
C 38	248.8	32.2	380	9	A1151261	A1151261 qc88a07.x
C 39	248.8	32.2	664	28	AQ343449	AQ343449 RPC111-12
40	248.6	32.2	541	14	CA437967	CA437967 UI-H-DH0-
C 41	248.6	32.2	721	12	EM679639	EM679639 UI-E-RO0-
C 42	248.4	32.2	745	29	AG092111	AG092111 Pan trogl
C 43	248	32.1	323	13	BU588591	BU588591 AGENCOURT
C 44	248	32.1	365	10	AW472872	AW472872 xs21all.x
C 45	248	32.1	457	28	AQ010278	AQ010278 HS_2172_B

ALIGNMENTS

BM976892	794 bp	mRNA	linear	EST 21-FEB-2003
UI-CF-EN1-adb-n-01-0-UI.s1	UI-CF-EN1	Homo sapiens	cdna clone	
UI-CF-EN1-adb-n-01-0-UI.3'			mRNA sequence.	
BM976892				
BM976892				
BM976892.1	GI:19594754			
EST.				
Homo sapiens (human)				
Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
1 (bases 1 to 794)				
Bonardo,M.F., Lennon,G. and Soares,M.B.				
Normalization and subtraction: two approaches to facilitate gene				
discovery				
Genome Res. 6 (9), 791-806 (1996)				
97044477				
8889548				
Contact: McCray, PB				
McCray Lab				
University of Iowa				
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA				
Tel: 319 356 4866				
Fax: 319 356 7171				
Email: paul-mccray@uiowa.edu				
Tissue Procurement: Dr. M. J. Welsh, University of Iowa				

polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NC1-CGAP-qc4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1259631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

	Query Match	34.7%;	Score 268;	DB 10;	Length 673;
	Best Local Similarity	79.9%;	Pred. No. 7.4e-45;		
	Matches 417;	Conservative	0;	Mismatches 65;	Indels 40; Gaps 7;
Qy	2	AAGCGTTCTCGGCGGAGCGCAACACTAGAACCGTGTAGAACGCGTCCAGCAACCGCGAC	61		
Db	649	AGCGCTCAGTCTGGGAGCGCGCAACACGAGATCCGTGTAGAACGCGTCCATCACTCGA-	591		
Qy	62	CCACGACGACGTACCTCTCGGGCAGCGCCCAAGGAGAGAAAGCCGACCTCTTAAGAAGAA	121		
Db	590	CCTCGACGACGGCGCTCTCGGGCACACAAAGGAGAGAAAGGCCAAGACCTCCAAAGAAGAA	531		
Qy	122	GCAGGGCTCCATGGCCAAAGCGTAGCGGAGGCGTCCCGCGAGACCTCCCCCATCGACCC	181		
Db	530	GAAGCGCTCCAGGGCCAGGCGGAGAGGGCGTCCCTGTGCGGACCTCCCCATCGACCC	471		
Qy	182	CAGCGAGCC-----CTCTACTGGGAGATGATCGCTGCGGA	217		
Db	470	CAACGAACCAACGTACTGTGTGTGCAACACGAGTCTCTATGGGGAATGATCGCTGCGGA	411		
Qy	218	CA----ACGATGCCCATCGATGGTTCGGCTTCTCGTGTGTGAGTCTCAACCATAAACC	274		

275	AAAGCCAAAGTGTCTAGTTCAGATGCCCGGGAAAGAAGCG-----ATGGCCAAAGC	326
Db		
350	CAAGGGCAATGTGTACTGTCCCAAGTGTCCGGGGGAGAACGAGAGACCATGGACAAAGC	291
Qy		
327	CCTGTGAAATCCAGAAAAAACAAGGGCTTATAACAGGTAGTTTGGGACATGCCGTCTA	386
Db		
290	CCTGGAGAAATCC- -AAAAAAGAGAGGGCTTACAACAGGTAGTTTGTGGACAGGCGCCTG	233
Qy		
387	ATAGTGAGGAGAACAAAAATAAGCCAGCTGTGTTGATTACATTGGCACTTTTCTGTGAGGTGC	446
Db		
232	GT-GTGAGGAGGACAAAATAAACG- GTGTATTATTACATTGCTGTCCTTTGTTGAGGTGC	175
Qy		
447	AGGAAGTGTAAAATGTATATTTTAAAGAATGTTGTTAGAGG	488
Db		
174	AAGGAGTGTAAATGTATATTTTAAAGAATGTAGAAAAAGG	133

BM042700/c	761 bp	linear	EST 07-NOV-2000
LOCUS			
DEFINITION	603616058T1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420510 3', mRNA sequence.		
ACCESSION	BM042700		
VERSION	BM042700.1		
KEYWORDS	GI:16771967		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1. (bases 1 to 761)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA sequencing by: Incyte Genomics, Inc.		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
Plate: LLCW1875 row: d column: 15	
High quality sequence start: 2	
High quality sequence stop: 754.	
FEATURES	Location/Qualifiers
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	/db_xref="taxon:9606"
	/clone="IMAGE:5420510"
	/tissue_type="melanotic melanoma, cell line"
	/lab_host="DH10B (phage-resistant)"
	/clone_lib="NIH MGC 112"
	/note="Organ: skin; Vector: pOTB7; Site: 1; XhoI; Site 2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN	
Query Match 34.3%; Score 265; DB 12; Length 761;	
Best Local Similarity 80.7%; Pred. No. 3.1e-44;	
Matches 422; Conservative 0; Mismatches 60; Indels 41; Gaps 8;	
QY	2 AAGCGTCTCGGGGCGGACGACACTAGACCGCTGAGACGCGTCCAGCAACCGCGAC 61
DB	
QY	566 AAGCGTCTACGGCGGCGGACGACGACGAGAACCGTGTGAGACGCGTCCAGCAACCGA- 508
DB	
QY	62 CCACGACGACGTCACCTCGGGCAGCCGCCAAGAGAGAAAGCCAGACCTTAAAGAGAA 121
DB	
QY	507 CCACGACGACGCGCGCTCGGGCAGACCCCAAGAGAGAAAGGCGCAAGACCTCCAGAGAA 448
DB	
QY	122 GCAGGCTCCATGTCGACGCGTAGCGGAGGCGTCCCGGAGACCTCCCGATCGACCC 181
DB	
QY	447 GAAGCGCTCCAGGCCAAGCGGAGGAGGCGGTCCCTGCGACCTCCCGATCGACCC 388
DB	
QY	182 CACGAGGCC-----CTCTACTGGGAGATGATCCGTGGGA 217
DB	
QY	387 CAACGAAACCCAGCTACTGTGTGTGCAACACGAGTCTCTATGGGAGATGATCGGTGGGA 328
DB	
QY	218 CA---ACGATGCCCATCGAGTGTTCGCTCTCGTGTGAGTCTCAACCATAAACC 274
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QY	327 CAACGACGAGTGCCTCCATCGAGTGTTCACCTTCTCGTGGTGGGCTCAATCAATACC 268
DB	
QY	275 AAAGCGCAAGTGGA-CTGTTCAGATGCGCGGGAAGAACG-----ATGGGCAAG 325
DB	
QY	326 CCCTTGAGAGTCAGAAAAAACAGGCTTATACAGTAGTGTGGGACATCGGTCT 385
DB	
QY	207 CCCTGGAGAAATCC--AAAAAGAGAGGGGCTTCAACAGAGTAGTGTGTGGACAGGCGCT 150
DB	
QY	386 AATAGTGAGAGAACAAAAATAAGCAGTGTGTGATTACATTGCCACCTTTGCTGAGGTG 445
DB	
QY	149 GGT-GTGAGGAGCAAAATAACC-GTGATTTATTATACATTGCTGCTTTGTGGAGTG 92
DB	
QY	446 CAGGAGGTGATAATGTATATTTTAAAGATGTTGTAGAG 488
DB	
QY	91 CAAGAGGTGTAATAATGTATATTTTAAAGATGTTAGAAAGG 49
DB	
RESULT 5	
A0877998	
LOCUS	
DEFINITION	
HS 2160 A2_c07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2160 Col=14 Row=E, genomic survey sequence.	
A0877998	
ACCESSION	
A0877998.1 GI:6309465	
GSS	
Homo sapiens (human)	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
1 (bases 1 to 503)	
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.	
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)	
99380589	
MEDLINE	
10449764	
PUBMED	
COMMENT	
Contact: Mahairas GG, Wallace JC, Hood L	
High Throughput Sequencing Center	
University of Washington	
401 Queen Anne Avenue North, Seattle, WA 98109, USA	
Tel: (206) 616-3618	
Fax: (206) 616-3887	
Email: jwallace@u.washington.edu	
Clones may be purchased from Research Genetics (info@resgen.com).	
BAC end Web Server: http://www.htsc.washington.edu	
Plate: 2160 row: E column: 14	
Seq primer: M13 Reverse	
Class: BAC ends	
High quality sequence stop: 503.	
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Location/Qualifiers	
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/clone="Plate=2160 Col=14 Row=E"	
/sex="male"	
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/notes="Organ: Sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"	
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Best Local Similarity 79.1%; Pred. No. 2.2e-43;	
Matches 307; Conservative 0; Mismatches 81; Indels 0; Gaps 0;	
QY	385 TAATAGTAGGAGAGACAAATAAGCCAGTGTGTGATTACATTGCCACCTTCTGAGGT 444
DB	
QY	80 TAGAACAGATATGAAAAAGTAATTCAATGATATCAGAAAAATAATTCTGAATG 139
DB	
QY	445 GCAGGAGTGTAAATGTATATTTTAAAGAAATGTTTGTAGAGCGCGCGCGTGGCTC 504
DB	
QY	140 AAAAAATCTACAAAGAGATATCATTTAAAAAGAAATATTGGGGCTGGCGCGTGGCTC 199
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QY	505 ACGCTGTAAATCCAGCACCTTGGGAGCGCGAGCGGTGGATCAAGAGTCAAGAGATC 564
DB	
QY	200 ACGCTGTAAATCCAGCACCTTGGGAGCGCGAGCGGTGGATCAAGAGTCAAGAGATC 259
DB	
QY	565 GAGACCATCTGGCTACAGGTGAACCCCGCTCTACTTAAAAATTCAAAAAATAATT 624
DB	
QY	260 GAGACCATCTGGCTAAACCGGTGAACCCCGCTCTCTATATAAATAACAAAAATAATT 319
DB	
QY	625 AGCTGGGCGTGGTGGCGGGCGCTGTAGTCCAGCTATTTCGGAGGCTGAGGAGAGAA 684
DB	
QY	320 AGCGGGCGTGGTGGTGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGAGAGAA 379
DB	
QY	695 TGGNTGAACTGGGAGGTGAGCTTGCAATGAGCAAGGTCCGGCCACTGCACTCCAGC 744
DB	
QY	380 TGGCGTGAACCCCGGAGCGGAGCTTGCAGTGAGCCGAGATGTTGCCACTGCACTCCAGC 439
DB	
QY	745 CTGGCGCAGACAGAGGAGACTCCATCTTA 772
DB	
QY	440 CTGGCAGCAGAACGAGACTCCGCTCTCA 467
DB	

RESULT 6
BG249643
LOCUS
DEFINITION 602319736F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4414905 5',
mRNA sequence.
ACCESSION BG249643
VERSION BG249643
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 822)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapsb-remail.nih.gov
Tissue Procurement: ATCC
cdna Library Preparation: Life Technologies, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M0143 row: h column: 10.
High quality sequence stop: 546.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:4414905"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 89"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES
source
1..822
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:4414905"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 89"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 33.4%; Score 258.2; DB 12; Length 822;
Best Local Similarity 90.8%; Pred. No. 7.8e-43;
Matches 286; Conservative 0; Mismatches 25; Indels 4; Gaps 1;
QY 458 AATGTATATTTTAAAGAAATGTTTGTAGAGCGCGCGGTGGCTACGCGCTGTAATCC 517
DB 178 ACTGAATTTTAAAAATTCAGATATCGCGCGCGGTGGCTACGCGCTGTAATCC 237
QY 518 CAGCACTTTGGAGCGCGCGGTGGCTACGAGGTCAGAGATCGAGACCATCCTGG 577
DB 238 CAGCACTTTGGAGCGCGCGGTGGCTACGAGGTCAGAGATCGAGACCATCCTGG 297
QY 578 CTAAACCGGTGAACCCCGTCTCTACTAAAAATTCAAAAAATAATTAGCTGGCGGTGGT 637
DB 298 CTAAACCGGTGAACCCCGTCTCTACTAAAAATTCAAAAAATAATTAGCTGGCGGTGGT 353
QY 638 GCGGCGCGCTAGTCCAGCTATTCGAGGCTGAGGAGGAGAGAGAGAGAGAGAGAGAG 697
DB 354 AGCGGCGCGCTAGTCCAGCTATTCGAGGCTGAGGAGGAGAGAGAGAGAGAGAGAG 413
QY 698 GGAGGTGAGCTTGCANTGAGCAAGGTGGCGCCACTGCACTCCAGCTGGGCGACAGAG 757
DB 414 GGAGGCGGAGCTTGCANTGAGCAAGGTGGCGCCACTGCACTCCAGCTGGGCGACAGAG 473
QY 758 CGAGACTCCATCTTA 772
DB 474 CGAGACTCCGCTTCA 488

AQ351424/c
LOCUS
DEFINITION RPC111-111K4_TV RPC1-11 Homo sapiens genomic clone RPC1-11-111K4,
genomic survey sequence.
ACCESSION AQ351424
VERSION AQ351424.1
KEYWORDS GI:4178759
SOURCE GSS.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 592)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
TITLE Use of BAC End Sequences from Library RPC1-11 for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: RPC111-111K4.TU
Contact: Shaving Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
Seq primer: 17
Class: BAC ends.
Location/Qualifiers
1..592
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/db_xref="taxon:9606"
/clone="RPC1-11-111K4"
/sex="Male"
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/clone_lib="RPC1-11"
/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
RPC111 Human Male BAC Library"

ORIGIN
Query Match 33.0%; Score 255; DB 28; Length 592;
Best Local Similarity 88.2%; Pred. No. 3.4e-42;
Matches 276; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 459 ATGTATATTTTAAAGAAATGTTTGTAGAGCGCGCGGTGGCTACGCGCTGTAATCC 518
DB 359 ATTCAGGTTATAAAAGTAGATACCTTTTGTAGCGCGGACGGGTGCTCATGCTGTAATCC 300
QY 519 AGCACTTTGGAGCGCGCGGTGGCTACGAGGTCAGAGATCGAGACCATCCTGGC 578
DB 299 AGCACTTTGGAGCGCGCGGTGGCTACGAGGTCAGAGATCGAGACCATCCTGGC 240
QY 579 TAAACAGCGTGAACCCCGTCTCTACTAAAAATTCAAAAAATAATTAGCTGGCGGTGGT 638
DB 239 TAACATGGTGAACCCCGTCTCTACTAAAAATTCAAAAAATAATTAGCGGCGGTGGT 180
QY 639 GCGGCGCGCTAGTCCAGCTATTCGAGGCTGAGGAGGAGAGAGAGAGAGAGAGAGAG 698
DB 179 GCGGCGCTTGTAGTCCAGCTACTCGGAGGCTGAGGAGGAGAGATGCGTGAACCTGG 120
QY 699 GAGGTGAGCTTGCANTGAGCAAGGTGGCGCCACTGCACTCCAGCTGGGCGACAGAG 758
DB 119 GAGGCGGAGCTTGCANTGAGCGGAGATTGCACCACTGCACTCCAGCTGGGCGACAGAG 60
QY 759 GAGACTCCATCTT 771
|||||

```

Db      59 AAGACTCTGTCTT 47
RESULT 8
BU615970/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strauberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 11-299, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
Location/Qualifiers
1..701
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-DF0-ben-c-08-0-UI"
/tissue_type="Subchondral Bone"
/dev_stage="Adult"
/lab_hosts="DH10B (Life Technologies)"
/clone_lib="NCI-CGAP DF0"
/notes="Organ: Bone; Vector: p7773-Pac (Pharmacia) with a
modified polylinker; Site: 1: Scor 1; Site_2: Not 1;
NCI CGAP DF0 is a cDNA library containing the following
tissue(s): Subchondral Bone. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p7773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GTTAAGCGTC.
TAG TISSUE-subchondral bone
TAG LIB-UI-H-DF0
TAG_SEQ-GTTAAGCGTC"
ORIGIN
Query Match 33.0%; Score 255; DB 13; Length 701;
Best Local Similarity 86.4%; Pred. No. 3.5e-42;
Matches 293; Conservative 0; Mismatches 42; Indels 4; Gaps 1;
QY 434 TTGTGAGTGCAGGAGTGAATATGTTATATTTTAAAGAACTTTTAGAGCGCGG 493
DB 352 TTGGGAGATGTTAATATGTTGAAGACACACATGTTTAAAGATTCGCCATCTGCGCGG 293
QY 494 CGCGGTGGCTCAGCGCTGTAATCCAGCACCTTTGGGAGCGCGAGCGGTCCGATCACGAG 553
DB 292 CGCGGTGGCTCAGCGCTGTAATCCAGCACCTTTGGGAGCGCGAGCGGTCCGATCACGAG 233
QY 554 GTCAGGAGATCGAGACCATCTCGGTACACAGGTGAACCCCGCTCTCTACTAAATTC 613
Db      232 GTCAGGAGATCGAGACCATCTCGGTACACAGGTGAACCCCGCTCTCTACTAAAT --- 176
QY 614 AAAAAAAAAATTAGCTGGCGCTGCTGGCGCGCGCTTAGTCCAGTATTCGGAGGCTG 673
DB 175 -ACAAAAAATTAGCGGGCGTGTAGCGGCGCGCTGTAGTCCAGCTACTTCGGAGGCTG 117
QY 674 AGGAGAGAGATGCGTGTACCTCGGAGGTGGAGCTTGCAATGAGCAAGGTCCGCCAC 733
DB 116 AGGAGAGAGATGCGGTGAACCCCGGAGGCGGAGCTTGCAGTGAGCGGAGATCGGCCAC 57
QY 734 TGCACTCCAGCTGGCGCGAGCGAGACTCCATCTTA 772
DB 56 TGCACTCCAGCTGGCGCGAGCGAGACTCCGCTCTCA 18
B80438 458 bp DNA linear GSS 24-OCT-1998
CIT-HSP-2045M21.TR CIT-HSP Homo sapiens genomic clone 2045M21,
genomic survey sequence.
ACCESSION B80438
VERSION B80438.1 GI:2867461
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 458)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuwa,H.,
Simon,K. and Venter,J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other GSSs: CIT-HSP-2045M21.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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/db_xref="taxon:9606"
/clone="2045M21"
/sex="Male"
/cell_type="Sperm"
/clone_lib="CIT-HSP"
/notes="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"
ORIGIN
Query Match 32.9%; Score 254.2; DB 28; Length 458;
Best Local Similarity 90.0%; Pred. No. 4.9e-42;
Matches 271; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 472 AAGATGTTGTAGAGCGCGCGGTGCTCAGCTGTATCCAGCACTTTGGGAG 531
DB 56 AAAAAATCTTGGGCTCGCGCGCGGTGCTCAGCTGTATCCAGCACTTTGGGAG 115
QY 532 GCCGAGCGCGTCCGATCACAGGTCCAGAGATCGAGACCATCTCGGTACACGTTGAA 591
DB 116 GCCAAGCGCGCGGATCAACAGGTCCAGAGATTGAGACCATCTCGGTAAACCGTTGAA 175

```


Matches 286; Conservative 0; Mismatches 38; Indels 2; Gaps 1;
QY 447 AGGAGTGTAAATGATATATTTTAAAGAAATTTCTAGAGCGCGCGGTGGCTCAC 506
Db 372 ATGTATTTTATTTTAAAGCTTAAATAAACATGTAGAGCGCGCGGTGGCTCAC 313
QY 507 GCTGTATCCAGACACTTTGGAGGCGGAGCGGTGCGATCACAGGTCTAGGAGATCGA 566
Db 312 GCTGTATCCAGACACTTTGGAGGCGGAGCGGTGCGATCACAGGTCTAGGAGATCGA 253
QY 567 GACCATCTGGGTAAACAGCGTGAACCCCGTCTCTACTAAATAATCAAAAAAAATTTAG 626
Db 252 GACCATCTGGGTAAACAGCGTGAACCCCGTCTCTACTAAATAATCAAAAAAAATTTAG 195
QY 627 CTGGGCGTGGTGGGCGGCGCTGTAGTCCAGACTATTCGGAGGCTGAGGCGAGGAGATG 686
Db 194 CCGGGCGTAGTGGGCGGCGCTGTAGTCCAGACTATTCGGAGGCTGAGGCGAGGAGATG 135
QY 687 GNTGAACTCTGGAGGTGAGCTTGCANTGAGCCAGGTTCGGGCGGCGTCCAGCGCT 746
Db 134 GCGTGAACCCGGAGCGGAGCTTGCGTGAAGCCGAGATTCGCCACCTGCACTCCAGCGCT 75
QY 747 GGGCGACAGAGCGAGACTCCATCTTA 772
Db 74 GGGCGACAGAGCGAGACTCCGTCCTCA 49

RESULT 14
AG144106 662 bp DNA linear GSS 08-JAN-2002
LOCUS Pan troglodytes DNA, clone: RP43-005A01.TJ, genomic survey
DEFINITION
ACCESSION AG144106
VERSION AG144106.1 GI:16673784
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of Library RPCI-43
JOURNAL Unpublished
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcorI
R.Site 2 : EcorI
Location/Qualifiers
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-005A01.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 32.7%; Score 252.2; DB 29; Length 662;
Best Local Similarity 92.0%; Pred. No. 1.3e-41;
Matches 277; Conservative 0; Mismatches 20; Indels 4; Gaps 1;
QY 472 AAGAAATTTGTAGAGCGCGCGGTGGCTCAGCCCTGTATATCCAGCACTTTGGGAG 531
Db 284 AAGAAATGCCACACCGCGCGCGGTGGCTCAGCCCTGTATATCCAGCACTTTGGGAG 343
QY 532 GCGAGGCGGTGCGATCAACAGGTCTAGGAGATCGAGACCATCTGCTTAACACGGTGA 591
Db 344 GCGAGGCGCGGTGCGATCAACAGGTCTAGGAGATCGAGACCATCTGCTTAACACGGTGA 403
QY 592 CCCGCTCTCTACTAAATAATCAAAAAAAATTTAGTGGCGGTGGTGGCGGCGCTGTA 651
Db 404 CCCGCTCTCTACTAAATAATCAAAAAAAATTTAGTGGCGGTGGTGGCGGCGCTGTA 459
QY 652 GTCCAGCTATTCGGAGGCTGAGGCGAGGAGATGCGTGAACCTGGGAGGTGAGCTTG 711
Db 460 GTCCAGCTATTCGGAGGCTGAGGCGAGGAGATGCGTGAACCTGGGAGGTGAGCTTG 519
QY 712 CANTGAGCAAGTCCGCGCACTGCACTCCAGCTGGGCGAGAGAGAGACTCCATCTT 771
Db 520 CAGTGAAGCGAGATCGCGCACTGCACTCCAGCTGGGCGAGAGAGACTCCATCTT 579
QY 772 A 772
Db 580 A 580

RESULT 15
BZ601227 1073 bp DNA linear GSS 08-JUN-2003
LOCUS WHADC89TR Human MCF7 breast cancer cell line library (MCF7.1) Homo
DEFINITION sapiens genomic clone MCF7.1-19P9, genomic survey sequence.
ACCESSION BZ601227
VERSION BZ601227.1 GI:31509689
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1073)
Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q., Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P., Gray, J.W. and Collins, C.
End-sequence profiling: Sequence-based analysis of aberrant genomes
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
TITLE
JOURNAL
MEDLINE 22709111
PUBMED 12788976
COMMENT Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
Class: BAC ends.
Location/Qualifiers
1. .1073
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="MCF7.1-19P9"
/sex="female"
/clone_lib="Human MCF7 breast cancer cell line library (MCF7.1)"
/note="Vector: pECBAC1; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

FEATURES
source
1. .1073
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="MCF7.1-19P9"
/sex="female"
/clone_lib="Human MCF7 breast cancer cell line library (MCF7.1)"
/note="Vector: pECBAC1; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

ORIGIN

Query Match	32.7%	Score 252.2	DB 28	Length 1073
Best Local Similarity	89.3%	Pred. No. 1.4e-41		
Matches 283	Conservative 0	Mismatches 30	Indels 4	Gaps 1

Qy	456	AAATGTATATTTTAAAGATTTGTAGAGCGCGCGGTGCTCACGCTGTAT	515
Db	302	AAATTTAGTGGCTTAAAAATGAAAAATGGCGCGGTGCTCACGCTGTAT	361
Qy	516	CCAGCACTTTGGAGCGCGGTGCGATCACGAGTTCAGAGATCGAGACCATCCT	575
Db	362	CCAGCACTTTGGAGCGCGGTGCGATCACGAGTTCAGAGATCGAGACCATCCT	421
Qy	576	GGCTAACACCGGTGAACCCCGTCTCTACTAAAAATTCAAAAATTTAGTGGCGTG	635
Db	422	GGCTAAAAACCGGTGAACCCCGTCTCTACTAAAAATAC-----AAAAATTTAGCGCGGTGA	477
Qy	636	GTGCGGGCGCTCTAGTCCAGCTATTTCGGAGGCTGAGGAGAGAGATGGCTGAACC	695
Db	478	GTGCGGGCGCTCTAGTCCAGCTATTTCGGAGGCTGAGGAGAGAGATGGCTGAACC	537
Qy	696	TGGAGGTGAGCTTGCAATGAGCCAGGTGCGCCACTGCACTCCAGCCTGGGCGACAG	755
Db	538	CGGAGGCGGAGCTTGCAATGAGCCAGGTGCGCCACTGCACTCCAGCCTGGGCGACAG	597
Qy	756	AGGAGACTCCATCTTA	772
Db	598	AGGAGACTCCGCTCA	614

Search completed: May 6, 2004, 11:48:52
 Job time : 2581.23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 06:25:29 ; Search time 3361.45 Seconds
(without alignments)
9954.293 Million cell updates/sec

Title: US-09-451-739H-8
Perfect score: 772
Sequence: 1 aaagcgtctcggcgagc.....cagagcgagactcattta 772

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.pl.*
8: gb.pr.*
9: gb.ro.*
10: gb.sts.*
11: gb.sy.*
12: gb.un.*
13: gb.vi.*
14: gb.ba.*
15: em.fun.*
16: em.hum.*
17: em.in.*
18: em.mu.*
19: em.om.*
20: em.ov.*
21: em.pat.*
22: em.ph.*
23: em.pl.*
24: em.ro.*
25: em.sts.*
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27: em.vi.*
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29: em.htg.inv.*
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32: em.htg.pln.*
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40: em.htgo.hum.*
41: em.htgo.mus.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	770	99.7	772	6	AX367049	Sequence
2	770	99.7	772	9	AF149724	AX367049 Homo sapi
3	754.8	97.8	86703	2	AL159989	AF149724 Homo sapi
4	754.8	97.8	248968	9	HSXDPB	AL159989 Homo sapi
5	277.6	36.0	97465	9	AL157820	AL159763 Homo sapi
6	277.6	36.0	159983	2	AC013713	AL157820 Human DNA
7	276	35.8	1074	9	AF149722	AC013713 Homo sapi
8	276	35.8	1143	6	AX367043	AF149722 Homo sapi
9	276	35.8	1189	9	AF149723	AX367043 Sequence
10	276	35.8	1533	6	AX367042	AF149723 Homo sapi
11	276	35.8	1533	9	AF149721	AX367042 Sequence
12	276	35.8	1902	6	AR079046	AF149721 Homo sapi
13	276	35.8	1902	6	AR087457	AR079046 Sequence
14	276	35.8	1902	6	AR110646	AR087457 Sequence
15	276	35.8	1902	6	AR154563	AR110646 Sequence
16	276	35.8	1905	6	AX839842	AR154563 Sequence
17	276	35.8	1980	9	AB024404	AX839842 Sequence
18	276	35.8	2061	6	AR087464	AB024404 Homo sapi
19	276	35.8	2061	6	AR110653	AR087464 Sequence
20	276	35.8	2061	6	AR154570	AR110653 Sequence
21	276	35.8	2061	6	AR171883	AR154570 Sequence
22	276	35.8	2061	9	AF001954	AR171883 Sequence
23	276	35.8	2096	9	HSP33ING2	AF001954 Homo sapi
24	276	35.8	2296	9	BC018348	HSP33ING2 Homo sapi
25	276	35.8	2306	9	AB031269	BC018348 Homo sapi
26	276	35.8	2444	9	AB024401	AB031269 Homo sapi
27	276	35.8	2552	9	HSING3	AB024401 Homo sapi
28	276	35.8	2886	9	AF181849	HSING3 Homo sapi
29	276	35.8	2891	9	AB024402	AF181849 Homo sapi
30	276	35.8	2897	9	AF181850	AB024402 Homo sapi
31	276	35.8	2925	9	AB037386S2	AF181850 Homo sapi
32	276	35.8	163350	6	AX839844	AB037386 Homo sapi
33	272.8	35.3	2061	6	AR219160	AX839844 Sequence
34	271.4	35.2	167691	9	HS406A7	AR219160 Sequence
35	270.6	35.1	124615	9	AC006019	AL023284 Human DNA
36	270.6	35.1	184526	9	AC114969	AC006019 Homo sapi
37	270.4	35.0	61027	9	AC034204	AC114969 Homo sapi
38	270.4	35.0	191308	9	AC034243	AC034204 Homo sapi
39	269.6	34.9	97653	2	AC137570	AC034243 Homo sapi
40	269.6	34.9	149110	9	AP003692	AC137570 Homo sapi
41	269.2	34.9	132433	9	HSJ210B1	AP003692 Homo sapi
42	269.2	34.9	213585	9	BS000086	AL078593 Human DNA
43	269	34.8	157834	2	AC022931	BS000086 Pan trogl
44	268.2	34.7	107848	9	AC105030	AC022931 Homo sapi
45	268.2	34.7	154604	2	AC104974	AC105030 Homo sapi

ALIGNMENTS

RESULT 1
AX367049
LOCUS AX367049
DEFINITION Sequence 8 from Patent WO0147959.
ACCESSION AX367049
VERSION AX367049.1 GI:18855271
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and
Chen,Y.T.
TITLE Isolated nucleic acid molecules encoding cancer associated

Pred. No. is the number of results predicted by chance to have a

antigens, the antigens per se, and uses thereof
Patent: WO 0147959-A 8 05-JUL-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL
SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation
(US)

LOCATION/Qualifiers
1. .772
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 99.7%; Score 770; DB 6; Length 772;
Best Local Similarity 100.0%; Pred. No. 4.1e-184;
Matches 772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACGGTCTTCGGCGGAGCGGACCACTAGACCGGTGAGACCGCTCCAGCAACCGCGA 60
Db 1 AAACGGTCTTCGGCGGAGCGGACCACTAGACCGGTGAGACCGCTCCAGCAACCGCGA 60
QY 61 CCCACGACGAGCTCACCTCGGCGACCGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGA 120
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Db 121 AGCAGGCTCCATGGCCAGCGGTAGCGGAGCGGTCCCGCGAGACCTCCCATGACG 180
QY 181 CCACGAGCGCCCTCTACTGGGAGATGATCGGCTGCGACCAACGAAAGTGCCTCCAGTGGT 240
Db 181 CCACGAGCGCCCTCTACTGGGAGATGATCGGCTGCGACCAACGAAAGTGCCTCCAGTGGT 240
QY 241 TCCGCTTCTCGTGTGTGAGTCTCAACCATAAACCAAGCGAAGTGTGTCTGTTCCAGAT 300
Db 241 TCCGCTTCTCGTGTGTGAGTCTCAACCATAAACCAAGCGAAGTGTGTCTGTTCCAGAT 300
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Db 301 GCCCGGGAAGAAACGATGGGCAAGCCCTTGAGAGTCCAGAAAAAAGAGCGGCTTATA 360
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Db 361 ACAGGTAGTTGGGACATGGCTCTAATAGTGGAGAGAAACAAATAGCCAGTGTGTGA 420
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Db 541 GTCCGATCAGAGGTCCAGGAGATCGAGACCATCTGGCTAACACGCTGAACCCCGTCTC 600
QY 601 TACTAAAAATTCAAAAAATTTAGTGGCGGTGGTGGCGGCGCTGTAGTCCAGCT 660
Db 601 TACTAAAAATTCAAAAAATTTAGTGGCGGTGGTGGCGGCGCTGTAGTCCAGCT 660
QY 661 ATTCCGGAGGCTGAGGAGGAGATGCGTGAACCTGGAGGTGAGCTTGCANTGAGCC 720
Db 661 ATTCCGGAGGCTGAGGAGGAGATGCGTGAACCTGGAGGTGAGCTTGCANTGAGCC 720
QY 721 AAGTTCGGCCACTGCACTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCT 772
Db 721 AAGTTCGGCCACTGCACTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCT 772

RESULT 2
AF149724 772 bp mRNA linear PRI 10-DEC-2001
LOCUS Homo sapiens INGI-like tumor suppressor protein mRNA, complete cds.

AF149724
AF149724.1 GI:8131966
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 772)
Jager, D., Stockert, E., Scanlan, M.J., Gure, A.O., Jager, E., Knuth, A.,
Old, L.J., and Chen, Y.T.
Cancer-testis antigens and INGI tumor suppressor gene product are
breast cancer antigens: characterization of tissue-specific INGI
transcripts and a homologue gene
Cancer Res. 59 (24), 6197-6204 (1999) 12/99
20090239
PUBMED 10626813
2 (bases 1 to 772)
Jaeger, D.
Direct Submission
Submitted (10-MAY-1999) Pathology, Cornell University, 1300 York
Avenue, New York, NY 10021, USA
Location/Qualifiers
1. .772
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/codon_start=1
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/translation="MIRCDNECPIEWFRFVSVLNHKKPKWYKRCRGRKNDGSP"

CDS
Query Match 99.7%; Score 770; DB 9; Length 772;
Best Local Similarity 100.0%; Pred. No. 4.1e-184;
Matches 772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGGTTCTCGGCGGAGCGCAACACTAGAACCGTGAGAACCGTCCAGCAACCGCGA 60
Db 1 AAAGGTTCTCGGCGGAGCGCAACACTAGAACCGTGAGAACCGTCCAGCAACCGCGA 60
QY 61 CCCACGACGAGCTCACCTCGGCGACCGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGA 120
Db 61 CCCACGACGAGCTCACCTCGGCGACCGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGA 120
QY 121 AGCAGGCTCCATGGCCAGCGGTAGCGGAGCGGTCCCGCGAGACCTCCCATCGACC 180
Db 121 AGCAGGCTCCATGGCCAGCGGTAGCGGAGCGGTCCCGCGAGACCTCCCATCGACC 180
QY 181 CCAGCGAGCCCTCTCTACTGGGAGATGATCCGCTGCGACCAACGAAATGCCATCGAGTGGT 240
Db 181 CCAGCGAGCCCTCTCTACTGGGAGATGATCCGCTGCGACCAACGAAATGCCATCGAGTGGT 240
QY 241 TCCGTTCTCGTGTGTGAGTCTCAACCATAAACCAAGCGCAAGTGTGTCTGTTCCAGAT 300
Db 241 TCCGTTCTCGTGTGTGAGTCTCAACCATAAACCAAGCGCAAGTGTGTCTGTTCCAGAT 300
QY 301 GCCCGGGAAGAAACGATGGGCAAGCCCTTGAGAGTCCAGAAAAAAGAGCGGCTTATA 360
Db 301 GCCCGGGAAGAAACGATGGGCAAGCCCTTGAGAGTCCAGAAAAAAGAGCGGCTTATA 360
QY 361 ACAGGTAGTTGGGACATGGCTCTAATAGTGGAGAGAAACAAATAGCCAGTGTGTGA 420
Db 361 ACAGGTAGTTGGGACATGGCTCTAATAGTGGAGAGAAACAAATAGCCAGTGTGTGA 420
QY 421 TTACATTGCCACCTTCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 480
Db 421 TTACATTGCCACCTTCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 480
QY 481 GTTAGGCGCGGCGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 540


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AL157820      97465 bp      DNA      linear      PRI 04-JAN-2002
LOCUS      Human DNA sequence from clone RP11-8D7 on chromosome 13, complete
DEFINITION
ACCESSION      AL157820
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 97465)
Direct Submission
Submitted (04-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
clonerequest@sanger.ac.uk
On Jan 6, 2002 this sequence version replaced gi:17154265.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; SW,
SWISSPROT; Tr, TrEMBL; Wp, WormPep; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
RP11-8D7 is from the library RP11-11.1 constructed by the group of
Pier de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-8D7
It may be shorter because we sequence overlapping sections only
once, except for a short overlap.
The true right end of clone RP11-8D7 is at 97465 in this sequence.
The true left end of clone RP11-120J20 is at 68161 in this
sequence. The true right end of clone RP11-90L1 is at 2000 in this
sequence.
FEATURES
Location/Qualifiers
1. 97465
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/mol_type="genomic DNA"
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/chromosomes="13"
/clone="RP11-8D7"
/clone_lib="RP11-11.1"
/clone_id="22847"
/note="Single clone region. Assembly confirmed by
restriction digest data."
misc_feature
51946..51960
/note="Single clone region. Assembly confirmed by
restriction digest data."
ORIGIN
Query Match 36.0%; Score 277.6; DB 9; Length 97465;
Best Local Similarity 81.0%; Pred. No. 2.2e-59;
Matches 423; Conservative 0; Mismatches 59; Indels 40; Gaps 7;
QY 2 AACGCTTCGGCGGACGACACTAGACCGTGAGACGCTCCAGCAGCGCGAC 61

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Db 57673 AAGCGCTCAGCGGCGGCGGCAACAAACAGAGAACCGTGAGAACGCGTCCAGCAACCAAGA- 57731
QY 62 CCACGACGAGTCACTCTGGGCGACGCCCAAGAGAGAGAAAGCCAGACCTCTAGAGAA 121
Db 57732 CCACGACGACGCGGCTCTGGGCGACACCCAGAGAGAGAGGCGCCAGACCTCCAGAGAA 57791
QY 122 GCAGGCGCTCCATGGCCAAAGGCGGTAGCGGCGAGGCGCTCCCCCGCAGACCTCCCATCGACCC 181
Db 57792 GAAGCGCTCCAGGCGCAAGCGGAGGAGAGGCGCTCCCTCCGACCTCCCATCGACCC 57851
QY 182 CAGCGAGCC-----CTCTACTGGGAGAGATCCGCTGGGA 217
Db 57852 CAACGAACCCACGTACTGTGTGTGCAACACAGCTCTCTATGGGAGATGATCGGCTGGGA 57911
QY 218 CA---ACGAATCCCCCATCGAGTGGTTCGGCTTCTCGTGTGTGAGTCTCAACCAATAAAC 274
Db 57912 CAACGAGAGTCCCATCGAGTGGTTCACATCTCTCGTGTGGGGCTCAATCATATAAAC 57971
QY 275 AAAGCGCAAGTGGTACTGTTCAGATGCGGGGGAAGAAGC-----ATGGGCAAGC 326
Db 57972 CAAGGCGCAAGTGGTACTGTCTCCCAAGTGCGGGGGAGAACAGAGACATCGGCAAGC 58031
QY 327 CTTGAGAGAGTCCAGAAAAAAGAGGGCTTATAACAGTAGTGTGGGAGCATGCGTCTA 386
Db 58032 CTTGAGAGATCA-AAAAAGAGGGCTTACACAGTAGTGTGTGACAGGCGCTG 58089
QY 387 ATAGTGAGGAGAACAAATAAGCCAGTGTGTGATTAATCCACCTTCTGAGGTGC 446
Db 58090 GT-GTGAGGAGGACAAATAAAC-GTGTATTATTATCATCTGCTCCTTTGTGAGGTGC 58147
QY 447 AGGAGTGTAAATGTATATTTTAAAGAAATGCTGTAGAG 488
Db 58148 AGGAGTGTAAATGTATATTTTAAAGAAATGTAGTAAGG 58189

RESULT 6
AC013713      159983 bp      DNA      linear      HTG 10-SEP-2000
LOCUS      Homo sapiens clone RP11-2207, WORKING DRAFT SEQUENCE, 19 unordered
DEFINITION      pieces.
ACCESSION      AC013713
VERSION      AC013713.5 GI:10047774
HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 159983)
AUTHORS      Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE      Homo sapiens, clone RP11-2207
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 159983)
AUTHORS      Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavskiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArillano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferrelira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, K., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 10, 2000 this sequence version replaced gi:7280307.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

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Db 149861 CCTGAGAAATCCA--AAAAAGAGAGGGCTTACAACAGGTAGTTTGTGGACAGCGGCTG 149918
QY 387 ATAGTGGAGGAAACAAATATAGCCAGTGTGTGATGATACATGTCACCTTTGCTGAGGTGC 446
Db 149919 GT-GTGGAGGAGCAAAATAAACCC-GTGTATTTATTACATTCGTGCTTTTGTGAGGTGC 149976
QY 447 AGGAGGTGTAATAATGTATATTTTAAAGAAATGTTGTTAGAGG 488
Db 149977 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGTAAAGG 150018

RESULT 7
AF149722 AF149722 1074 bp mRNA linear PRI 05-MAR-2000
LOCUS Homo sapiens INGI1 tumor suppressor, variant B (ING1) mRNA, complete
DEFINITION cds.
ACCESSION AF149722
VERSION AF149722.1 GI:7158366
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1074)
AUTHORS Jager,D., Stockert,E., Scanlan,M.J., Gure,A.O., Jager,E., Knuth,A.,
Old,L.J. and Chen,Y.T.
TITLE Cancer-testis antigens and INGI1 tumor suppressor gene product are
breast cancer antigens: characterization of tissue-specific INGI1
transcripts and a homologue gene
Cancer Res. 59 (24), 6197-6204 (1999)
JOURNAL
MEDLINE 20090239
PUBMED 10626813
REFERENCE 2 (bases 1 to 1074)
AUTHORS Jager,D.
Direct Submission
TITLE Submitted (11-MAY-1999) Pathology, Cornell University, 1300 York
Avenue, New York, NY 10021, USA
JOURNAL
FEATURES
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1. .1074
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ORIGIN
Query Match 35.8%; Score 276; DB 9; Length 1074;
Best Local Similarity 80.8%; Pred. No. 4e-59;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
QY 2 AAGCGTTCTCGCGGAGCGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAACCGCGAC 61
Db 433 AAGCGTCTACCGCGGAGCGCAACAAACGAGAACCGGTGAGAACCGGTCCAGCAACCGCA- 491
QY 62 CCACGACGACGTCACCTCGGGGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGAA 121
Db 492 CCACGACGACGCGGCTCGGGGACACCCCAAGAGAGAGAGGACCAAGACCTCCAGAGAA 551
QY 122 CGAGGGCTCCATGGCAAGGCTAGCGGAGCGGCTCCCGCGAGACCTCCCATCGACCC 181
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552 GAAGCGCTCAAGGCCAAGGCGGAGCGAGAGCGGTCCCTCCGACCTCCCATCGACCC 611
182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTGCGA 217
612 CAACGACCCAGTACTCTCTGTGCAACAGAGTCTCCTATGCGGAGATGATCGGCTGCGA 671
218 CA---ACGAATGCCCATCGAGTGGTTCCGCTTCTCGTGTGTGAGTCTCAACCATTAACC 274
672 CAACGACGAGTCCCGCATCGAGTGGTTCCACTTCTCGTGGTGGGCTCAATCATTAACC 731
275 AAAGCGCAAGTGTACTGTTCAGATGCCGGGAAGAACG-----ATGGGCAAAAGC 326
732 CAAGGCGAAGTGTACTGTCCCAAGTGCGGGGGAGAACGAGAACCATGGAACAAAGC 791
327 CTTGAGAAAGTCCAGAAACCAAGGCTTATAACAGTAGTTTGGGAGCATCGCTCTA 386
792 CTTGAGAAATCCA--AAAAAGAGAGGCTTACACAGTAGTTTGTGACAGGCGCGCTG 849
387 ATAGTGGAGAGCAAAATAATAGCCAGTGTGTGATTACATTGCCACCTTTGCTGAGGTGC 446
850 GT-GTGGAGGAGCAAAATTAACCC-GTGTATTTATTACATTCGCTTGTGAGGTGC 907
447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTTAGAGG 488
908 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGAAAGG 949

RESULT 8
AX367043 AX367043 1143 bp DNA linear PAT 16-FEB-2002
LOCUS Sequence 2 from Patent WO0147959.
DEFINITION AX367043
ACCESSION AX367043
VERSION AX367043.1 GI:18855268
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and
Chen,Y.T.
TITLE Isolated nucleic acid molecules encoding cancer associated
antigens, the antigens per se, and uses thereof
Patent: WO 0147959-A 2 05-JUL-2001;
LUDWIG-INSTITUT FOR CANCER RESEARCH (US); MEMORIAL
SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation
(US)
FEATURES
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1. .1143
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ORIGIN
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Best Local Similarity 80.8%; Pred. No. 4e-59;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
QY 2 AAGCGTTCTCGCGGAGCGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAACCGCGAC 61
Db 502 AAGCGTCTACCGCGGAGCGCAACAAACGAGAACCGGTGAGAACCGGTCCAGCAACCGCA- 560
QY 62 CCACGACGACGTCACCTCGGGGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGAA 121
Db 561 CCACGACGACGCGGCTCGGGGACACCCCAAGAGAGAGAGGACCAAGACCTCCAGAGAA 620
QY 122 GCAGGGCTCCATGCCAAGCGGTAGCGGAGCGGCTCCCGCGAGACCTCCCATCGACCC 181
Db 621 GAAGCGCTCCAGGCCCAAGCGGAGGAGCGGCTCCCTGCGGACCTCCCATCGACCC 680
182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTGCGA 217
681 CAACGAAACCAACGTACTGTCTGTGTGCAACAGGTCTCTATGCGGAGATGATCGGCTGCGA 740
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QY 62 CCACGACGCTCACCTGGGACGCCCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGAA 121
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 QY 122 GCAGGGCTTCATGGCCAAAGGCTAGCGGACGGGTCCCGCCAGACCTCCCGCATCGACCC 181
 Db 1011 GAAGCGCTCCAAAGGCCAAAGCGGAGCGAGCGGCTCCCGTCCCGACCTCCCGATCGACCC 1070
 QY 182 CAGCGAGCC-----CTCTACTGGGAGATGATCGCTCCGA 217
 Db 1071 CAACGAACCCAGTACTGTCTGTGCAACCAAGTCTCTATGGGAGATGATCGCTCCGA 1130
 QY 218 CA---ACGAATGCCCATCGAGTGTCCGTTCTCGGTGTGTGAGTCTCAACCATAAACC 274
 Db 1131 CAACGACGAGTGGCCCATCGAGTGTCCCACTTCTCGTGGTGGGCTCAATCATAAACC 1190
 QY 275 AAAGCGCAAGTGTACTGTCCAGATGCCGGGGAAGACG-----ATGGGCAAGC 326
 Db 1191 CAAGGCGAAGTGTACTGTCTGTGCGGGGAGAACGAGAACCATGGCAAGC 1250
 QY 327 CTTGAGAGTCCAGAAAAAAGCAGGCTTTATACAGGTAGTTTGGGGACATGCGTCTA 386
 Db 1251 CTTGAGAGTCCCA---AAAAAGAGAGGCTTTACACAGGTAGTTTGGGACAGGCGCTG 1308
 QY 387 ATAGTGAGGAGACAAATAAGCCAGTGTGTGATTACATTGCCACCTTTGCTGAGTGC 446
 Db 1309 GT-GTGGAGGACAAATAAACC-GTGTATTATTACATTGCTGCTTTGTTGAGTGC 1366
 QY 447 AGGAGTGTAAATGTATATTTTAAAGATGTTGTTAGAGG 488
 Db 1367 AAGGAGTGTAAATGTATATTTTAAAGATGTTGTTAGAGG 1408

RESULT 11

AF149721 1533 bp mRNA linear PRI 05-MAR-2000
 LOCUS Homo sapiens INGI tumor suppressor, variant A (ING1) mRNA, complete cds.
 DEFINITION
 ACCESSION AF149721
 VERSION AF149721.1 GI:7158364
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Jager D., Stockert, E., Scanlan, M.J., Gure, A.O., Jager, E., Knuth, A., Old, L.O. and Chen, Y.T.
 Cancer-testis antigens and INGI tumor suppressor gene product are breast cancer antigens: characterization of tissue-specific INGI transcripts and a homologue gene
 Cancer Res. 59 (24), 6197-6204 (1999)

JOURNAL

MEDLINE 20090239
 PUBMED 10626813
 Jager D.
 Direct Submission
 TITLE Submitted (11-MAY-1999) Pathology, Cornell University, 1300 York Avenue, New York, NY 10021, USA
 JOURNAL

FEATURES

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 /mol_type="mRNA"
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gene

1. 1533
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CDS

451..1290
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 YNR"

ORIGIN

Query Match 35.8%; Score 276; DB 9; Length 1533;
 Best Local Similarity 80.8%; Fred. No. 4.1e-59;
 Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
 QY 2 AAGCGTCTTCGCGCGCAGCGCAACAACTAGAACCGTGTGAGACGGCTCCAGCAACCGCAC 61
 Db 892 AAGCGTCTCACGCGCGCAGCGCAACAAACGAGAACCGTGTGAGACGGCTCCAGCAACCA 950
 QY 62 CCACGACGACGTCACTCTGGGACGCCCAAGAGAGAGAGAGCCCGACACTCTAAGAAGAA 121
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 QY 122 GCAGGCTCCATGGCCAAAGCGGTAGCGGACGGCTCCCGCCGACAGACCTCCCGCATCGACCC 181
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 QY 182 CAGCGAGCC-----CTCTACTGGGAGATGATCGCTCCGA 217
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 QY 218 CA---ACGAATGCCCATCGAGTGTCCGTTCTCGGTGTGTGAGTCTCAACCATAAACC 274
 Db 1131 CAACGACGAGTGGCCCATCGAGTGTCTCACTTCTCGTGGTGGGCTCAATCATAAACC 1190
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 Db 1191 CAAGGCGAAGTGTACTGTCTGTGCGGGGAGAACGAGAACCATGGCAAGC 1250
 QY 327 CTTGAGAGTCCAGAAAAAAGCAGGCTTTATACAGGTAGTTTGGGGACATGCGTCTA 386
 Db 1251 CTTGAGAGTCCCA---AAAAAGAGAGGCTTTACACAGGTAGTTTGGGACAGGCGCTG 1308
 QY 387 ATAGTGAGGAGACAAATAAGCCAGTGTGTGATTACATTGCCACCTTTGCTGAGTGC 446
 Db 1309 GT-GTGGAGGACAAATAAACC-GTGTATTATTACATTGCTGCTTTGTTGAGTGC 1366
 QY 447 AGGAGTGTAAATGTATATTTTAAAGATGTTGTTAGAGG 488
 Db 1367 AAGGAGTGTAAATGTATATTTTAAAGATGTTTAGAGG 1408

RESULT 12

AR079046 1902 bp DNA linear PAT 31-AUG-2000
 LOCUS Sequence 1 from patent US 5965398.
 DEFINITION AR079046
 ACCESSION AR079046
 VERSION AR079046.1 GI:10005792
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE

1 (bases 1 to 1902)
 Garkavtsev, I. and Riabowol, K.
 DNA sequence encoding a tumor suppressor gene
 Patent: US 5965398-A 1 12-OCT-1999;

FEATURES

source

1. 1902
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 35.8%; Score 276; DB 6; Length 1902;

Best Local Similarity 80.8%; Pred. No. 4.2e-59;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY 2 AAGCGTCTCGGGGAGCGGCAACACTAGAACCGTGAAGCGGTCCAGCAACCGCGAC 61
DB 343 AAGCGTCTCGGGGAGCGGCAACACTAGAACCGTGAAGCGGTCCAGCAACCGCGA- 401

QY 62 CCACGACGACGTCACCTCGGGGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGAA 121
DB 402 CCACGACGACGTCACCTCGGGGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGAA 461

QY 122 GCAGGCTCCATGGCCCAAGGCTAGCGGAGCGGCTCCCGGAGACCTCCCATCGACCC 181
DB 462 GAAGCGCTCCAGGCGCAAGCGGAGCGGAGCGGCTCCCGGAGACCTCCCATCGACCC 521

QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCGGCTGCGA 217
DB 522 CAACGAACCCAGTACTGTCTGTGCAACCCAGGTCTCCTATGGGAGATGATCGGCTGCGA 581

QY 218 CA---ACGATGCCCATCGAGTGGTTCGGCTTCTCGTGTGAGTCTCAACCATAAACC 274
DB 582 CAACGACGAGTGGCCCATCGAGTGGTTCGGCTTCTCGTGTGAGTCTCAACCATAAACC 641

QY 275 AAGCGCAAGTGGTACTGTTCAGATGCGGGGAAAGAACG-----ATGGGCAAGC 326
DB 642 CRAAGGCAAGTGGTACTGTTCAGATGCGGGGAAAGAACG-----ATGGGCAAGC 701

QY 327 CCTTGAGAGTCCAGAAAACAGGCTTATATTTTAAAGAAATGTTGTAGAGG 488
DB 818 AAGGAGTGTAAATGTTATATTTTAAAGAAATGTTAGAAAGG 859

QY 387 ATAGTGAGGAGAAACAAATAGCCAGTGTGTGATTTACATTCGACCTTGTGAGGTGC 446
DB 760 GT-GTGAGGAGGACAAATAAACCC-GTGATTTATTATACATTCGCTCTGTTGAGGTGC 817

QY 447 AGGAAGTGTAAATGTTATATTTTAAAGAAATGTTGTAGAGG 488
DB 818 AAGGAGTGTAAATGTTATATTTTAAAGAAATGTTAGAAAGG 859

RESULT 13
LOCUS AR087457
DEFINITION Sequence 1 from patent US 5986078.
ACCESSION AR087457
VERSION AR087457.1 GI:10014220
KEYWORDS source
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1902)
AUTHORS Garkavtsev, I. and Riabowol, K.
TITLE DNA sequence encoding the tumor suppressor gene INGI
JOURNAL Patent: US 5986078-A 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..1902
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 35.8%; Score 276; DB 6; Length 1902;
Best Local Similarity 80.8%; Pred. No. 4.2e-59;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY 2 AAGCGTCTCGGGGAGCGGCAACACTAGAACCGTGAAGCGGTCCAGCAACCGCGAC 61
DB 343 AAGCGTCTCGGGGAGCGGCAACACTAGAACCGTGAAGCGGTCCAGCAACCGCGA- 401

QY 62 CCACGACGACGTCACCTCGGGGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGAA 121
DB 402 CCACGACGACGTCACCTCGGGGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGAA 461

QY 122 GCAGGCTCCATGGCCCAAGGCTAGCGGAGCGGCTCCCGGAGACCTCCCATCGACCC 181
DB 462 GAAGCGCTCCAGGCGCAAGCGGAGCGGAGCGGCTCCCGGAGACCTCCCATCGACCC 521

QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCGGCTGCGA 217
DB 522 CAACGAACCCAGTACTGTCTGTGCAACCCAGGTCTCCTATGGGAGATGATCGGCTGCGA 581

QY 218 CA---ACGATGCCCATCGAGTGGTTCGGCTTCTCGTGTGAGTCTCAACCATAAACC 274
DB 582 CAACGACGAGTGGCCCATCGAGTGGTTCGGCTTCTCGTGTGAGTCTCAACCATAAACC 641

QY 275 AAGCGCAAGTGGTACTGTTCAGATGCGGGGAAAGAACG-----ATGGGCAAGC 326
DB 642 CRAAGGCAAGTGGTACTGTTCAGATGCGGGGAAAGAACG-----ATGGGCAAGC 701

QY 327 CCTTGAGAGTCCAGAAAACAGGCTTATATTTTAAAGAAATGTTGTAGAGG 488
DB 818 AAGGAGTGTAAATGTTATATTTTAAAGAAATGTTAGAAAGG 859

DB 462 GAAGCGTCTCGGGGAGCGGCAACACTAGAACCGTGAAGCGGTCCAGCAACCGCGAC 521
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCGGCTGCGA 217
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QY 387 ATAGTGAGGAGAAACAAATAGCCAGTGTGTGATTTACATTCGACCTTGTGAGGTGC 446
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QY 447 AGGAAGTGTAAATGTTATATTTTAAAGAAATGTTGTAGAGG 488
DB 818 AAGGAGTGTAAATGTTATATTTTAAAGAAATGTTAGAAAGG 859

RESULT 14
LOCUS AR110646
DEFINITION Sequence 1 from patent US 6117633.
ACCESSION AR110646
VERSION AR110646.1 GI:12827460
KEYWORDS source
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1902)
AUTHORS Garkavtsev, I., Riabowol, K. and Gudkov, A.
TITLE DNA sequence encoding the tumor suppressor gene INGI
JOURNAL Patent: US 6117633-A 12-SEP-2000;
FEATURES Location/Qualifiers
source 1..1902
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
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Best Local Similarity 80.8%; Pred. No. 4.2e-59;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY 2 AAGCGTCTCGGGGAGCGGCAACACTAGAACCGTGAAGCGGTCCAGCAACCGCGAC 61
DB 343 AAGCGTCTCGGGGAGCGGCAACACTAGAACCGTGAAGCGGTCCAGCAACCGCGA- 401

QY 62 CCACGACGACGTCACCTCGGGGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGAA 121
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QY 122 GCAGGCTCCATGGCCCAAGGCTAGCGGAGCGGCTCCCGGAGACCTCCCATCGACCC 181
DB 462 GAAGCGCTCCAGGCGCAAGCGGAGCGGAGCGGCTCCCGGAGACCTCCCATCGACCC 521

QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCGGCTGCGA 217
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QY 218 CA---ACGATGCCCATCGAGTGGTTCGGCTTCTCGTGTGAGTCTCAACCATAAACC 274
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 QY 387 ATAGTGAGGAGAACAAATAAGCCAGTGTGTTGATTACATTGCCACCTTTGCTGAGGTGC 446
 Db 760 GT-GTGAGGAGGACAAATAAACCC-GTGTATTATTACATTGCTGCCCTTTGTTGAGGTGC 817
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RESULT 15
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 DEFINITION Sequence 1 from patent US 6238918.
 ACCESSION ARI154563
 VERSION ARI154563.1 GI:15122616
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1902)
 AUTHORS Garkavtsev, I. and Riabowol, K.
 TITLE DNA sequence encoding the tumor suppressor gene ING1
 JOURNAL Patent: US 6238918-A 1 29-MAY-2001;
 FEATURES
 Location/Qualifiers
 source
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 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 35.8%; Score 276; DB 6; Length 1902;
 Best Local Similarity 80.8%; Pred. No. 4.2e-59;
 Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
 QY 2 AAGCGTTCTCGGCGGAGCGCAACAACCTAGAACCGGTGAGAACCGCTCCAGCAACCGCGAC 61
 Db 343 AAGCGTCTACGGCGGAGCGCAACAACAGAACCGGTGAGAACCGCTCCAGCAACCGCA- 401
 QY 62 CCAGGAGCGTCACTCGGCGGAGCGCCAGGAGAGAGAGCCAGACCTCTAAGAGAA 121
 Db 402 CCAGGAGCGGCGCTCGGCGGAGCGCCAGGAGAGAGAGCCAGACCTCTAAGAGAA 461
 QY 122 GCAGGGCTCCATGGCCAAAGCGGTAGCGGAGCGGTCCCGGAGAGACCTCCCATCGACCC 181
 Db 462 GAAGCGCTCCAGGCGCAAGCGGAGGAGGCGTCCCTGCGGACCTCCCATCGACCC 521
 QY 182 CAGGGAGCC-----CTCTACTGGAGATGATCGCTGCGA 217
 Db 522 CAACGACCCACGCTACTGCTGTGCAACCAAGGTCTCTATGGGGAGATGATCGCTGCGA 581
 QY 218 CA---ACGAATGCCATCGAGTGGTTCGCTTCTCGTGTGAGTCTCAACCATTAACC 274
 Db 582 CACGACGAGTGCCCATCGAGTGGTTCCTCTCTCGTGGTGGGCTCAATCATTAACC 641
 QY 275 AAAGCGCAAGTGGTACTGTTCCAGATGCCGGGAGAGAACG-----ATGGGCAAGC 326
 Db 642 CAAGGCAAGTGGTACTGTTCCAGATGCCGGGAGAGAACG-----ATGGGCAAGC 701
 QY 327 CTTTGAAGTCCAGAAAAAACAAGGGCTTATAACAGGTAGTTTGGGACATGCGTCTA 386
 Db 702 CTTGAGAAATCCA--AAAAAGAGAGGCTTACACAGGTAGTTTGTGGACAGCGCCCTG 759
 QY 387 ATAGTGAGGAGAACAAATAAGCCAGTGTGTTGATTACATTGCCACCTTTGCTGAGGTGC 446
 Db 760 GT-GTGAGGAGGACAAATAAACCC-GTGTATTATTACATTGCTGCCCTTTGTTGAGGTGC 817
 QY 447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTGTTAGAGG 488

Db 818 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGAAAAGG 859
 Search completed: May 6, 2004, 10:18:00
 Job time : 3364.45 secs

OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 18:25:05 ; Search time 5261 Seconds

(without alignments)
11522.567 Million cell updates/sec

Title: US-09-451-739H-15

Perfect score: 2030

Sequence: 1 ctctgcgcgttaagatggt.....gaaaaaanaaaaaa 2030

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estov:*
- 7: em_estro:*
- 8: em_hci:*
- 9: gb_estcl:*
- 10: gb_estcl:*
- 11: gb_hci:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: gb_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gssl:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	540.4	26.6	565	10 AW373574	AW373574 QV4-BT053
2	514.2	25.3	574	10 BF328582	BF328582 RC5-BN019
3	485.8	23.9	3443	11 BC028407	BC028407 Homo sapi
4	478.8	23.6	490	9 AI951118	AI951118 wx63g05.x

C	5	471.8	23.2	650	10	BE177744	BE177744 RCI-HT059
C	6	399.2	19.7	492	13	BX282243	BX282243 BX282243
C	7	381.8	18.8	3794	11	BC036210	BC036210 Homo sapi
C	8	319.4	15.7	886	13	BQ437838	BQ437838 AGENCOURT
C	9	318	15.7	904	12	BG539426	BG539426 602568046
C	10	314.6	15.5	638	13	BU678550	BU678550 UI-CF-DU1
C	11	309	15.2	443	10	BF746270	BF746270 RCI-BT025
C	12	309	15.2	443	10	BF746270	BF746270 RCI-BT025
C	13	308	15.2	684	14	CA394381	CA394381 cs50h08.Y
C	14	306.8	15.1	862	12	BG431116	BG431116 602498742
C	15	290.4	14.3	821	12	BG622779	BG622779 602647567
C	16	285.4	14.1	683	14	CF181571	CF181571 818415.WA
C	17	269.2	13.3	700	14	CB527418	CB527418 UI-M-FY0-
C	18	251.2	12.4	751	14	CD000265	CD000265 AGENCOURT
C	19	251	12.4	546	10	BE292777	BE292777 RC3-GN004
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C	21	249.8	12.3	633	10	AW976709	AW976709 EST388818
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C	23	247.4	12.2	504	10	BF512258	BF512258 UI-H-BW1-
C	24	247.2	12.2	642	10	AW976715	AW976715 EST388824
C	25	244	12.0	1014	13	BQ298279	BQ298279 220016.re
C	26	241.6	11.9	630	14	CB298279	CB298279 220016.re
C	27	238.8	11.8	641	14	CB044222	CB044222 NISC 9C03
C	28	235.2	11.6	596	13	BQ429618	BQ429618 AGENCOURT
C	29	234.8	11.6	1105	13	BQ071543	BQ071543 AGENCOURT
C	30	229.2	11.3	574	14	CB298280	CB298280 220016.re
C	31	216.2	10.7	597	14	CB228494	CB228494 AGENCOURT
C	32	213.2	10.5	858	14	CD244895	CD244895 AGENCOURT
C	33	210.6	10.4	555	29	CF750511	CF750511 tigr-gss-
C	34	208.8	10.3	388	10	B939777	B939777 CM1-UT001
C	35	200.8	9.9	521	10	BF895056	BF895056 RCI-MT013
C	36	198.6	9.8	505	14	CB220242	CB220242 lAbol9C03
C	37	198.6	9.8	1093	11	BC022380	BC022380 Homo sapi
C	38	197	9.7	817	12	BG622137	BG622137 602646759
C	39	192.6	9.5	694	9	AI687645	AI687645 tp82d07.x
C	40	187.8	9.3	644	13	BU680626	BU680626 UI-CF-DU1
C	41	186.8	9.2	774	14	CA324174	CA324174 UI-M-FY0-
C	42	184.8	9.1	608	10	BE900060	BE900060 RC6-BT071
C	43	184.2	9.1	462	10	BF840427	BF840427 RCI-HT097
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C	45	178.2	8.8	639	10	BE384138	BE384138 601272967

ALIGNMENTS

RESULT 1	AW373574	QV4-BT0534-281299-053-a01	BT0534	Homo sapiens	cdna, mRNA	linear	EST 04-FEB-2000
LOCUS	AW373574	QV4-BT0534-281299-053-a01	BT0534	Homo sapiens	cdna, mRNA	linear	EST 04-FEB-2000
DEFINITION	AW373574	QV4-BT0534-281299-053-a01	BT0534	Homo sapiens	cdna, mRNA	linear	EST 04-FEB-2000
ACCESSION	AW373574	QV4-BT0534-281299-053-a01	BT0534	Homo sapiens	cdna, mRNA	linear	EST 04-FEB-2000
VERSION	AW373574.1	QV4-BT0534-281299-053-a01	BT0534	Homo sapiens	cdna, mRNA	linear	EST 04-FEB-2000
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ORGANISM	Homo sapiens	QV4-BT0534-281299-053-a01	BT0534	Homo sapiens	cdna, mRNA	linear	EST 04-FEB-2000
REFERENCE	1	(bases 1 to 565)	QV4-BT0534-281299-053-a01	BT0534	Homo sapiens	cdna, mRNA	linear
AUTHORS	HCGP	http://www.ludwig.org.br/ORESTES.	QV4-BT0534-281299-053-a01	BT0534	Homo sapiens	cdna, mRNA	linear
TITLE	The FAPESP/LICR Human Cancer Genome Project	QV4-BT0534-281299-053-a01	BT0534	Homo sapiens	cdna, mRNA	linear	EST 04-FEB-2000
JOURNAL	Unpublished (1999)	QV4-BT0534-281299-053-a01	BT0534	Homo sapiens	cdna, mRNA	linear	EST 04-FEB-2000
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-BT0534-281299-053-a01&t3=1999-12-28&t4=1)	QV4-BT0534-281299-053-a01	BT0534	Homo sapiens	cdna, mRNA	linear	EST 04-FEB-2000

ORIGIN	Query Match	25.3%;	Score 514.2;	DB 10;	Length 574;
	Best Local Similarity	98.3%;	Pred. No. 1e-73;		
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					Gaps 1;
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Qy	254	TTGGGATTC-TGAGAGTCTCTGTGAGACTGTTCACAGAGGATGTGTGTTTACCCAAGG	312		
Db	96	TTGGGGGGCGTGAGAGTCTCTGTGAGACTGTTCACAGAGGAGTGTGTGTTTACCCAAGG	155		
Qy	313	CTACACATCAAAAAGAAATAGATAAATAAATCGGAAAAATTAGAAAGAGTCTCCCTGATAATG	372		
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Db	276	TGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGCCATCTGCCTTCGAGCGCTG	335		
Qy	493	CCATTGAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTTGAAGAATGAAACAAACAT	552		
Db	336	CCATTGAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTTGAAGAATGAAACAAACAT	395		
Qy	553	TGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAAGAGGTTGAGAGAAATTCCTT	612		

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 QY 673 CACATCAAAAGAAATCGATTAATAAATAGTGGAAATAGAGATTCAACTAGCCTATCA 731
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RESULT 3
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 LOCUS Homo sapiens breast cancer antigen NY-BR-1.1, mRNA (cDNA clone
 IMAGE:4821910), containing frame-shift errors.
 ACCESSION BC028407
 VERSION BC028407.1 GI:22382096
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 3443)

REFERENCE
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullen, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Kzyvinski, M.I., Skalska, U., Smallos, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE 2238257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 3443)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (23-APR-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadnan@systemsbiology.org
 Anup Madan, Jessica Fahney, Erin Helton, Mark Kettman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 46 Row: i Column: 20
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF

analysis
 This clone has the following problem: frame shifted.

FEATURES

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ORIGIN

Query Match 23.9%; Score 485.8; DB 11; Length 3443;
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 Matches 571; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
 QY 5 TGCCGTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAGTTTCTTATCCAACTAA 64
 Db 1991 TCCTGATAAAGATGGTCTTCTGAAGCCTACCTGTGGAAGGAAGTTCTCTTCCAAATAA 2050
 QY 65 AGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAAGAGCCATCTGC 124
 Db 2051 AGCCTTAGAATTAAAGGACAGAGAAACACTCAAGCAGAGTCTCTGTATATGATGGTCT 2110
 QY 125 CTTGAGGCTGCCATTGAATGCAAAAGTCTGTTCCTCAAAATAAGCCTTGAATGAAGAA 184
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 QY 605 AATTTCTGGATTCTGAGAGTCTCCGTGAGACTGTTTTCACAGAAGGATGTGTGTATCC 664
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RESULT 4
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 AI951118
 ACCESSION AI951118

VERSION AI951118.1 GI:5743428
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 490)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapb@mail.nih.gov
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
 Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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 Seq primer: -40UP from Gibco
 High quality sequence stop: 423.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:2548376"
 /tissue_type="four pooled high-grade tumors, including two
 primary tumors and two metastatic to ovary"
 /lab_hosts="DHIOB"
 /clone_lib="NCI-CGAP Br18"
 /note="Organ: breast; Vector: pCMV-SPORT6; Site: 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
 Library constructed by Life Technologies."
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 Best Local Similarity 98.6%; Pred. No. 5.7e-68;
 Matches 483; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 320 TCAAAAGAAATAGATAAATAAATGAAATAGAGAGTCTCTGATATGATGTTT 379
 DB 490 TCAAAAGAAATAGATAAATAAATGAAATAGAGAGTCTCTGATATGATGTTT 431
 QY 380 TCTGAAGCTCCCTGCGAGATGAAGTTCTATTCGAATAGAGCTTAGAATGATGA 439
 DB 430 TCTGAAGCTCCCTGCGAGATGAAGTTCTATTCGAATAGAGCTTAGAATGATGA 371
 QY 440 CATGCAAACTTTCAAAGCAGAGCTCCGAGAGCCATCTGCTTCGAGCTGCCATTGA 499
 DB 370 CATGCAAACTTTCAAAGCAGAGCTCCGAGAGCCATCTGCTTCGAGCTGCCATTGA 311
 QY 500 AATGCAAAAGTCTGTGTTCAAAATAAGCTTGGAAATGAGATGAACAAACATTGAGGC 559
 DB 310 AATGCAAAAGTCTGTGTTCAAAATAAGCTTGGAAATGAGATGAACAAACATTGAGGC 251
 QY 560 AGATCAGATGTTCCCTTCAGATCAAAACAAAGAGGTTGAGAAATCTTGGGATTC 619
 DB 250 AGATCAGATGTTCCCTTCAGATCAAAACAAAGAGGTTGAGAAATCTTGGGATTC 191
 QY 620 TGAGAGTCTCCGTGAGAGCTGTTTCACAGAGAGATGTGTGTACCCAGGCTACATCA 679
 DB 190 TGAGAGTCTCCGTGAGAGCTGTTTCACAGAGAGATGTGTGTACCCAGGCTACATCA 131
 QY 680 AAAGCAATGGAATAAATAGTGGAAATTAGAGATTCAACTAGCCTATCAAAAATCTT 739
 DB 130 AAAGCAATGGAATAAATAGTGGAAATTAGAGATTCAACTAGCCTATCAAAAATCTT 71
 QY 740 GGATACAGTTCATCTTGTGAAGAGCAGAGGAAGCTTCAAAAAGATCACTGTGAACACG 799

DB 70 GGATACAGTTCATCTTGTGAAGAGAAAGAGGAACTTCAAAAGACCCCTGTGACCCACG 11
 QY 800 TACAGGAAAA 809
 DB 10 TTAGGAAAA 1
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 LOCUS BE177744
 DEFINITION RC1-HT0598-140300-021-b02 HT0598 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BE177744
 VERSION BE177744.1 GI:8656896
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 650)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Ngai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC1-HT0598-140>)
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 High quality sequence start: 24
 High quality sequence stop: 569.
 Location/Qualifiers
 1..650
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 /mol_type="mRNA"
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 /note="Organ: head neck; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196.716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 ORIGIN
 Query Match 23.2%; Score 471.8; DB 10; Length 650;
 Best Local Similarity 85.8%; Pred. No. 7.1e-67;
 Matches 548; Conservative 0; Mismatches 87; Indels 4; Gaps 2;
 QY 983 AAAAATTAGGAGAAATTAGGAGAAATCGAGAGCAGCATAGGAAGAGTTAGAGTCAA 1042
 DB 638 AAGAAGCTGAAAGAAAGAAAATTTAGACCCGAGAGCGCTGAGGAAGATTAGAG-GGA 580
 QY 1043 ACAACAACCTTGACAGCGCTCTCAGATAACAAGATAGAGTTAGAGGTGAGAGTAA 1102
 DB 579 ACAGCGCTGACAGACTCTCAGATACAGATATAGATTGAAAGAGTTGAACAGTAA 520

1103	QY	TTTGAATCAGGTTTCTCACACTCATGAAATGAAATTTATCTCTTACATGAAAATTCGAT	1162
519	Db	TGTGAATCAGGTTTCTCACACTCATGAAAGTGAATGATCTCTTTTCATGAAAATTCGAT	460
1163	QY	GTTGAAAAAGGAATTTGCCATGCTAAAACTGGAATAGCCACACTGAAACACCAATACCA	1222
459	Db	GTTGAAAAAGGAATTTGCCATGCTAAACTGGAAGTAGCCACACTGAAACATCAACACCA	400
1223	QY	GGAAAAAGGAAAAATAATACCTTTGAGGACATTAAGATTTTAAAGAAAAGAACTCTGAACT	1282
399	Db	GGTGAAGGAAAAATAATACCTTTGAGGACATTAAGATTTTACCGAAGAAAGAACTCTGAACT	340
1283	QY	TCAGATGACCCCTAAAACTGAAAGAGGAATCATTTAACTTAAAGGGCATCTCAATATAGTGG	1342
339	Db	TCAAATGACCCCTAAACTGATACAGAAAAAGTAAACCAAGGCGCATCTCAGTATAGAGA	280
1343	QY	GCAGCTTAAAGTTCTGTAGTCTGAGAACACAATGTCTCACTTTAAATTGAAGAAAACA	1402
279	Db	GCAGCTTAAAGTTCTGTAGCGCAGAGAACAGATGCTGACTTCTAAATTGAAGAAAACCT	220
1403	QY	AGACAAAGAAATTAAGTCTAGAGGCAGAAATTGAAATCACACATCTTAGAGCTGGCTTCTGCTGT	1462
219	Db	AGACAAAGAAATTAAGTCTGAGACAGAAATTGAAATCACACATCTTAGAGCTGGCTTCTGCTTT	160
1463	QY	ACAAGACCATGATCAAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTTCCACATGTC	1522
159	Db	ACAAGACCATGATCAAAAGTGTCAATCAAGAAAAAACCTAGAACTTCTCTTTTCCACAGTGC	100
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99	Db	AGGATGCTCCTTTGCGAGGAATTAAGAAATGTTGATGTGAGTAATACATATAT--AAC	43
1583	QY	ATGAGGTGCTCCATCAACCACTTTCTGAAAGCTCAAGGA	1621
42	Db	ATGAGGTGCTCCATCAACCACTTTATGAAAGCTCAAGGA	4

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RESULT 6
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LOCUS
DEFINITION
BX282243 Soares NFL T GBC S1 Homo sapiens cDNA clone
IWAG9981196637; IMAGE:2659290, mRNA sequence.
ACCESSION
BX282243
VERSION
BX282243.1 GI:28615040
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 492)
Ebert,U., Hall,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,J., Schneider,D. and Korn,B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE9981196637.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/cloneCards/cgi-
bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from rzpd;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTCACACAGGAACACTATGAC.
Location/Qualifiers
1..492
/organism="Homo sapiens"
FEATURES
source

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ORIGIN

Query Match	19.7%; Score 399.2; DB 13; Length 492;
Best Local Similarity	95.0%; Pred. No. 4.4e-55;
Matches 459; Conservative	0; Mismatches 19; Indels 5; Gaps 5;
QY 1549	TGAATGTTGATGTGAGTAGTACCGATATATAACAATGAGGTGCTCATCAACACATTCT 1608
DB 1	TGAATGTTGATGTGAGTAGTA-CCATATATAACAATGAGGTGCTCCATCAACACATTCT 59
QY 1609	GAAGCTCAAGGAAATCCANAAAGCCTTAAATTAATCTCAATTTATGAGGAGATGCTCTA 1668
DB 60	GAAGCTCAAGGAAATCCAAAGCCCTAAATTTAACTCAATTTATGAGGAGATGCTCTA 119
QY 1669	AGAGAAATACATTTGGTTTCAGGAACATGCACAAAGAGACCAACGTTGAACACAGTGCTCA 1728
DB 120	AGAGAAATACATTTGGTTTCA-GAATGTCACAAAGAGACCAACGTTGAACACAGTGCTCA 178
QY 1729	AATGAAGGAGCTGAACACATGTTCAAAACGACACAGATNATGTGAACAAACACACTGA 1788
DB 179	AATGAAGGAGCTGAACACATGTTCAAAACGACACAGATNATGTGAACAAACACACTGA 238
QY 1789	NCAGCAGAGTCTTAGATCAGAAATATTTTCAACTACAAAGCAAAATATGTGGCTTCA 1848
DB 239	ACAGCAGAGTCTTAGATCAGAAATATTTTCAACTACAAAGCAAAATATGTGGCTTCA 298
QY 1849	ACAGCAATTAGTTCATGCACATGAAGAAAGCTGACAAACAAAGCAAGATTAACATTGATN 1908
DB 299	ACAGCAATTAGTTCATGCACATAA-GAAGCTGACAAACAAAGCAAGATTAACATTGATN 357
QY 1909	TTCAATTTCCTTGAGAGGAAATGCG-NCATCATCTTCTTAAAGAGAAAAATGAGGAGATAT 1967
DB 358	TTCAATTTCCTTGAGAGGAAATGCAACATCATCTCTTAAAGAGAAAAATGAGGAGATAT 417
QY 1968	TTNATTACNATAACCAATTTAAAAACCCGTATATTTCAATATGAAAAAANAANAANA 2027
DB 418	TTNATTACNATAACCAATTTAAAAA-CGGTATATATCAATATGAAAAAGAGAAAGCGAA 476
QY 2028	AAA 2030
DB 477	ACA 479

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RESULT 7
BC036210
LOCUS BC036210 Homo sapiens, clone IMAGE:5265638, mRNA.
DEFINITION BC036210
ACCESSION BC036210
VERSION BC036210.1 GI:23242519
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3794)
AUTHORS Strausberg,R.
```

TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NEHRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcdepaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 63 Row: e Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
This clone has the following problem: frame shifted.

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Matches 838; Conservative 0; Mismatches 364; Indels 172; Gaps 7;

QY 687 ATGGATAAATTAAGTGGAAATAGACATTCACATAGCCTATCAAAATCTTGATACA 746
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DB 1507 AAAATGAAAAAATGAAAATGAGGTCCATGTACTTACAAAAGGAGTTATCTGAAACACA 1566
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DB 1567 GAATATAAATTACAGTTAGACATCAAGTGTATGTAATGGAAACGAGATTTCTACAGTTG 1626
QY 927 AGATTGACTTTAAACAAGAGAGAGAGAGAGAGAGATGCCGATATATTAAATGAAGAAA 986
DB 1627 AGATCTACCTTACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1686
QY 987 ATTGGGAGAAATTAGAGAGATTCGAAGAGCAGCAGTAGGAGAGAGTTAGAGTTGAACAA 1046
DB 1687 ATCAGGGGACACTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1746
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QY 1109 ----- 1108
DB 1867 AGAATATTACAAGTGAATTTCTGACCAATCACTTTGCAAAACAAAGAGAGATAGCACTG 1926
QY 1109 -----TCAGGTTTCTCAACACTCATGAAATGAAATATATCTCTTA 1148
DB 1927 GCTGAGGAAAGAGATTTCTCAGATTTCTTCAGCCATGACAAAGTACAAATCTGTTG 1986
QY 1149 CATGAAATATGATGTTGAAAGAGAAATTCATGCTTAAACTGGAATAGCAACACTG 1208
DB 1987 CATGAAATATGATGTTGAGGAGAAATTTGCCACCTCAGCTGGAATAGCAACATA 2046
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QY 1329 TCTCAATATAGTGGGAGCTTTAAAGTTTCTGATAGCTGAGAACACAATGCTCACTTTAAA 1388
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QY 1389 TT---GAAGGAAAAACAAGACAAAGAAATCTAGAGGAGAAATTAATCAACACATCCT 1445
DB 2206 CTGGAGAGGAAAAACAAGAAAGAGCCTGGAGACAGAAAGTTGAATCAACCCGTTGC 2265
QY 1446 AGACTGGCTTCTGCTGTACAGAGCCATGATCAAAATTTGACATCAAGAAAGAAAGTCAAGAA 1505
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QY 1506 CTTGCTTTTCCATTCAGAGGAGATGCTTTGTTGCAAGAAAGAAATGAATGTTGATGAGT 1565
DB 2326 CTTGCTTTTCCAGGAGCAAAAGATGAATGTTTATTACCGAGAA--AATGAATTTTGA 2384
QY 1566 AGTACCGATATATAAATGAGTGGTCTCCATCAACCACTTTCTGAAGCTCAAGAGAAATC 1625
DB 2385 TGACTTAAAGCTAAGTGTCTTCTGTTCTCAGCAACTGTCTAGAACTCAAGTAATCTT 2444
QY 1626 CANAAGCCTTAAATTAATCTCAATTTATGCGAGGAGATGCTCTTAAGAGA-----AAATA 1678
DB 2445 GGAAGCCTTAAGCTTAAAGTTCCAAACACACAGAGATGCTCTTACAGAAAGAGAGAAAG 2504
QY 1679 CATTTGTTTTCAGGACATGCAACAGAGACCAAGCTGAAACACACAGTGTCAATGAAGAA 1738
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QY 1739 GCTGAACACATGTTCAAACGAAACAGATNATGTGAACAAACACACTGAGACAGAGAG 1798
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QY 1799 TCTTAGATCAGAAATTTTCAACTACAAAGCAAAATATGTTGGCTTCAACAGCAATTA 1858
DB 2624 TCTGTAGAGCGGAGGCTGTCTCACTGAGAGTGAATATGTTGTTTCCACAGCACTG 2683
QY 1859 GTTCATGCAATGAAGAAAGCTGACAAACAAAGAGCAAGTAAACAATTTGATTTCA 1912
DB 2684 GATGATGCTTACAC--AAAGCTGACAAATCAAGAAAGAGCAATAATTTACTATCCA 2736

RESULT 8
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LOCUS BQ437838
DEFINITION AGENCOURT 7892743 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6157635
5', mRNA sequence.
ACCESSION BQ437838
VERSION BQ437838.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 886)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DC/DTP
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM13503 row: n column: 04
High quality sequence stop: 682.
Location/Qualifiers
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ORIGIN
Query Match 15.7%; Score 319.4; DB 13; Length 886;
Best Local Similarity 64.9%; Pred. No. 3e-42;
Matches 514; Conservative 0; Mismatches 273; Indels 5; Gaps 3;

QY 1103 TTGTAATCAGGTTTCACATCATGAAATGAAATATCTCTTACATGAAATTTGCAT 1162
DB 791 TTTATTTAGGATTTTTCATATCATGAAATGAAATGAAATCTGTGATTTAAATTTGCAT 732
QY 1163 GTTGAAGAAGAAATGCGATGCTTAAATGGAATAGCCACTGAAACACCAATACCA 1222
DB 731 TTTGTAATCAGATATTTGTTATATTCAGACAGGAATGTGCAATGAAATGCAACCT 672
QY 1223 GGAAGAAGAAATTAATATCTTTGAGCAGATTAAGATTTTAAAGAAAGAAATGCTGAAT 1282
DB 671 GGAAGAAGAAATTAATATCTTTGAGCAGATTAAGATTTTAAAGAAAGAAATGCTGCT 612
QY 1283 TCAGATGACCCCTAAACTGAAAGAGGAATCATTAACCTAAAGGGGATCTCAATATAGTGG 1342
DB 611 TGAAAGATATATAAACTCAATGAGGAATTTGATACAAATACAGCAATTCGGTATCAACA 552
QY 1343 CGAGCTTAAAGTTCTGATAGCTGAGACACATGCTCACTTCTAAA---TTGAAGGAAA 1399
DB 551 AGAGCTTAAATGATCTCAAGCTGGAATATACAGGCTCAGTCCGACTGTTGAGGAGA 492
QY 1400 ACAAGCAAGAAATATCTAGAGCGGAGAAATTTGAATCAACCAATCTAGACTGGCTTTCG 1459
DB 491 AGAAGACACAAAGACTGGAAGCTGAACTGAATCTTATCAGTCTAGACTGGCTGCTTC 432
QY 1460 TGTACAAGACCATGATCAATTTGTCACATCAAGAAAGATCAAGAACTGTTTCCCAT 1519
DB 431 TATAGTAAACAGTGAAGTGTGAACACAGAAAGAACCTTAAATCTGTTAGAGAG 372
QY 1520 TCGAGGAGATGCTTTGTTTCAAGAAAGAAATGAAATGATGTTGAGTACCGCATATATA 1579
DB 371 AACTCAAGATGTTTCGTACAAAGTAAAGATGATTTCTGATAT-TTCCGAAGTGAAGATA 313
QY 1580 ACATGAGTGTCTCATCAACACTTCTGAGCTCAAGGAAATCCANAGCCCTAAAA 1639
DB 312 AGAATGAGTTTCTTACTGAAACACTTCTTAAACCAAAATTAATTAATACCTTTAAAG 253
QY 1640 TTAATCTCAATATGAGGAGATGCTCTTAAGGAAAGAAATACATGTTGTTTCAAGAAATGCA 1699

Db 252 ATAAGTTCGTAAAGACAAGAGATATCTCTCAGAAAAAAGTCATTGGCTTTAGAAAC-TGTA 194
QY 1700 CAAAGAGACCAACGTAACACAGTGTCAATTAAGAGAGAGCTGAACACATGTTTCAAAC 1759
Db 193 CATACAACTTAAGCCAAACACAGCAGCAATTAAGGAAATGAAGACAGATGTATGAAAT 134
QY 1760 GAACAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATATT 1819
Db 133 GCAGAGCTTAAAGAGATAATTCCTGAAAGTGGAGCTGTGTAGAAAGAGAGATATGT 74
QY 1820 CCACTTAAAGCAAAATATGCTTCAACAGCAATTAGTTTCATGCATATAAGCAAGC 1879
Db 73 CAACTCCACATGAATAATCCGTCATTTGAACAGCACTAGATGATGATGTTTCATCAGAAAG 14
QY 1880 TGACAAACAAAG 1891
Db 13 TATCATTAAGAG 2

RESULT 9
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LOCUS 602568046F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4692635 5',
DEFINITION mRNA sequence.
ACCESSION EG539426
VERSION EG539426.1 GI:13531659
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 904)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1513 row: 1 column: 12
High quality sequence stop: 608.
Location/Qualifiers
1. 904
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4692635"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1: SfiI (ggccattagcc); Site 2: SfiI (ggccattagcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCCATTAGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGCCGACATG-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

FEATURES
source
1. 904
Location/Qualifiers

ORIGIN
Query Match 15.7%; Score 318; DB 12; Length 904;
Best Local Similarity 68.0%; Pred. No. 5.1e-42;
Matches 506; Conservative 0; Mismatches 225; Indels 13; Gaps 4;

QY 767 AAGGGAATTTCAAAAAATGATCTGTGAACACAGTACAGAAAAATGGACAAATGAAAA 826
Db 2 AATAAACTTAAAGATAACCACTGTGAGCAACTTAGAGTAAAAATTCGAAAACTGAAAA 61

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..638
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-DUI-aar-o-16-0-UI"
/tissue_type="Primary Lung Epithelial Cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-DUI"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-DUI is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCTGTAGGC.
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-DUI
TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 15.5%; Score 314.6; DB 13; Length 638;
Best Local Similarity 72.9%; Pred. No. 2e-41;
Matches 461; Conservative 0; Mismatches 160; Indels 11; Gaps 4;

QY 1117 CTCACACTCATGAATGAATATCTTACATGAAATTTGCTGTTGAAAAAGGAAA 1176
Db 638 CTCATAGTCATGAAGAAGAAAAGACCTTCATCCATAAATAGCATGTCGAGGAGAAA 579
QY 1177 TTGCCATGCTAAAACCTGGAATAGCCCACT-GAAACACCAATACCCAGAAAAGGAAAAT 1235
Db 578 TTGCTATGCTAAGACTAGAAATAGACACAATAAAAAATCAACCCAGGAAAAGAAAAG 519
QY 1236 AATACCTTTGAGGACATTAAGATTTTAAAGAAAAGAAATGCTGAACCTTCAGATGCCCTA 1295
Db 518 AATGTTTGGAGACCTTAAATTTGAAAGAAAAGAAATGAAGACCTTCAGAGACTATA 459
QY 1296 AAACCTGAAAGAGGAATCATTAACCTAAAGGGGCAATCTCAATATATAGTGGGAGCTTAAAGTT 1355
Db 458 AAACAGATGAGGAAAACATTAAACACAACAATATCCAGTATAATGAGCGGCTTAGTGT 399
QY 1356 CTGATAGCTGAGAACACAATGCTCCTCTTAATTT---GAAGGAAAACAACAGCAAGAAA 1412
Db 398 CTGACAGCTGAGAAATCAATGCTTAAATTTAACTGGAAGTGAAGAAAAGCAAGAGGAA 339
QY 1413 ATACTAGAGGAGCAAAATTTGAATCACACCAATCTTAGACTGGCTTCTGCTGTACAAGACCT 1472
Db 338 AGACTGGAAGCAGAAAGTTGNAATCATACCATCTTAGATTGGCTGCTGTATACATGATCGT 279
QY 1473 GATCAAAATTTGTGATCAAGAAAAGTCAAGAACCTGCTTCCACATCTCCAGGAGATG--- 1530
Db 278 GATCAAAAGTGAGACATCAAAAAGAGAACTAGAACTTGTCTTCCAGAGACGAGAGATGAA 219

QY 827 GAAGCTTTGTGTAAGTAAAGAACTGTGAGAGCAAAAGAAATATAATCACAGTTAGA 886
Db 62 TAAGGCTAGTGTACTACAAAGAGAAATATCTGAAAGAAAGAAATATAATCGCAGTTAA 121
QY 887 GAACCAAAAGTAAATGGGACACAGAGCTGTCGAGTGTGAGATTGATTTAAACCAAGA 946
Db 122 GCATGAATATCTGAATTTGAAAAGAACTGTGAGTTTGGATTTGCCATACAGCAAGA 181
QY 947 AGAAGAGAGAGAGAAATGCGGATATATTAATTAAGTAAAGAAATTAGGGAAGAAATAGGAAG 1006
Db 182 AAAAAAGAAAGAAAGAAATTTGAAGAGTTGCACCAAAAGTTAGGGAAGAAATTAAGAAT 241
QY 1007 AATCGAAGAGAGAGATAGGAAGATTTAGAGTGAACACCAACTTGAACAGGCTCTCAG 1066
Db 242 AACGAGAGAGCAATATAGGATAGAGCTGTGTGACAAACCAATTAACCGGCTCTCAA 301
QY 1067 AATCAAGATATAGAAATTTGAAGAGTGTAGAAGTAAATTTGAATCAGGTTTCTCACACTCA 1126
Db 302 ATCAGCAGAGTGGAAATTTGAAGACAGGAGGAATAATTCAAATCAGGTTTCTGAAACTGA 361
QY 1127 TGAATTAAGAAATTTATCTCTTACATGAATTTGATGTTGAAAAGGAAATTTGCCATGCT 1186
Db 362 TGAATAAGAGAC---CTGCTGCATGAATAACCGCTTGTATGAAGATGAATTTGCCAGGCT 418
QY 1187 AAAACTGGAATAGCCACACTGAACACCAATACAGGAAAGGAAAATATAATACTTTGA 1246
Db 419 CAGGCTGGAAGAGACACAATAAAGAACCAAACTGGAAAAGAAATACTTAAC---A 473
QY 1247 GGACATTAAGATTTTAAAGAAAGATGCTGAATCTCAGATGACCTTAAACCTGAAGA 1306
Db 474 AGACTTTGAAATTTGAAAAGAAAGCATGAAGACCTTCAAAGGCTCTAAACCGAATGG 533
QY 1307 GGAATCATTAATAAAGGGCA-TCTCAATATAGTGGCAGCTTAAAGTTTCTGATAGCTG 1365
Db 534 GGAACATTAAGAAAAGCATAGCTGCTGTATAGTGACAGCTAGCTGCTGACATG 593
QY 1366 AGAACACATGCTCACTTCTTAATTAAG-----GAAAACAAAGCAAGAAATTAAGTACAG 1421
Db 594 ACAACACACGCTCGCTTACAACTGGAGAGACGAAGCGAAGCAGCAACGATGGGAA 653
QY 1422 GCAGAAATTTGAATCACACATCTAGACTGCTTCTGCTGTACAGACCATGATCAATTT 1481
Db 654 ACAGAAAGCAATATACATGCTGCTGAGCTGCTGAGGCTGCCAAGGACCATGACCAAAGG 713
QY 1482 GTGACATCAAGAAAAGTCAAGAA 1505
Db 714 CATCCCATCAGAAGAAGACAAAA 737

RESULT 10

BU678550/c

LOCUS

DEFINITION

UI-CF-DUI-aar-o-16-0-UI.s1 UI-CF-DUI Homo sapiens cDNA clone

UI-CF-DUI-aar-o-16-0-UI 3', mRNA sequence.

ACCESSION

BU678550

VERSION

BU678550.1 GI:23525612

KEYWORDS

EST.

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 638)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: McCray, PB

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

1531 ----CTTGTTGCAAGAAAATGAATGTTGATGTAGTAGTACCGGATATATACAAATGA 1586
218 TGTCTCGTTTACAGGACAAAATGAATTTTGATGTCTA-ACCTAAAGATAACAATGA 160
1587 GGTCTCATCAACCACTTCTGAGCTCAAGGAAATCCANAGAGCCCTAAATATATCT 1646
159 GATTCTTCTCAACAACATATTAAACATGAAGTAACCTCAATAGCCCTAGAAAATTGAGTT 100
1647 CAATATATCAGAGATGCTCTAAAGAGAAAAATACATTTGGTTTTCAGGAACATGCACAAAGAG 1706
99 CCATACACAGAGAGATGCCCTCAGAGAAAAGACTTTGGGTTTAGAACGGGTACAAAGGA 40
1707 ACCACGTGAACACACAGTGTCAATGAAGAA 1738
39 CCTAAGCCCTAAACACAGTGTCAAAAAA 8

RESULT 11
BF746270 443 bp mRNA linear EST 10-JAN-2001
LOCUS RCI-BT0254-071100-119-a03 BT0254 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF746270
ACCESSION BF746270.1 GI:12072946
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

Zukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 443)
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RCI&t2=RCI-BT0254-
071100-119-a03&t3=2000-11-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 439.
Location/Qualifiers
1. .443
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BT0254"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORFEST PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

15.2%; Score 309; DB 10; Length 443;
Query Match 98.4%; Pred. No. 1.8e-40;
Best Local Similarity

FEATURES
source
1. .443
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BT0254"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORFEST PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN
Query Match 15.2%; Score 309; DB 10; Length 443;
Best Local Similarity 98.4%; Pred. No. 1.8e-40;

Matches 312; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 93 TTCAAAGCAGAGCCCTCCGAGAGCCATCTGCTCGAGCGCTGCCATTGAATGCARAAG 152
DB 127 TTACAATCAGAGCCCTCCGAGAGCCATCTGCTCGAGCGCTGCCATTGAATGCARAAG 186
QY 153 TCTGTTCCTCAATTAAGAGCCCTTGAATTTGAAGATGAACAAACATTTGAGAGCAGATGAGATA 212
DB 187 TCTGTTCCTCAATTAAGAGCCCTTGAATTTGAAGATGAACAAACATTTGAGAGCAGATGAGATA 246
QY 213 CTCCCATCAGAAATCCAAACAAAGAGCCTATGAAGAAAGTTCTTGGGATTTGAGAGTCTC 272
DB 247 CTCCCATCAGAAATCCAAACAAAGAGCCTATGAAGAAAGTTCTTGGGATTTGAGAGTCTC 306
QY 273 TGTGAGACTGTTTCACAGAGAGGATGTGTGTTTACCAAGGCTACACATCAAAAAGAAATA 332
DB 307 TGTGAGACTGTTTCACAGAGAGGATGTGTGTTTACCAAGGCTACACATCAAAAAGAAATA 366
QY 333 GATAAATAAATGGAATAATTAAGAGAGTCTCTGATATATGATGGTTTCTGAAGGCTCC 392
DB 367 GATAAATAAATGGAATAATTAAGAGAGTCTCTGATATATGATGGTTTCTGAAGGCTCC 426
QY 393 TGCAGAAATGAAGTTTC 409
DB 427 TGCAGAAATGAAGTTTC 443

RESULT 12
BF746340 443 bp mRNA linear EST 10-JAN-2001
LOCUS RCI-BT0254-081100-119-a03 BT0254 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF746340
ACCESSION BF746340
VERSION BF746340.1 GI:12073016
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 443)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RCI&t2=RCI-BT0254-
081100-119-a03&t3=2000-11-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 439.
Location/Qualifiers
1. .443
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BT0254"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORFEST PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

15.2%; Score 309; DB 10; Length 443;
Query Match 98.4%; Pred. No. 1.8e-40;
Best Local Similarity

FEATURES
source
1. .443
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BT0254"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORFEST PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN
Query Match 15.2%; Score 309; DB 10; Length 443;
Best Local Similarity 98.4%; Pred. No. 1.8e-40;

SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 15.2%; Score 309; DB 10; Length 443;
Best Local Similarity 98.4%; Pred. No. 1.8e-40;
Matches 312; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 93 TTCAAGCAGAGCTCCGAGAGCCATCTGCTTCAGAGCTGCAATGAAATGCAAAAG 152
Db 127 TTCAATCAGAGCTCCGAGAGCCATCTGCTTCAGAGCTGCAATGAAATGCAAAAG 156
QY 153 TCTGTTCCAAATAAGCTTCGAATTAAGAAATGAACAAACATTTGAGAGATGAGATA 212
Db 187 TCTGTTCCAAATAAGCTTCGAATTTGAAGAAATGAACAAACATTTGAGAGATGAGATA 246
QY 213 CTCCATCAGATCCAAACAAAGGACTATCAAGAAAGTTCTTGGGATTTCTGAGATCTC 272
Db 247 CTCCATCAGATCCAAACAAAGGACTATCAAGAAAGTTCTTGGGATTTCTGAGATCTC 306
QY 273 TGTGAGACTGTTTACAGAGAGATGTTGTTTACCCAGGCTACACATCAAAAAGAAATA 332
Db 307 TGTGAGACTGTTTACAGAGAGATGTTGTTTACCCAGGCTACACATCAAAAAGAAATA 366
QY 333 GATTAATAAATGGAATTAAGAGCTCTCTGTAATGATGTTTCTGAGGCTCCC 392
Db 367 GATTAATAAATGGAATTAAGAGCTCTCTGTAATGATGTTTCTGAGGCTCCC 426
QY 393 TGCAGATGAAAGTTTC 409
Db 427 TGCAGATGAAAGTTTC 443

RESULT 13

CA394381
LOCUS
DEFINITION
cs50h08.y1 Human Retinal pigment epithelium/choroid cDNA
5', mRNA sequence.

ACCESSION

CA394381
CA394381.1 GI:24728876
EST.
Homo sapiens (human)

KEYWORDS

Homo sapiens
Eukaryota; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

Wistow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A.,
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of human RPE/choroid for the
NIH Bank Project: Over 6000 non-redundant transcripts, novel genes
and splice variants
Mol. Vis. 8 (4), 205-220 (2002)

JOURNAL

MEDLINE
22103460

PUBMED

12107410
COMMENT

Contact: Wistow G
Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 50 row: b column: 08

Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

1..684

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

FEATURES

source

RESULT 14

BG431116

LOCUS

BG431116

862 bp

mRNA

linear

EST 14-MAR-2001

/clone="cs50h08"
/tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Retinal pigment epithelium/choroid cDNA"
(Un-normalized, unamplified): cs"
(Note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
eyes (75-80 years old) yielded approximately 600 mg of
dissected RPE/choroid tissue. This in turn yielded 340 ug
of total RNA and 7 ug of mRNA. A directionally cloned cDNA
library in the pCMVSPORT6 vector was constructed at Life
Technologies (Rockville, MD; now part of Invitrogen Corp),
essentially following the protocols of the SuperScript
Plasmid System (Invitrogen Corp).
http://www.invitrogen.com/>". The library code
designation was cs. For this library, cDNA inserts were
cloned into the NotI/MluI sites of the vector. EST
analysis was performed on the unamplified library at the
NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 15.2%; Score 308; DB 14; Length 684;
Best Local Similarity 69.0%; Pred. No. 2.3e-40;
Matches 454; Conservative 0; Mismatches 195; Indels 9; Gaps 2;
QY 687 ATGGATAAAATAGTGGAAATTAAGAGATCAATAGCTTCAAAAATCTTGGATACA 746
Db 36 ATTGATCAACATGAATGAAGTGTAAAGATTGTGTTCACCTATTGAAATTAATAATACA 95
QY 747 GTTCATTCTTGAAGAGCAAGGAACTTCAAAAAGATCACTGTGAACAACGTACAGGA 806
Db 96 TTTTGTGTTATGGAAGAATTAATAAACTTAAGATAACCTGTGACCACTTAGAGTA 155
QY 807 AAAATGGAACAAATGAAAAAGATTTTGTGTACTGAAAAAGAACTGTCTAGAGCAAAA 866
Db 156 AAAATTCGAAACTGAAAAATAGGCTAGTGTACTACAAAAGAGAAATATCTGAAAAAGAA 215
QY 867 GAAATTAATCACAGTTAGAGAACCCAAAAGCTTAATGGAACAGAGCTCTGCAGTGTG 926
Db 216 GAAATTAATCACAGTTAGAGAACCCAAAAGCTTAATGGAACAGAGCTCTGCAGTGTG 275
QY 927 AGATTGACATTTAAACCAAGAGAGAGAGAGAGAAATGCCGATATATTAATTAATGAAA 986
Db 276 AGATTGACATTTAAACCAAGAGAGAGAGAGAGAAATGCCGATATATTAATTAATGAAA 335
QY 987 ATTAGGAAGATTAGGAAGATCCAAAGCAGCAGATGGAAGAGTGAAGTGAAGTGAACAA 1046
Db 336 GTTAGGGAAGATTAGGAAGATCCAAAGCAGCAGATGGAAGAGTGAAGTGAAGTGAACAA 395
QY 1047 CAACCTTGAACGGCTCTCAGAAATACAGATATAGAAATTAAGAGAGTGAAGTGAAGTGA 1106
Db 396 CCATTTAAACCGCTCTCAATCACAGAGGTGGAAATTAAGAGAGTGAAGTGAAGTGAAC 455
QY 1107 ATCAGGTTTCTCACATCTGAAAATGAAAATATCTCTTACATGAAAATGCAATGTTG 1166
Db 456 AATCAGGTTTCTGAAACTGTATGAAAAAGAA---GACCTGCTGCATGAAAAACCGCTTGA 512
QY 1167 AAAAGGAAATTTGCCATGTCTAAACCTGGAATATAGCCACATGAAACACCAATACAGAA 1226
Db 513 CAAGATGAATTTGCCAGGCTCAGGCTGGAAGAAAGACAAATAAAAAACCAAACTGGAA 572
QY 1227 AGGAAATTAATATCTTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAATTCAG 1286
Db 573 AAG-----AAATACTTTAAAGACTTTGAATTTGAAAAAGAAAGCATGAAGACCTTCAA 626
QY 1287 ATGACCTTAAACTGAAAGAGGAATCAATTAATAAAGGCGCATCTCAATATATAGTGGC 1344
Db 627 AAGGCTCTAAACGGAAATGCGGAACACATTAAGCAAAACAGATAGCTGTTATAGTGGAC 684

DEFINITION 602498742F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4612186 5', mRNA sequence.

ACCESSION BG431116

VERSION BG431116.1 GI:13337622

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC http://mgc.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1360 row: d column: 11
High quality sequence stop: 730.

FEATURES
Location/Qualifiers
1..862
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4612186"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site: 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 15.1%; Score 306.8; DB 12; Length 862;
Best Local Similarity 68.3%; Pred No. 3.4e-40;
Matches 516; Conservative 0; Mismatches 224; Indels 16; Gaps 6;

QY 1013 AGAGCAGCATAGGAAGAGTAGAGTGAAGTGAACCAACTTGAACAGGCTCTCAGATACA 1072

DB 76 AGAAGAGATGCCAGATGTTACAGATGGAATCTGACCAATCACCTTTCCAAACAAA 135

QY 1073 AGATATAGATTTGAAGAGTGTAGAAGTAATTTGAATCAGTCTTCTACACTCATGAAA 1132

DB 136 GGAGATTGAATGGCTCAAGAGAATGAATTT---CTGAGATTCTCATGCTATGAGA 192

QY 1133 TGAATAATTATCTTTACATGAAAATTCATGTTGAAAAGGAAATTCATGCTTAAACT 1192

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QY 1662 TGCTTAAGAGAAATACATTTGTTTTCAGGACATGCAAGAGACCAACGTTGAAACAC 1721

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QY 1722 AGTGTCAAAATGAAGAACTGAAACACATGTTTCAAA 1757

DB 791 AGGTTCATGAGGCAATGACCAACGTTTCACA 826

RESULT 15

BG622779

LOCUS

DEFINITION BG622779 821 bp mRNA linear EST 18-APR-2001

ACCESSION BG622779

VERSION BG622779.1 GI:13674150

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC http://mgc.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1633 row: f column: 17
High quality sequence stop: 818.

FEATURES
source

Location/Qualifiers
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_79"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match		14.3%;	Score 290.4;	DB 12;	Length 821;
Best Local Similarity		68.2%;	Pred. No. 1.5e-37;		
Matches 510;		Conservative 0;	Mismatches 221;	Indels 17;	Gaps 7;
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Qy	747	GTTCATTCTTGTGAAGAGCAAGGAACTTCAAAAGATCACTGTGAAACACGTACAGGA	806		
Db	80	-TTTGTATTATGAAGATTAAAGATTAAAGAACTTAAGATATACCTGTGAGCACTTAGGTA	138		
Qy	807	AAATGGAAACAATGAAGAAAGATTTTGTGTACTGAAAGAAACTGTGAGAGCAAAA	866		
Db	139	AAAATTCGAAACTGAAATTAAGCTAGTGTACTACAAAAGAGACTATCTGAAAAGAA	198		
Qy	867	GAAATAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTG	926		
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Qy	927	AGATTGACTTTAAACCAAGAAAGAGAGAGAAATGCCGATATATTAAATGAAAAA	986		
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Qy	987	ATTAGGGAGAAATTAGGAGAAATCGAGAGCAGATAGGAAGAGTTAGAGTGAAACAA	1046		
Db	319	GTTAGGGAAAGTTAAGAAATCACAGAGAGCAATATAGGATAGAGCTGTGTGACAAA	378		
Qy	1047	CAACTTGAACAGGCTCTCAGAAATCAAGATATAGAAATTGAAGAGTGTAGAAAGTAATTG	1106		
Db	379	CCAAATTAACCGG-TCTCAATCAGCAGAGGTGGAATTTGAAGACAGGAGGAAATTAATCA	437		
Qy	1107	AATCAGGTTTCTCACACTCATGAAATGAATTAATTTATCTTTACATGAATTTGCATGTTG	1166		
Db	438	AATCAGGTTTCTGAAACTGATGAAAGAGAGAC---CTGCTGCATGAAACCGT-TGATG	493		
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Qy	1287	ATGACCTTAAACTGAAAGAGGAATCAATTAACATAAAGGGCATCTCAATATAGTGGG-CA	1345		
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Qy	1346	GCTTAAAGTTCTGATAGCTGAGACACAATGCTCACTTCTTAATTG-----AAGGAAAAAC	1401		
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Search completed: May 6, 2004, 22:30:59
Job time : 5265 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 21:03:19 ; Search time 960 Seconds
(without alignments)

10692.886 Million cell updates/sec

Title: US-09-451-739H-15

Perfect score: 2030

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1940	95.6	4047	14	US-10-007-805-566
2	1940	95.6	4047	15	Sequence 566, App
3	1940	95.6	4047	15	Sequence 566, App
4	1940	95.6	4458	13	US-10-124-805-566
5	1940	95.6	4458	14	US-10-058-270A-3
6	1940	95.6	4458	14	US-10-007-805-564
7	1940	95.6	4458	15	US-10-076-622-564
8	1940	95.6	4458	15	US-10-177-293-333
9	1938.4	95.5	3288	14	US-10-007-805-490
10	1938.4	95.5	3288	15	US-10-076-622-490
11	1938.4	95.5	3288	15	US-10-124-805-490
12	1938.4	95.5	3865	9	US-09-604-287A-474
13	1938.4	95.5	3865	10	US-09-551-621-474
14	1938.4	95.5	3865	14	US-10-007-805-474

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Sequence 463, App
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Sequence 19, Appl
Sequence 24, Appl
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ALIGNMENTS

RESULT 1

US-10-007-805-566
; Sequence 566, Application US/10007805
; Publication No. US20020150581A1

GENERAL INFORMATION:

; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepier, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 566
; LENGTH: 4047
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-007-805-566

Query Match 95.6%; Score 1940; DB 14; Length 4047;

Best Local Similarity 98.7%; Pred. No. 0;

Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;

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Db 2016 TCCTGTTAAAGATGGCTTCTGAGGCTAATCGCGAATGAAAGTTCTATTCCAACTAA 2075

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QY	185	TGAAACAAACATTGAGAGCAGATGAGATATCTCCCATCAGAAATCCAAACAAAGAGCATATGA	244
Db	2196	TGAAACAAACATTGAGAGCAGATGAGATATCTCCCATCAGAAATCCAAACAAAGAGCATATGA	2255
QY	245	AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCACAGAAGGATGTGTGTTT	304
Db	2256	AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCACAGAAGGATGTGTGTTT	2315
QY	305	ACCCRAGGCTACACATCCTAAAAGAAATAGATAAAATAAATGAAAAATTGAGAGAGTCTCC	364
Db	2316	ACCCRAGGCTACACATCCTAAAAGAAATAGATAAAATAAATGAAAAATTGAGAGAGTCTCC	2375
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RESULT 2

US-10-076-622-566

; Sequence 566, Application US/10076622

Publication No. US20030023036A1

GENERAL INFORMATION:

APPLICANT: Houghton, Raymond L.

APPLICANT: Sleath, Paul R.

APPLICANT: Persing, David H.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 310121.470C11

CURRENT APPLICATION NUMBER: US/10/076,622

; CURRENT FILING DATE: 2002-02-13

Query Match	95.6%	Score 1940	DB 15	Length 4047
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QY	125	CTTCGAGCCCTGCCATTTGAAATGCAAAAGCTGTCTTCCAAATTAAGCCCTTGAATTGAAGAA	184	
Db	2136	CTTCGAGCCCTGCCATTTGAAATGCAAAAGCTGTCTTCCAAATTAAGCCCTTGAATTGAAGAA	2195	
QY	185	TGAACAAACATTCAGAGCAGATCAGATACCTCCCATCAGAAATCCAAACAAAGGACTATGA	244	
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QY	245	AGAAAGTCTTGGATTCCTGAGAGTCTCTGTGAGACTGTTCACAGAGGATGTGTGTT	304	
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QY	305	ACCCAAGGCTACACATCAAAAGAAATAGATAAAATAAAATGGAATAATTAAGAGAGTCTCC	364	
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QY	365	TGATATATGATGGTTTCTGAAAGGCTCCCTGCAGANTGAAGATTTCTATTCCAACTAAAGC	424	
Db	2376	TGATATATGATGGTTTCTGAAAGGCTCCCTGCAGANTGAAGATTTCTATTCCAACTAAAGC	2435	
QY	425	CTTAGAATTCATGGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAGCCATCTGCCTT	484	
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QY	485	CGAGCCTGCCATTTGAAATGCAAAAGCTGTCTTCCAAATTAAGCCCTTGAANTGAAGATGA	544	
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QY	545	ACAAACATTCAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA	604	
Db	2556	ACAAACATTCAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA	2615	
QY	605	AAATTCCTGGATTCAGAGTCTCCCTGAGACTGTTCACAGAGGATGTGTGTACC	664	
Db	2616	AAATTCCTGGATTCAGAGTCTCCCTGAGACTGTTCACAGAGGATGTGTGTACC	2675	
QY	665	CAAGGCTACACATCAAAAGAAATTGGATAAAATAAGTGGAAAAATTAGAAGATCAACATAG	724	
Db	2676	CAAGGCTACACATCAAAAGAAATTGGATAAAATAAGTGGAAAAATTAGAAGATCAACATAG	2735	
QY	725	CCATATCAAAATCTTGGATACAGTTCACTTCTGTGGAAGCGAGGGAATTCACAAAGA	784	
Db	2736	CCATATCAAAATCTTGGATACAGTTCACTTCTGTGGAAGCGAGGGAATTCACAAAGA	2795	
QY	785	TCACGTGTGAACCAACGTACAGAAAAAATGGAAACAAATGAAAAAGAGTTTGTGTACTGAA	844	
Db	2796	TCACGTGTGAACCAACGTACAGAAAAAATGGAAACAAATGAAAAAGAGTTTGTGTACTGAA	2855	
QY	845	AAAGAACTGTTCAGAGCAGAAAGAAATAAATATCAAGTTAGAGAACCAAAAGTTAAATG	904	
Db	2856	AAAGAACTGTTCAGAGCAGAAAGAAATAAATATCAAGTTAGAGAACCAAAAGTTAAATG	2915	
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; Sequence 566, Application US/10124805			
; Publication No. US20030166022A1			
; GENERAL INFORMATION:			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Sleath, Paul R.			
; APPLICANT: Persing, David H.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER			
; FILE REFERENCE: 210121.470C12			
; CURRENT APPLICATION NUMBER: US/10/124.805			
; CURRENT FILING DATE: 2002-04-15			
; NUMBER OF SEQ ID NOS: 627			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 566			
; LENGTH: 4047			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
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Best Local Similarity 98.7%; Pred. No. 0;			
Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;			
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QY	245	AGAAAGTTCTTGGGATCTGAGAGTCTCTGAGAGTCTTTTCAAGAGGATGTTGTTT	304
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QY	305	ACCCAGGCTACACATCAAAAGAAATAGATAAATTAATGGAATTAAGAGAGTCTCC	364
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QY	365	TGATAATGATGTTTCTGAAGGCTCCCTGAGAGTGAAGTTTCTATTTCCAACTAAAGC	424
Db	2376	TGATAATGATGTTTCTGAAGGCTCCCTGAGAGTGAAGTTTCTATTTCCAACTAAAGC	2435
QY	425	CTTAGAATTGATGACATGCAAACTTTCAAGCAGAGGCTCCCGAGAGGCTATGCTT	484
Db	2436	CTTAGAATTGATGACATGCAAACTTTCAAGCAGAGGCTCCCGAGAGGCTATGCTT	2495
QY	485	CGAGGCTGCAATGAAATGCAAAAGTCTGTTCCAAATTAAGCCTTGGAAATGAAGATGA	544
Db	2496	CGAGGCTGCAATGAAATGCAAAAGTCTGTTCCAAATTAAGCCTTGGAAATGAAGATGA	2555
QY	545	ACAAACATTTGAGCAGATGATGTTTCCATCAGAACTCAAAAGAGGTTGAAGA	604
Db	2556	ACAAACATTTGAGCAGATGATGTTTCCATCAGAACTCAAAAGAGGTTGAAGA	2615
QY	605	AAATTTCTGGGATTTCTGAGGTTCTCCGTGAGACTGTTTCAAGAGGATGTTGTTGACC	664
Db	2616	AAATTTCTGGGATTTCTGAGGTTCTCCGTGAGACTGTTTCAAGAGGATGTTGTTGACC	2675
QY	665	CAAGGCTACACATCAAAAGAAATGATTAATTAAGTGGAAATTAAGATTTCAACTAG	724
Db	2676	CAAGGCTACACATCAAAAGAAATGATTAATTAAGTGGAAATTAAGATTTCAACTAG	2735
QY	725	CTATCAAAAAATCTTGGATACAGTTTCATTTCTGTGAAAGCAAGGAACTTCAAAAAA	784
Db	2736	CTATCAAAAAATCTTGGATACAGTTTCATTTCTGTGAAAGCAAGGAACTTCAAAAAA	2795
QY	785	TCATGTGAACAACTGACAGGAAATGGAACAAATGGAAGAGGTTTGTGTACTGAA	844
Db	2796	TCATGTGAACAACTGACAGGAAATGGAACAAATGGAAGAGGTTTGTGTACTGAA	2855
QY	845	AAAGAACTGTGAGAGCAAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT	904
Db	2856	AAAGAACTGTGAGAGCAAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT	2915
QY	905	GGACAAAGAGTCTGAGTGTGAGATTTGACTTTTAAACCAAGAGAGAGAGAGAA	964
Db	2916	GGACAAAGAGTCTGAGTGTGAGATTTGACTTTTAAACCAAGAGAGAGAGAGAA	2975
QY	965	TGCCGATATATTAAATGAAAAATTTAGGGAAGAAATTAAGAAAGATTCGAAGAGCAGATAG	1024
Db	2976	TGCCGATATATTAAATGAAAAATTTAGGGAAGAAATTAAGAAAGATTCGAAGAGCAGATAG	3035
QY	1025	GAAGAGTTAGAGTGAACCAACTTTGAAACAGGCTCTCAGATACAGATATAGATTT	1084
Db	3036	GAAGAGTTAGAGTGAACCAACTTTGAAACAGGCTCTCAGATACAGATATAGATTT	3095
QY	1085	GAAGAGTTAGAGTGAACCAACTTTGAAACAGGCTCTCAGATACAGATATAGATTT	1144
Db	3096	GAAGAGTTAGAGTGAACCAACTTTGAAACAGGCTCTCAGATACAGATATAGATTT	3155
QY	1145	CTTACATGAAATTCATGTTGAAAGAAATTCGCAATGCTTAAACCTGGAATAGCCAC	1204
Db	3156	CTTACATGAAATTCATGTTGAAAGAAATTCGCAATGCTTAAACCTGGAATAGCCAC	3215
QY	1205	ACTGAAACCACTACAGGAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT	1264
Db	3216	ACTGAAACCACTACAGGAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT	3275
QY	1265	AGAAAGATGCTGAACTTCAGATCACTTAACTGAAAGAGGAAATCAATTAACATAAG	1324
Db	3276	AGAAAGATGCTGAACTTCAGATCACTTAACTGAAAGAGGAAATCAATTAACATAAG	3335
QY	1325	GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGATGCTGAGACACAACTGCTCCTC	1384
Db	3336	GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGATGCTGAGACACAACTGCTCCTC	3395
QY	1385	TAAATTAAGGAGAAACCAAGACAAAGAAATCTAGAGGCAAGAAATTTGAATCACCATCC	1444
Db	3396	TAAATTAAGGAGAAACCAAGACAAAGAAATCTAGAGGCAAGAAATTTGAATCACCATCC	3455
QY	1445	TAGACTGGCTTCTGCTGACAGACCATGATCAAAATTTGACATCAAGAAAAGTCAAGA	1504
Db	3456	TAGACTGGCTTCTGCTGACAGACCATGATCAAAATTTGACATCAAGAAAAGTCAAGA	3515
QY	1505	ACCTGCTTTCCATTTGAGGAGATGCTTTGTTGCAAAAGAAAAATGAATTTGATGTCAG	1564
Db	3516	ACCTGCTTTCCATTTGAGGAGATGCTTTGTTGCAAAAGAAAAATGAATTTGATGTCAG	3575
QY	1565	TAGTACCGATATATAAATGAGTGTCTCCATCAACCACTTTCTGAGCTCAAGGAAAT	1624
Db	3576	TAGTACCGATATATAAATGAGTGTCTCCATCAACCACTTTCTGAGCTCAAGGAAAT	3634
QY	1625	CCAAAGGCTTAAATTAATTTCAATTAATGAGGAGATGCTCTTAAGAGAAATACATTTG	1684
Db	3635	CCAAAGGCTTAAATTAATTTCAATTAATGAGGAGATGCTCTTAAGAGAAATACATTTG	3694
QY	1685	TTTCAGGAACTGCAAAAGAGACCAACCTGAAAACACAGTGTCAATGAGAGAACTGAA	1744
Db	3695	TTTCAGGAACTGCAAAAGAGACCAACCTGAAAACACAGTGTCAATGAGAGAACTGAA	3753
QY	1745	CACATGTTCAAAACCAACCAAGATGTAAGCAAAACACACTGAGCAGAGGCTCTCTA	1804

Db 3754 CACATGTATCAAAACGACAAAGATATGTGAAACAAACACACTGAACAGCAGGAGTCTCTA 3813
Qy 1805 GATCAGAAATTAATTTCAACTACAAACCAAAATATATGTGGCTTCAACAGCAATAGTTTCAT 1864
Db 3814 GATCAGAAATTAATTTCAACTACAAACCAAAATATATGTGGCTTCAACAGCAATAGTTTCAT 3873
Qy 1865 GCACATAAGAAAGCTGACACAAACAAAGCAAGATAGAAATTTGATNTTTCATTTCTTGAGAG 1924
Db 3874 GCACATAA-GAAAGCTGACACAAACAAAGCAAGATAGAAATTTGATNTTTCATTTCTTGAGAG 3932
Qy 1925 GAAATGCG-NCATCATCTTTCTAAAGAGAAATATGAGGAGATATTTNATTCNATTAACCA 1983
Db 3933 GAAATGCAACATCATCTCTCTAAAGAGAAATATGAGGAGATATTTNATTCNATTAACCA 3992
Qy 1984 TTTAAAAACCCGTATATTTTCAATATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 2030
Db 3993 TTTAAAAACCCGTATATATTTTCAATATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 4038

RESULT 4
US-10-058-270A-3
; Sequence 3, Application US/10058270A
; Publication No. US20040029114A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Afar, Daniel
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer
; FILE REFERENCE: 018501-0052100S
; CURRENT APPLICATION NUMBER: US/10/058,270A
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,965
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/265,928
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/829,472
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/282,698
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/288,590
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,443
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-058-270A-3

Query Match 95.6%; Score 1940; DB 13; Length 4458;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;

Qy 5 TGCCGCTTAAGATGCTCTCTGAAGCTAACTGCGGAATGAAGTTTCTATTCCAACTAA 64
Db 2091 TCCCTGTTAAAGATGCTCTCTGAAGCTAACTGCGGAATGAAGTTTCTATTCCAACTAA 2150
Qy 65 AGCCTTAGAATTTGATGGACATGCAAACTTTCAAGCAGAGCCTCCCGAGAGCCATTCGC 124
Db 2151 AGCCTTAGAATTTGATGGACATGCAAACTTTCAAGCAGAGCCTCCCGAGAGCCATTCGC 2210
Qy 125 CTTGAGCTGCTGATTAAGTCAAAAGTCTGTTCCCAATGAAGCTTTGGATTTGAAGAA 184
Db 2211 CTTGAGCTGCTGATTAAGTCAAAAGTCTGTTCCCAATGAAGCTTTGGATTTGAAGAA 2270
Qy 185 TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGGACTATGA 244
Db 2271 TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGGACTATGA 2330

Qy 245 AGAAGTTCTTGGATTTCTGAGACTCTCTGTGAGACTGTGTTTCACAGAAAGATGTGTGTTT 304
Db 2331 AGAAGTTCTTGGATTTCTGAGACTCTCTGTGAGACTGTGTTTCACAGAAAGATGTGTGTTT 2390
Qy 305 ACCCAAGCTACACATCAAAAGAAATAGATAAATAAATGGAATTTAGAAAGTCTCC 364
Db 2391 ACCCAAGCTACACATCAAAAGAAATAGATAAATAAATGGAATTTAGAAAGTCTCC 2450
Qy 365 TGATAATGATGTTTCTTGAAGGCTCCCTGCAGAAATGAAAAGTTTCTATTCCAACTAAAGC 424
Db 2451 TGATAATGATGTTTCTTGAAGGCTCCCTGCAGAAATGAAAAGTTTCTATTCCAACTAAAGC 2510
Qy 425 CTTAGAATTTGATGACATGCAAACTTTCAAGAGAGCCTCCCGAGAGCCATCTGCGTT 484
Db 2511 CTTAGAATTTGATGACATGCAAACTTTCAAGAGAGCCTCCCGAGAGCCATCTGCGTT 2570
Qy 485 CGAGCCTGCCATTTGAATGCAAAAGTCTGTTCCAAATGAAGCTTTGGAATTTGAAGATGA 544
Db 2571 CGAGCCTGCCATTTGAATGCAAAAGTCTGTTCCAAATGAAGCTTTGGAATTTGAAGATGA 2630
Qy 545 ACAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 604
Db 2631 ACAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 2690
Qy 605 AAATTTCTTGGATTTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAAGGATGTGTGTACC 664
Db 2691 AAATTTCTTGGATTTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAAGGATGTGTGTACC 2750
Qy 665 CAAAGCTACACATCAAAAGAAATGGAATAAATAAAGTCGAAATTTAGAAGATTTCAACTAG 724
Db 2751 CAAAGCTACACATCAAAAGAAATGGAATAAATAAAGTCGAAATTTAGAAGATTTCAACTAG 2810
Qy 725 CTTATCAAAATTTTGGATACAGATTCATCTGTGAAAGAGCAAGGAACTTCAAAAAGA 784
Db 2811 CTTATCAAAATTTTGGATACAGATTCATCTGTGAAAGAGCAAGGAACTTCAAAAAGA 2870
Qy 785 TCACTGTGAACCAACGTCAGAGAAATGGAACAAATGAAAAGAAAGTTTGTGTACTGAA 844
Db 2871 TCACTGTGAACCAACGTCAGAGAAATGGAACAAATGAAAAGAAAGTTTGTGTACTGAA 2930
Qy 845 AAAGAACTGTGAGAGCAAAAGAAATAAATCAAGTTAGAGACCAAAAGTTAAATG 904
Db 2931 AAAGAACTGTGAGAGCAAAAGAAATAAATCAAGTTAGAGACCAAAAGTTAAATG 2990
Qy 905 GGAACAAAGAGCTCTGAGTGTGAGATTTGAACTTTAAACCAAGAGAGAGAGAGAGAA 964
Db 2991 GGAACAAAGAGCTCTGAGTGTGAGATTTGAACTTTAAACCAAGAGAGAGAGAGAGAA 3050
Qy 965 TGCCGATATTTAAATGAAAAAATTTAGGAGAAATTTAGGAGAAATTTAGGAGAGAGAGAGAG 1024
Db 3051 TGCCGATATTTAAATGAAAAAATTTAGGAGAAATTTAGGAGAAATTTAGGAGAGAGAGAGAG 3110
Qy 1025 GAAAGAGTTAGAGTGAACCAACCTTGAACAGAGCTCTCAGAAATCAAGATATAGAAT 1084
Db 3111 GAAAGAGTTAGAGTGAACCAACCTTGAACAGAGCTCTCAGAAATCAAGATATAGAAT 3170
Qy 1085 GAAAGAGTTAGAGTGAATTTGAATTTGATTTCTCAGCTCTGAAATGAAATTAICT 1144
Db 3171 GAAAGAGTTAGAGTGAATTTGAATTTGATTTCTCAGCTCTGAAATGAAATTAICT 3230
Qy 1145 CTTACATGAATTTGATTTGAAAGGAAATTTGCAATGCTTAAACTGGAATAGCCAC 1204
Db 3231 CTTACATGAATTTGATTTGAAAGGAAATTTGCAATGCTTAAACTGGAATAGCCAC 3290
Qy 1205 ACTGAAACCACTACACAGAAAGGAAATTAATTAATTTGAGGACATTTAAGATTTTAA 1264
Db 3291 ACTGAAACCACTACACAGAAAGGAAATTAATTAATTTGAGGACATTTAAGATTTTAA 3350
Qy 1265 AGAAAGAGTGTGAATTTGATTTGAAAGGAAATTTGCAATGCTTAAACTGGAATAGCCAC 1324
Db 3351 AGAAAGAGTGTGAATTTGATTTGAAAGGAAATTTGCAATGCTTAAACTGGAATAGCCAC 3410
Qy 1325 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATGCTGAGAGACAAATGCTCACTTC 1384

[illegible]

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US-10-076-622-564
; Sequence 564, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INFECTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 564
; LENGTH: 4458
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-076-622-564

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[illegible]

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Db      3889  GATCAGAAATATTATTTCCTAACATACAAAGCAAAATAATGTGGCTTCAACAGCAATTAGTTTCAT 3948
Qy      1865  GCACATAANGAAAGCTGCACACCAACAAAGCAAGATACAAATGTGATNTTCATTTTCTTTGAGAG 1924
Db      3949  GCACATAAA-GAAAGCTGCACACCAAAAGCAAGATAACAAATGTGATATTCATTTTCTTTGAGAG 4007
Qy      1925  GAAATATGC-NCATCATCATCTTCTTAAAGAGAGAAAATAATGAGGAGATATTATTNATTCACNATAACCA 1983
Db      4008  GAAATATGCACATCATCTTCTTAAAGAGAGAAAATAATGAGGAGATATTATTAAATCAATAACCA 4066
Qy      1984  TTTTAAAAACCCGTATATTTTCATATGCGAAAAAATAAAAAAATAAAAAA 2030
Db      4068  TTTTAAAAAA-CCGTATATATCAATATGAAAAAGAAAGAAAGACAGAAACA 4113

RESULT 7
US-10-177-293-333
; Sequence 333, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: East Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSAY
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 333
; LENGTH: 4458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-333

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		95.6%;	Score 1940;	DB 15;	Length 4458;
		Best Local Similarity 98.7%;	Pred. No. 0;		
		Matches 2001;	Conservative 0;	Mismatches 21;	Indels 5; Gaps 5;
Qy	5	TGCGGTAAAGATGCTCTGTGAAGCTTAAC	TGCGGAATGAAAGTTCTTATTCCAACTAA	64	
Db	2091	TCTGTTTAAGATGGTCTCTGAAGCTTAAC	TGCGGATGAAAGTTCTTATTCCAACTAA	2150	
Qy	65	AGCCTTAGAATTGATGGACATGCAAACTTT	CAAGAGAGCCCTCCGAGAGCGCATCTGC	124	

Db 2151 AGCTTAGAATTTGATGGACATGCAAACTTTCAAAGCAGAGGCTCCCGAGAAGCCATCTGC 2210
Qy 125 CTTGAGGCTGCAATGTAATCAAAAGTCTGTTCCAAATAAAGCCTTTGGAATGAAGAA 184
Db 2211 CTTGAGGCTGCAATGTAATCAAAAGTCTGTTCCAAATAAAGCCTTTGGAATGAAGAA 2270
Qy 185 TGAACAAACATTTGAGAGCAGATGAGATCTCCATCAGATCCCAACCAAAAGGACTATGA 244
Db 2271 TGAACAAACATTTGAGAGCAGATGAGATCTCCATCAGATCCCAACCAAAAGGACTATGA 2330
Qy 245 AGAAGTCTTGGATTTCTGAGGCTCTGTCGAGACTGTTTCAACAAGAGGATGTGTGTT 304
Db 2331 AGAAGTCTTGGATTTCTGAGGCTCTGTCGAGACTGTTTCAACAAGAGGATGTGTGTT 2390
Qy 305 ACCAAGGCTACACATCAAAAAGAAATAGATAAAATAAATGAAATTAAGAGAGGCTGCC 364
Db 2391 ACCAAGGCTACACATCAAAAAGAAATAGATAAAATAAATGAAATTAAGAGAGGCTGCC 2450
Qy 365 TGATAATGATGTTTCTGAGGCTCCCTGAGAAATGAAGTTCCTATTCCAACTAAAGC 424
Db 2451 TGATAATGATGTTTCTGAGGCTCCCTGAGAAATGAAGTTCCTATTCCAACTAAAGC 2510
Qy 425 CTTAGAAATGATGGACATCAAACTTTCAAAGCAGGCTCCCGAGAAGCCATCTGCCTT 484
Db 2511 CTTAGAAATGATGGACATCAAACTTTCAAAGCAGGCTCCCGAGAAGCCATCTGCCTT 2570
Qy 485 CGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTTGGAATTAAGAAATGA 544
Db 2571 CGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTTGGAATTAAGAAATGA 2630
Qy 545 ACAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 604
Db 2631 ACAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 2690
Qy 605 AAATCTTGGGATCTGAGAGTCTCCGTGAGACTGTTTCAACAAGAGGATGTGTGTACC 664
Db 2691 AAATCTTGGGATCTGAGAGTCTCCGTGAGACTGTTTCAACAAGAGGATGTGTGTACC 2750
Qy 665 CAAAGCTACACATCAAAAAGAAATGATAAAATAGTGGAATTAAGAGATTCAACTAG 724
Db 2751 CAAAGCTACACATCAAAAAGAAATGATAAAATAGTGGAATTAAGAGATTCAACTAG 2810
Qy 725 CTTATCAAAAATCTTGATACAGTTTCACTTTGTAAGAGAGCAAGGAACTTCAAAAAGA 784
Db 2811 CTTATCAAAAATCTTGATACAGTTTCACTTTGTAAGAGAGCAAGGAACTTCAAAAAGA 2870
Qy 785 TCATGTGAAACCTGACAGGAAATGGAACAAATGAAAGAAAGTGTGTACTGAA 844
Db 2871 TCATGTGAAACCTGACAGGAAATGGAACAAATGAAAGAAAGTGTGTACTGAA 2930
Qy 845 AAAGAACTGTGAGAGCAAGAAATGAAATCAGTTGAGACCAAGTAAAGTTAAATG 904
Db 2931 AAAGAACTGTGAGAGCAAGAAATGAAATCAGTTGAGACCAAGTAAAGTTAAATG 2990
Qy 905 GGAACAAGAGCTCTGAGGTGTGAGATTTGACTTTAAACCAAGAGAGAGAGAGAGAA 964
Db 2991 GGAACAAGAGCTCTGAGGTGTGAGATTTGACTTTAAACCAAGAGAGAGAGAGAA 3050
Qy 965 TGCCGATATTTAAATGAAATTAAGGAAATTAAGGAAATTAAGGAAATTAAGGAAATTAAG 1024
Db 3051 TGCCGATATTTAAATGAAATTAAGGAAATTAAGGAAATTAAGGAAATTAAGGAAATTAAG 3110
Qy 1025 GAAAGAGTTAGAGTGAACCAACAACTTGAACAGGCTCTCAGAAATCAAGATATAGAAT 1084
Db 3111 GAAAGAGTTAGAGTGAACCAACAACTTGAACAGGCTCTCAGAAATCAAGATATAGAAT 3170
Qy 1085 GAAGAGTTAGAGTGAATTTGAATCAGGTTTCTACACTATGAATGAATTAATCT 1144
Db 3171 GAAGAGTTAGAGTGAATTTGAATCAGGTTTCTACACTATGAATGAATTAATCT 3230
Qy 1145 CTTACATGAATTTGATGTTGAAAAGGAAATGCAATGCTTAAACTGGAATAGCCAC 1204
Db 3231 CTTACATGAATTTGATGTTGAAAAGGAAATGCAATGCTTAAACTGGAATAGCCAC 3290

Qy 1205 ACTGAAACACCAATACACAGAAAGGAAATAAATACCTTTGAGGACATTAAGATTTTAA 1264
Db 3291 ACTGAAACACCAATACACAGAAAGGAAATAAATACCTTTGAGGACATTAAGATTTTAA 3350
Qy 1265 AGAAAGAAATGCTGAACTTTCAGATGACCTTAAAGAACTGAAAGAGGAAATCAATTAACATAAAG 1324
Db 3351 AGAAAGAAATGCTGAACTTTCAGATGACCTTAAAGAACTGAAAGAGGAAATCAATTAACATAAAG 3410
Qy 1325 GGATCTCAATATAGTGGGAGCTTAAAGTCTGATAGCTGAGAACACAAATGCTCACTTC 1384
Db 3411 GGATCTCAATATAGTGGGAGCTTAAAGTCTGATAGCTGAGAACACAAATGCTCACTTC 3470
Qy 1385 TAAATGAAAGGAAACCAAGACAAAGAAATCTAGAGGACAGAAATGAAATCACCATCC 1444
Db 3471 TAAATGAAAGGAAACCAAGACAAAGAAATCTAGAGGACAGAAATGAAATCACCATCC 3530
Qy 1445 TAGATGGCTTCTGCTTCAAGACCAATGATCAAAATTTGACATCAAGAAAAGTCAAGA 1504
Db 3531 TAGATGGCTTCTGCTTCAAGACCAATGATCAAAATTTGACATCAAGAAAAGTCAAGA 3590
Qy 1505 ACCTGCTTTCCATTCAGAGGAGATGCTTGTGTAAGAAAGAAATGAAATGATGTGAG 1564
Db 3591 ACCTGCTTTCCATTCAGAGGAGATGCTTGTGTAAGAAAGAAATGAAATGATGTGAG 3650
Qy 1565 TAGTACCGATATATAAATGAGGCTCCATCAACCACTTTCTGAAGCTCAAGGAAT 1624
Db 3651 TAGTACCGATATATAAATGAGGCTCCATCAACCACTTTCTGAAGCTCAAGGAAT 3709
Qy 1625 CCNAGGCTTAAATTAATCTCAATATGAGGAGATCTCTAAGAGAAATACATTCG 1684
Db 3710 CCNAGGCTTAAATTAATCTCAATATGAGGAGATCTCTAAGAGAAATACATTCG 3769
Qy 1685 TTTTCAAGCAATGACCAAGAGAGACCAAGCTGAAACACAGTGTCAATGAGAAAGCTGAA 1744
Db 3770 TTTTCAAGCAATGACCAAGAGAGACCAAGCTGAAACACAGTGTCAATGAGAAAGCTGAA 3828
Qy 1745 CACATGTCNCAAGCAAGATGATGTAAGCAACACACTGANCAGAGGAGTCTCTA 1804
Db 3829 CACATGTCNCAAGCAAGATGATGTAAGCAACACACTGANCAGAGGAGTCTCTA 3888
Qy 1805 GATCAGAAATTTTCAACTTCAAGCAAGAAATATGCTGCTTCAACAGCAATTAGTTCAT 1864
Db 3889 GATCAGAAATTTTCAACTTCAAGCAAGAAATATGCTGCTTCAACAGCAATTAGTTCAT 3948
Qy 1865 GCACATGAAGAGAGTGAACCAAGAGAGATACAAATGATTTTCAATTTCTTGAGAG 1924
Db 3949 GCACATGAAGAGAGTGAACCAAGAGAGATACAAATGATTTTCAATTTCTTGAGAG 4007
Qy 1925 GAAATGTCNCATCATCTTCTAAAGAGAAATATGAGGAGATTTTAAATGAGGAGATTTTAAATGAGGAG 1983
Db 4008 GAAATGTCNCATCATCTCTTAAAGAGAAATATGAGGAGATTTTAAATGAGGAGATTTTAAATGAGGAG 4067
Qy 1984 TTTTAAAGAGAGGAGATTTTCAATATGAGGAGATTTTAAATGAGGAGATTTTAAATGAGGAG 2030
Db 4068 TTTTAAAGAGAGGAGATTTTCAATATGAGGAGATTTTAAATGAGGAGATTTTAAATGAGGAG 4113

RESULT 8

US-10-124-805-564
; Sequence 564, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCES: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10/124,805
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: Fast-Seq for Windows Version 4.0

[illegible]

Qy	965	TGCCGATATATTAAATGAAAAATTTAGGGAAGAAATTAGGAAGAAATCGAAGACAGCATAG	1024
Db	3051	TGCCGATATATTAAATGAAAAATTTAGGGAAGAAATTAGGGAAGAAATCGAAGACAGCATAG	3110
Qy	1025	GAAAGAGTTAGAGTGAAAGTGAACCAACTTGAAACAGGCTCTCAGAAATCAAGATATAGAAAT	1084
Db	3111	GAAAGAGTTAGAGTGAAAGTGAACCAACTTGAAACAGGCTCTCAGAAATCAAGATATAGAAAT	3170
Qy	1085	GAAAGAGTGAGAAAGTAAATTTGAAATCAGGTTTCTCAGCTCATGAAATTCGAATTTATCT	1144
Db	3171	GAAAGAGTGAGAAAGTAAATTTGAAATCAGGTTTCTCAGCTCATGAAATTCGAATTTATCT	3230
Qy	1145	CTTTACATGAAATTTGCAATGTTGAAAAAGGAAATTTGCCATGCTTAAAACTGGAATATGCCAC	1204
Db	3231	CTTTACATGAAATTTGCAATGTTGAAAAAGGAAATTTGCCATGCTTAAAACTGGAATATGCCAC	3290
Qy	1205	ACTGAAACACCAATACAGGAAAGGAAATTAATTAATTTTGAGGACATTTAAGATTTTAAA	1264
Db	3291	ACTGAAACACCAATACAGGAAAGGAAATTAATTAATTTTGAGGACATTTAAGATTTTAAA	3350
Qy	1265	AGAAAAGAAATGCTGAACTTCAGATGACCCCTTAAAACTGAAAGAGGAAATCAATTAACATAAAG	1324
Db	3351	AGAAAAGAAATGCTGAACTTCAGATGACCCCTTAAAACTGAAAGAGGAAATCAATTAACATAAAG	3410
Qy	1325	GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACAAATGCTCACTTC	1384
Db	3411	GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACAAATGCTCACTTC	3470
Qy	1385	TAAATTTGAAGGAAAAACAAGACAAAGAAATTAATCTAGAGGCGAGAAATTTGAATTCACCATCC	1444
Db	3471	TAAATTTGAAGGAAAAACAAGACAAAGAAATTAATCTAGAGGCGAGAAATTTGAATTCACCATCC	3530
Qy	1445	TAGACTGGCTTCTGCTGTACAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA	1504
Db	3531	TAGACTGGCTTCTGCTGTACAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA	3590
Qy	1505	ACCTGCTTTCCACATTCAGAGAGATGCTTTGTTGCAAGAAAAATGAATTTGATGTGTAG	1564
Db	3591	ACCTGCTTTCCACATTCAGAGAGATGCTTTGTTGCAAGAAAAATGAATTTGATGTGTAG	3650
Qy	1565	TAGTACCGATATATAACAAATGAGGTGCTCCATCAACACACATTTCTGAAAGCTTCAAGAGAAAT	1624
Db	3651	TAGTACCGATATATAACAAATGAGGTGCTCCATCAACACACATTTCTGAAAGCTTCAAGAGAAAT	3709
Qy	1625	CCANAAGCCTAAAAATTAATCTCAATTTATGACAGAGATGCTCTAAGAGAAAAATACATTTGG	1684
Db	3710	CCANAAGCCTAAAAATTAATCTCAATTTATGACAGAGATGCTCTAAGAGAAAAATACATTTGG	3769
Qy	1695	TTTCAGGAGACATGCACAAAGAGACCAACGTTGAAACACAGTGTCAAAATGAAGGAAAGCTGAA	1744
Db	3770	TTTCCA-GAACATGCACAAAGAGACCAACGTTGAAACACAGTGTCAAAATGAAGGAAAGCTGAA	3828
Qy	1745	CACATGNTCAAACGAAACAAGATNATGTGAAACAAAACACTGAGACAGAGAGTCTCTA	1804
Db	3829	CACATGNTCAAACGAAACAAGATNATGTGAAACAAAACACTGAGACAGAGAGTCTCTA	3888
Qy	1805	GATCAGAAATTTATTTCAACTACAAAGCAAAAAATATGTGGCTTCAACAGCAATTTAGTTTCAT	1864
Db	3889	GATCAGAAATTTATTTCAACTACAAAGCAAAAAATATGTGGCTTCAACAGCAATTTAGTTTCAT	3948
Qy	1865	GCACATAANGAAAGCTGACAAACAAAGCAAGATTAACATTTGATTTTCATTTCTTTGAGAG	1924
Db	3949	GCACATAANGAAAGCTGACAAACAAAGCAAGATTAACATTTGATTTTCATTTCTTTGAGAG	4007
Qy	1925	GAAAAATGC-NCATCATCTTCTTAAAGAGAAAAATGAGGAGATATTTTATTTACNATAACCA	1983
Db	4008	GAAAAATGC-NCATCATCTTCTTAAAGAGAAAAATGAGGAGATATTTTATTTACNATAACCA	4067
Qy	1984	TTTTAAAAAACCCGTTATTTTCAATATGAAAAAAAANAAAAAAA 2030	
Db	4069	TTTTAAAAAACCCGTTATTTTCAATATGAAAAAAAAGAAAGCAGAAACA 4113	

RESULT 9									
US-10-007-805-490									
; Sequence 490, Application US/10007805									
; Publication No. US20020150581A1									
; GENERAL INFORMATION:									
; APPLICANT: Jiang, Yuguo									
; APPLICANT: Dillon, Devin C.									
; APPLICANT: Mitcham, Jennifer L.									
; APPLICANT: Xu, Jiangchun									
; APPLICANT: Harlocker, Susan L.									
; APPLICANT: Hepler, William T.									
; APPLICANT: Henderson, Robert A.									
; APPLICANT: Fanger, Gary R.									
; APPLICANT: Vedick, Thomas S.									
; APPLICANT: McNeill, Patricia D.									
; APPLICANT: Durham, Margareta									
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY									
; FILE REFERENCE: 210121.470C10									
; CURRENT APPLICATION NUMBER: US/10/007.805									
; CURRENT FILING DATE: 2001-12-07									
; NUMBER OF SEQ ID NOS: 593									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 490									
; LENGTH: 3288									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-007-805-490									
Query Match 95.5%; Score 1938.4; DB 14; Length 3288;									
Best Local Similarity 98.5%; Pred. No. 0;									
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;									
QY	5	TGCCGTTAAAGATGGTCTTCTGAAGGCTAACTGGGGAATGAAGTTCTATTCCAACTAA	64						
Db	1254	TCTCTTAAAGATGGTCTTCTGAAGGCTAACTGGGGAATGAAGTTCTATTCCAACTAA	1313						
QY	65	AGCCTTAGAATGATGGACATGCAAACTTTCAGAGAGAGCTCCCGAGAGCCATCTGC	124						
Db	1314	AGCCTTAGAATGATGGACATGCAAACTTTCAGAGAGAGCTCCCGAGAGCCATCTGC	1373						
QY	125	CTTCGAGGCTGCATTGAAATGCAAAAGTCTGTTCCAAATGAAGCTTTGGAAATGAAGAA	184						
Db	1374	CTTCGAGGCTGCATTGAAATGCAAAAGTCTGTTCCAAATGAAGCTTTGGAAATGAAGAA	1433						
QY	185	TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGGACTATGA	244						
Db	1434	TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGGACTATGA	1493						
QY	245	ACAAAGTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTACAGAAAGGATGTGTGTTT	304						
Db	1494	AGAAAGTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTACAGAAAGGATGTGTGTTT	1553						
QY	305	ACCCAAGGCTACACATCAAAAGAAATAGATAAATGAATGAATGAAGAGTCTCC	364						
Db	1554	ACCCAAGGCTRCATCAAAAGAAATAGATAAATGAATGAATGAAGAGTCTCC	1613						
QY	365	TGATATGATGTTTCTCAAGGCTCCCTGAGAGTGAAGTTCTATTCCAACTTAAGC	424						
Db	1614	TGATATGATGTTTCTCAAGGCTCCCTGAGAGTGAAGTTCTATTCCAACTTAAGC	1673						
QY	425	CTTAGAATGATGGACATCAAACTTTCAAAGCAGAGCTCCCGAGAGGCCATCTGCCTT	484						
Db	1674	CTTAGAATGATGGACATCAAACTTTCAAAGCAGAGCTCCCGAGAGGCCATCTGCCTT	1733						
QY	485	CGAGGCTGCCATTGAATCAAAAGTCTGTTCCAAATGAAGCTTTGGAATGAAGATGA	544						
Db	1734	CGAGGCTGCCATTGAATCAAAAGTCTGTTCCAAATGAAGCTTTGGAATGAAGATGA	1793						
QY	545	ACAAACATTGAGAGCAGATCAGATGTTCCTTTCAAGATCAAAACAAAGAGGTTGAAGA	604						
Db	1794	ACAAACATTGAGAGCAGATCAGATGTTCCTTTCAAGATCAAAACAAAGAGGTTGAAGA	1853						

QY	605	AAATCTTTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTTCACAGAAAGATGTGTGTGATCC	664
Db	1854	AAATCTTTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTTCACAGAAAGATGTGTGTGATCC	1913
QY	665	CAAGGCTACACATCAAAAGAAATGGATTAATTAAGTGGAAATTTAGAAGATTTCAACTAG	724
Db	1914	CAAGGCTACACATCAAAAGAAATGGATTAATTAAGTGGAAATTTAGAAGATTTCAACTAG	1973
QY	725	CCTATCAAAATCTTTGGATACAGATTCATTCTTTGTAAGACCAAGGAACTTCAAAAGA	784
Db	1974	CCTATCAAAATCTTTGGATACAGATTCATTCTTTGTAAGACCAAGGAACTTCAAAAGA	2033
QY	785	TCATCTGTAACAACTGACAGAAATGGAAATTAATTAAGTGGAAATTTAGAAGATTTCAACTAG	844
Db	2034	TCATCTGTAACAACTGACAGAAATGGAAATTAATTAAGTGGAAATTTAGAAGATTTCAACTAG	2093
QY	845	AAAGAACTCTGACAGAAACAAAGAAATTAATTAAGTGGAAATTTAGAAGATTTCAACTAG	904
Db	2094	AAAGAACTCTGACAGAAACAAAGAAATTAATTAAGTGGAAATTTAGAAGATTTCAACTAG	2153
QY	905	GGAAACAAGAGCTCTGAGATGAGATTCATTCACTTTAAACCAAGAAAGAGAGAGAGAA	964
Db	2154	GGAAACAAGAGCTCTGAGATGAGATTCATTCACTTTAAACCAAGAAAGAGAGAGAGAA	2213
QY	965	TGCCGATATATTAATGAAGAAATTTAGGAAAGATTTAGGAAAGATTCGAAAGAGCAGATAG	1024
Db	2214	TGCCGATATATTAATGAAGAAATTTAGGAAAGATTTAGGAAAGATTCGAAAGAGCAGATAG	2273
QY	1025	GAAAGATTTAGAAAGTGAACCAACTTTGAAACAGGCTCTCAGAAATACAGATATAGATTT	1084
Db	2274	GAAAGATTTAGAAAGTGAACCAACTTTGAAACAGGCTCTCAGAAATACAGATATAGATTT	2333
QY	1085	GAAAGATTTAGAAAGTGAACCAACTTTGAAACAGGCTCTCAGAAATACAGATATAGATTT	1144
Db	2334	GAAAGATTTAGAAAGTGAACCAACTTTGAAACAGGCTCTCAGAAATACAGATATAGATTT	2393
QY	1145	CTTACATGAAATTTGCATGTTGAAAGAGAAATTTCCATGCTTAAACTGGAAATAGCCAC	1204
Db	2394	CTTACATGAAATTTGCATGTTGAAAGAGAAATTTCCATGCTTAAACTGGAAATAGCCAC	2453
QY	1205	ACTGAAACCAATACACAGAAAGAAATTAATTAAGTGGAAATTTAGAAGATTTAA	1264
Db	2454	ACTGAAACCAATACACAGAAAGAAATTAATTAAGTGGAAATTTAGAAGATTTAA	2513
QY	1265	AGAAAGATTTGCTGAACTTCAGATGACCTTAAACTGAAAGAGGAAATCAATTAACATAAG	1324
Db	2514	AGAAAGATTTGCTGAACTTCAGATGACCTTAAACTGAAAGAGGAAATCAATTAACATAAG	2573
QY	1325	GGCATCTCAATATAGTGGGAGCTTAAAGTCTGTAGTGTGAGACACAACTGCTCCTTC	1384
Db	2574	GGCATCTCAATATAGTGGGAGCTTAAAGTCTGTAGTGTGAGACACAACTGCTCCTTC	2633
QY	1385	TAAATTTGAAGGAAACAAAGACAAAGAAATTAATTAAGTGGAAATTTAGAAGATTTAA	1444
Db	2634	TAAATTTGAAGGAAACAAAGACAAAGAAATTAATTAAGTGGAAATTTAGAAGATTTAA	2693
QY	1445	TAGACTGGCTTCTGCTGTACAAGACCAATGATCAAAATTTGTGACATCAAGAAAGTCAAG	1504
Db	2694	TAGACTGGCTTCTGCTGTACAAGACCAATGATCAAAATTTGTGACATCAAGAAAGTCAAG	2753
QY	1505	ACCTGCTTTCCATTTGAGAGGATCTGTTTGAAGAAAGAAATTAATTAAGTGTGATGTAG	1564
Db	2754	ACCTGCTTTCCATTTGAGAGGATCTGTTTGAAGAAAGAAATTAATTAAGTGTGATGTAG	2813
QY	1565	TAGTACCGATATATAAATGAGGCTGCTCAATCAACCTTTCTGAGCTCAAGAGAAAT	1624
Db	2814	TAGTACCGATATATAAATGAGGCTGCTCAATCAACCTTTCTGAGCTCAAGAGAAAT	2872
QY	1625	CCAAAGCTTAAATTAATCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1684
Db	2873	CCAAAGCTTAAATTAATCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2932

QY	365	TGATAATGATGGTTTTCTGAAGGCTCCCTGCAGAAATGAAAGTTTCTATTCCAACCTAAAGC	424
Db	1614	TGATAATGATGGTTTTCTGAAGGCTCCCTGCAGAAATGAAAGTTTCTATTCCAACCTAAAGC	1673
QY	425	CTTTAGAATTGATGGACATGCAAACTTTTAAAGCAGAGCCTCCCGAGAGCCATCTGCCTT	484
Db	1674	CTTTAGAATTGATGGACATGCAAACTTTTAAAGCAGAGCCTCCCGAGAGCCATCTGCCTT	1733
QY	485	CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGGAAGATGA	544
Db	1734	CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGGAAGATGA	1793
QY	545	ACAAACATTGAGAGCAGATCAGATGTTTCCTTCAGAAATCAAAACAAAGAAGGTTGAAGA	604
Db	1794	ACAAACATTGAGAGCAGATCAGATGTTTCCTTCAGAAATCAAAACAAAGAAGGTTGAAGA	1853
QY	605	AAATTCTTGGATTCTTGAGAGTCTCCGTGAGACTGTTTTCACAGAAGGATGTGTGTACC	664
Db	1854	AAATTCTTGGATTCTTGAGAGTCTCCGTGAGACTGTTTTCACAGAAGGATGTGTGTACC	1913
QY	665	CAGGGCTACACATCAAAAGAAATGATAAATTAAGTGGAAATATAGAGATTCAACTAG	724

	QY	725	CCTATCAAAAACCTTGGATACAGTTCAITTCCTGTGTAAGAAGCAAGGAACCTTCAAAAAACA	784
	DB	1974	CCTATCAAAAACCTTGGATACAGTTCAITTCCTGTGTAAGAAGCAAGGAACCTTCAAAAAACA	2033
	QY	785	TCAGTGGAACAACGTACAGAAATAATGAAACAAATGAAAAAGNAGCTTTTGTGTACTGAA	844
	DB	2034	TCAGTGGAACAACGTACAGAAATAATGAAACAAATGAAAAAGNAGCTTTTGTGTACTGAA	2093
	QY	845	AAAGAAACTGTGAGAACCAAGAAATAAATAACACAGTTTAGAGAACCAAAAAAGTTAAATG	904
	DB	2094	AAAGAACTGTGAGAACCAAGAAATAAATAACACAGTTTAGAGAACCAAAAAAGTTAAATG	2153
	QY	905	GGAAACAAGAGCTGTGAGTGTGAGATTGACTTTAAACCAGAGAGAGAGAGAGAGAAA	964
	DB	2154	GGAAACAAGAGCTGTGAGTGTGAGATTGACTTTAAACCAGAGAGAGAGAGAGAGAAA	2213
	QY	965	TGCCGATATATTAATGAAAAAATTAGGGAAGAATAATAGGAAGAATCGAAGAGCAGCATAG	1024
	DB	2214	TGCCGATATATTAATGAAAAAATTAGGGAAGAATAATAGGAAGAATCGAAGAGCAGCATAG	2273
	QY	1025	GAAAGAGTTAGAGTGAACAACAACCTTGAAACAGGCTCTCAGAAATCAAGATATAGAATT	1084
	DB	2274	GAAAGAGTTAGAGTGAACAACAACCTTGAAACAGGCTCTCAGAAATCAAGATATAGAATT	2333
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	DB	2334	GAAAGAGTTAGAAAAGTAATTGAAATCAGGTTTTCTCACACTCATGAAAAATGAAAATTTATCT	2393
	QY	1145	CTTACATGAAAATTGCATGTTGAAAAAGGAAATTCCTATGCTTAAACTGGAATATAGCCAC	1204
	DB	2394	CTTACATGAAAATTGCATGTTGAAAAAGGAAATTCCTATGCTTAAACTGGAATATAGCCAC	2453
	QY	1205	ACTGAAACACCAAATACCAAGGAAAAAGGAAAAATAATCTTTTGAGGACATTTAAGATTTTAAA	1264
	DB	2454	ACTGAAACACCAAATACCAAGGAAAAAGGAAAAATAATCTTTTGAGGACATTTAAGATTTTAAA	2513
	QY	1265	AGAAAAGAAATGCTGNACTTCAGATGACCCCTAAACTGAAAGAGAAATCAITTAACATAAAG	1324
	DB	2514	AGAAAAGAAATGCTGNACTTCAGATGACCCCTAAACTGAAAGAGAAATCAITTAACATAAAG	2573
	QY	1325	GGCATCTCAATATAGTGGCGAGCTTAAAGTTCTGATAGTGAGAACACAATGCTCACCTTC	1384
	DB	2574	GGCATCTCAATATAGTGGCGAGCTTAAAGTTCTGATAGTGAGAACACAATGCTCACCTTC	2633
	QY	1385	TAAATTTGAGGAAAAACAAGACAAGAAATACTAGAGCGAAAAATGGAATCACACCATCC	1444
	DB	2634	TAAATTTGAGGAAAAACAAGACAAGAAATACTAGAGCGAAAAATGGAATCACACCATCC	2693

1205 ACTGAACACCAATACAGGAAAGGAAATATAATCTTTGAGCAGCAATTAAGATTTTAA 1264
1265 AGAAAGAAATGCTGAATCTGATGACCCCTAAATCTGAAAGAGGAATCAATTAAG 1324
2514 AGAAAGAAATGCTGAATCTGATGACCCCTAAATCTGAAAGAGGAATCAATTAAG 2573
1325 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGACCAATGCTCACTTC 1384
2574 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGACCAATGCTCACTTC 2633
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2634 TAAATGAGGAAACCAAGCAAAAGAAATCTAGAGGAGCAAAATGGAATCAGACCACTCC 2693
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2754 ACCTGCTTCCCATGTCAGGAGATGCTTTGTCGAAAGAAATGGAATGATGATGAG 2813
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2814 TAGTACCGATATATACATGAGGCTCCATCAACCACTTTCTGAGCTCAAGAGGAAT 2872
1625 CCNAAAGCCTTAAATTAATCTCAATATGCGAGAGTCTCTAAGAGAAATACATGG 1684
2873 CCNAAAGCCTTAAATTAATCTCAATATGCGAGAGTCTCTAAGAGAAATACATGG 2932
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2933 TTTTCA-GAAGAGTGAACAGAGAGCAGCAAGTGAACACAGTGTCAATGAAGAGAGCTGAA 2991
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1805 GATCAGAAATATTTCAACTACAGCAAAATATGTCCTTCAAGCAAGATTTTCAAT 1864
3052 GATCAGAAATATTTCAACTACAGCAAAATATGTCCTTCAAGCAAGATTTTCAAT 3111
1865 GCACATAAGAGAGCTGCAACAAAGAGCAAGATTAACATTTGATTTTCAATTTCTTGAGAG 1924
3112 GCACATAAGAGAGCTGCAACAAAGAGCAAGATTAACATTTGATTTTCAATTTCTTGAGAG 3170
1925 GAAATGCT-NCATCTCTTAAAGAGAGAAATGAGGAGATATTTNATGATNATACCA 1983
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1984 TTTTAAAGAGAGCTGCAACAAAGAGCAAGATTAACATTTGATTTTCAATTTCTTGAGAG 2030
3231 TTTTAAAGAGAGCTGCAACAAAGAGCAAGATTAACATTTGATTTTCAATTTCTTGAGAG 3276

RESULT 12
US-09-604-287A-474
; Sequence 474, Application US/09604287A
; Patent No. US20020064872A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillot, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604, 287A
; CURRENT FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 474
; LENGTH: 3865
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2448)...(2631)
; OTHER INFORMATION: 184 bp insert of B726P splice form
US-09-604-287A-474

Query Match 95.5%; Score 1938.4; DB 9; Length 3865;
Best Local Similarity 98.5%; Pred No. 0;
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;

QY 5 TCCGTTAAAGATGGTCTTCTGAAGCTAACTGCGGAATGAAGTTCTATTCCAACTAA 64
DB 1526 TCCGTTAAAGATGGTCTTCTGAAGCTAACTGCGGAATGAAGTTCTATTCCAACTAA 1585
QY 65 AGCTTTAGAAATGATGAGCATCAAACTTTCAAGCAGAGCTCCCGAAGAGCCATCTGC 124
DB 1586 AGCTTTAGAAATGATGAGCATCAAACTTTCAAGCAGAGCTCCCGAAGAGCCATCTGC 1645
QY 125 CTTTGAAGCTCCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATGAAGAA 184
DB 1646 CTTTGAAGCTCCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATGAAGAA 1705
QY 185 TGAACAAACATTTGAGAGCAGATGAGATCTCCCATCAGAAATCAAAACAAAGAGCTATCA 244
DB 1706 TGAACAAACATTTGAGAGCAGATGAGATCTCCCATCAGAAATCAAAACAAAGAGCTATCA 1765
QY 245 AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGAGTCTTTTCAAGAGAGTGTGTGTT 304
DB 1766 AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGAGTCTTTTCAAGAGAGTGTGTGTT 1825
QY 305 ACCCAGGCTTACATCAAAAGAGATAGATAATTAATAATGAAGATTTAGAGAGTCTCC 364
DB 1826 ACCCAGGCTTACATCAAAAGAGATAGATAATTAATAATGAAGATTTAGAGAGTCTCC 1885
QY 365 TGATAATGATGGTTTCTGAGAGTCTCCCTGCAAGTGAAGTTTCTATTCCAACTAAAGC 424
DB 1886 TGATAATGATGGTTTCTGAGAGTCTCCCTGCAAGTGAAGTTTCTATTCCAACTAAAGC 1945
QY 425 CTTAGAAATGATGAGCATGCAAACTTTCAAGCAGAGCTCCCGAAGAGCCATCTGCCTT 484
DB 1946 CTTAGAAATGATGAGCATGCAAACTTTCAAGCAGAGCTCCCGAAGAGCCATCTGCCTT 2005
QY 485 CGAGCTTGCCATGCAAAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATGAAGATGA 544
DB 2006 CGAGCTTGCCATGCAAAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATGAAGATGA 2065
QY 545 ACAAACATTTGAGAGCAGATGATGTTCCCTTCAAGATCAAAACAAAGAGAGTTGAAGA 604
DB 2066 ACAAACATTTGAGAGCAGATGATGTTCCCTTCAAGATCAAAACAAAGAGAGTTGAAGA 2125
QY 605 AAATTTCTTGGATTTCTGAGAGTCTCCGTGAGAGTCTTTTCAAGAGAGTGTGTGTACC 664
DB 2126 AAATTTCTTGGATTTCTGAGAGTCTCCGTGAGAGTCTTTTCAAGAGAGTGTGTGTACC 2185
QY 665 CAAGCTTACATCAAAAGAGAAATGGAATAAATAAGTGAAGATTTAGAGATTTCAACTAG 724
DB 2186 CAAGCTTACATCAAAAGAGAAATGGAATAAATAAGTGAAGATTTAGAGATTTCAACTAG 2245
QY 725 CCTATCAAAATCTTGGATTCAGTTCAATCTTGTGAAGAGAGCAAGGAGCTTCAAAAGA 784
DB 2246 CCTATCAAAATCTTGGATTCAGTTCAATCTTGTGAAGAGAGCAAGGAGCTTCAAAAGA 2305
QY 785 TCACGTGTGAACACGTACAGGAAATTAAGTGAAGAGAGAGTTTGTGTACTGAA 844
DB 2306 TCACGTGTGAACACGTACAGGAAATTAAGTGAAGAGAGAGTTTGTGTACTGAA 2365
QY 845 AAGAGAACTGTGAGAGCAAGAGAAATTAATCACAGTTAGAGAGCAAAAGAGTAAATG 904

QY 545 ACAAACATTGAGAGAGATCAGATGTTCCCTTCAGAAATCAAAACAAAAGAGGTTGAGA 604
 Db 2066 ACAAACATTGAGAGAGATCAGATGTTCCCTTCAGAAATCAAAACAAAAGAGGTTGAGA 2125
 QY 605 AAATTCITGGGATTCAGAGTCTCCGTGAGACTGTTTTCAGAGAGGATGTTGTGTACC 664
 Db 2126 AAATTCITGGGATTCAGAGTCTCCGTGAGACTGTTTTCAGAGAGGATGTTGTGTACC 2185
 QY 665 CAAGCTACACATCAAAAGAAAGTGAATAAATAGTGGAAATAGAAATTCNACTAG 724
 Db 2186 CAAGCTACACATCAAAAGAAAGTGAATAAATAGTGGAAATAGAAATTCNACTAG 2245
 QY 725 CCTATCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAATCTCAAAAAGA 784
 Db 2246 CCTATCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAATCTCAAAAAGA 2305
 QY 785 TCACGTGAAACAACTGACAGAAATAATGGAACAAATGAAAGAAAGCTTTTGTGACTGAA 844
 Db 2306 TCACGTGAAACAACTGACAGAAATAATGGAACAAATGAAAGAAAGCTTTTGTGACTGAA 2365
 QY 845 AAAGAAACTGTGAGAGCAAAAGAAATAAATACAGTTCAGAGAACCAAAAAGTTAAATG 904
 Db 2366 AAAGAAACTGTGAGAGCAAAAGAAATAAATACAGTTCAGAGAACCAAAAAGTTAAATG 2425
 QY 905 GGAACAAGAGCTCTGAGTGTGAGTTCAGTCTTTAAACCAAGAAAGAGAGAGAGAAA 964
 Db 2426 GGAACAAGAGCTCTGAGTGTGAGTTCAGTCTTTAAACCAAGAAAGAGAGAGAGAAA 2485
 QY 965 TGCCCATATATTAAATGAAATAATAGGGAAGAAATAGGAAGATCGAAGAGCAGCATAG 1024
 Db 2486 TGCCCATATATTAAATGAAATAATAGGGAAGAAATAGGAAGATCGAAGAGCAGCATAG 2545
 QY 1025 GAAAGAGTTAGAGTGAACAACTTGAACAGGCTCTCAGATACAGATATAGAAAT 1084
 Db 2546 GAAAGAGTTAGAGTGAACAACTTGAACAGGCTCTCAGATACAGATATAGAAAT 2605
 QY 1085 GAAGAGTGTAGAGTGAATTTGAATCAGGTTCTCAGACTCATGAAATGAAATTTACT 1144
 Db 2606 GAAGAGTGTAGAGTGAATTTGAATCAGGTTCTCAGACTCATGAAATGAAATTTACT 2665
 QY 1145 CTTACATGAAATTCATGTTGAAAGAAATGCTGATGCTGAAAGTGAAGTGAAGTGAAG 1204
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 Db 3026 ACCTGCTTTCCATTCGAGGAGATGCTTGTGTTGCAAGAAATAATCAATGTTGATGTGAG 3085
 QY 1565 TAGTACGATATATACATAGGCTGCTCCATCAACCATCTTCTGAGAGTCAAGGAAAT 1624
 Db 3086 TAGTA-CGATATATACATAGGCTGCTCCATCAACCATCTTCTGAGAGTCAAGGAAAT 3144

QY 1625 CCANAAGCCTAAATTAATCTCAATTTATGAGAGATGCTCTAAGAGAAAATACATGG 1684
 Db 3145 CCANAAGCCTAAATTAATCTCAATTTATGAGAGATGCTCTAAGAGAAAATACATGG 3204
 QY 1685 TTTTCAAGACATGCAAAAGAGACCAAGCTGCAAGTGTCAATGAGGAGGCTGAA 1744
 Db 3205 TTTTCA-GAACATGCAAAAGAGACCAAGCTGCAAGTGTCAATGAGGAGGCTGAA 3263
 QY 1745 CACATGTTTCAAAAGCAAAAGATGTTGAAACAAACACACTGACAGCAGGAGTCTCTA 1804
 Db 3264 CACATGTTTCAAAAGCAAAAGATGTTGAAACAAACACACTGACAGCAGGAGTCTCTA 3323
 QY 1805 GATCAGAAATTTTCAACTCAAAAGCAAAATATGTTGGCTTCAACAGCAATTTAGTTCA 1864
 Db 3324 GATCAGAAATTTTCAACTCAAAAGCAAAATATGTTGGCTTCAACAGCAATTTAGTTCA 3383
 QY 1865 GCACATTAAGAAAGCTGCAAAAGCAAAAGATGTTGAAACAAACACTGATTTCTTGAGAG 1924
 Db 3384 GCACATTAAGAAAGCTGCAAAAGCAAAAGATGTTGAAACAAACACTGATTTCTTGAGAG 3442
 QY 1925 GAAATGTC-NCATCATCTTTTAAAGAGAAAATGAGAGATATTTNATTACNATAACCA 1983
 Db 3443 GAAATGTCNATCATCTCTTAAAGAGAAAATGAGAGATATTTNATTACNATAACCA 3502
 QY 1984 TTTAAAAAACCCCTATATTTCATATGAAAAAANAAAAA 2030
 Db 3503 TTTAAAAA-CCGTATATCAATATGAAAAAGAGAGAGAGAAACA 3548

RESULT 14
 ; US-10-007-805-474
 ; Sequence 474, Application US/10007805
 ; Publication No. US20020150581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Yuhui
 ; APPLICANT: Dillon, Devin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Durham, Margarita
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
 ; FILE REFERENCE: 210121.470C10
 ; CURRENT FILING DATE: 2001-12-07
 ; CURRENT APPLICATION NUMBER: US/10/007,805
 ; NUMBER OF SEQ ID NOS: 593
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 474
 ; LENGTH: 3865
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-007-805-474

Query Match 95.5%; Score 1938.4; DB 14; Length 3865;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;

QY 5 TGCGGTAAAGATGCTTCTGAGGCTAACTGCGAATGAAAGTTTCTATTCCAACTAA 64
 Db 1526 TCCTGTTAAAGATGGTCTTCTGAGGCTAACTGCGAATGAAAGTTTCTATTCCAACTAA 1585
 QY 65 AGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCTCCCGAAGAGCCATCTGC 124
 Db 1586 AGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCTCCCGAAGAGCCATCTGC 1645
 QY 125 CTTGAGCCTGCCATTGAAATGAAAGTCTGTTCCAAATAAGCCCTTGAATTTGAAGAA 184
 Db 1646 CTTGAGCCTGCCATTGAAATGAAAGTCTGTTCCAAATAAGCCCTTGAATTTGAAGAA 1705

QY	185	TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAATCCAAACAAAGACTATGA	244
Db	1706	TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAATCCAAACAAAGACTATGA	1765
QY	245	AGAAAGCTCTTGGAATCTCAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTT	304
Db	1766	AGAAAGCTCTTGGAATCTCAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTT	1825
QY	305	ACCCAAGGCTACACATCAAAAAGAAATAGATATAAATAAATGGAAAAATTGAAGAGCTCC	364
Db	1826	ACCCAAGGCTCTCATCAAAAAGAAATAGATATAAATAAATGGAAAAATTGAAGAGCTCC	1885
QY	365	TGATAATGATGGTTTCTTGAAGCTCCCTCGCAAGATGAAGATTTCTATTCCAACTAAAGC	424
Db	1886	TGATAATGATGGTTTCTTGAAGCTCCCTCGCAAGATGAAGATTTCTATTCCAACTAAAGC	1945
QY	425	CTTAGAATTGATGGACATGCAAACTTTTCAAAGCAGAGCCTCCCGAAGCCATCTGCTTT	484
Db	1946	CTTAGAATTGATGGACATGCAAACTTTTCAAAGCAGAGCCTCCCGAAGCCATCTGCTTT	2005
QY	485	CGAGCTGCCATTGAANAATGCAAAAGCTGTCTCCAAATAAAGCCCTCGGAATTGAGGAATGA	544
Db	2006	CGAGCTGCCATTGAANAATGCAAAAGCTGTCTCCAAATAAAGCCCTCGGAATTGAGGAATGA	2065
QY	545	ACAAACATTGAGAGCAGATCAGATGTTTCCCTTTCAGAAATCAAAACAAAGAAAGTTTGAAGA	604
Db	2066	ACAAACATTGAGAGCAGATCAGATGTTTCCCTTTCAGAAATCAAAACAAAGAAAGTTTGAAGA	2125
QY	605	AAATTCTTGGGATTCGAGAGTCTCCGTGAGACTGTTTTCACAGAAGATGTGTGTATCC	664
Db	2126	AAATTCTTGGGATTCGAGAGTCTCCGTGAGACTGTTTTCACAGAAGATGTGTGTATCC	2185
QY	665	CAAGGCTTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAAATTAGAAGATTCAACTAG	724
Db	2186	CAAGGCTTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAAATTAGAAGATTCAACTAG	2245
QY	725	CCATACAAAATCTTGGATACAGTTCTATTCTGTGAAAGACGAAGGAACCTTCAAAAAGA	784
Db	2246	CCATACAAAATCTTGGATACAGTTCTATTCTGTGAAAGACGAAGGAACCTTCAAAAAGA	2305
QY	785	TCACGTGTGAACAAACGTACAGGAAAAATCGAACAAATGAAAAAGAAAGTTTGTGTACTGAA	844
Db	2306	TCACGTGTGAACAAACGTACAGGAAAAATCGAACAAATGAAAAAGAAAGTTTGTGTACTGAA	2365
QY	845	AAAGAAACTGTACAGACCAAAAGAAATAAATAATCACAGTTAGAGNACCAAAAAGTTAAATG	904
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QY	905	GGAAACAAGAGCTCTGCAGTGTGAGATTGACTTTTAAACCAAGAAGACAGAAAGAGAGAAA	964
Db	2426	GGAAACAAGAGCTCTGCAGTGTGAGATTGACTTTTAAACCAAGAAGACAGAAAGAGAGAAA	2485
QY	965	TGCCGATATATAAATGAAAAAATTAGGGAAGAAATTAGGAAGANTCGAAGACGAGATAG	1024
Db	2486	TGCCGATATATAAATGAAAAAATTAGGGAAGAAATTAGGAAGANTCGAAGACGAGATAG	2545
QY	1025	GAAAGAGTTAGAAGTGAACCAACAACTTGAACAGGCTCTCAGAAATCAAGATATAGAATT	1084
Db	2546	GAAAGAGTTAGAAGTGAACCAACAACTTGAACAGGCTCTCAGAAATCAAGATATAGAATT	2605
QY	1085	GAAGAGTGTGAAAGTAAATTTGAAATCAGGTTTTCTCACACTCATGAAAAATGAAAATTATCT	1144
Db	2606	GAAGAGTGTGAAAGTAAATTTGAAATCAGGTTTTCTCACACTCATGAAAATGAAAATTATCT	2665
QY	1145	CTTACATGAAAATTCGATGTTTGAANAAGGAATTCGCATGCTAAAACTGGAAATPAGCCAC	1204
Db	2666	CTTACATGAAAATTCGATGTTTGAANAAGGAATTCGCATGCTAAAACTGGAAATPAGCCAC	2725
QY	1205	ACTGAAACCAACAATCCAGGAAAAAGGAAAAATAAATATCTTTGAGACATTAAGATTTTAA	1264
Db	2726	ACTGAAACCAACAATCCAGGAAAAAGGAAAAATAAATATCTTTGAGACATTAAGATTTTAA	2785

Qy	1265	AGAAAGAAAGTCTGAACCTTCAGNATGACCCCTAAAACCTGAAGAGGANTCATTTAACTAAAAG	1322
Db	2786	AGAAAGAAAGTCTGAACCTTCAGNATGACCCCTAAAACCTGAAGAGGANTCATTTAACTAAAAG	2845
Qy	1325	GGCATCTCAATATAGTGGGAGCTTAAAGTTCGTAGCTAGCTGAGAAACACAATGCTCACTTC	1384
Db	2846	GGCATCTCAATATAGTGGGAGCTTAAAGTTCGTAGCTAGCTGAGAAACACAATGCTCACTTC	2905
Qy	1385	TAAATTGAAGGAAAAACAGACAAAAAATACTAGAGGGCAGAGAAATTTGAATTCACACCATCC	1444
Db	2906	TAAATTGAAGGAAAAACAGACAAAAAATACTAGAGGGCAGAGAAATTTGAATTCACACCATCC	2965
Qy	1445	TAGACTGGCTTCTGCTGTACAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA	1504
Db	2966	TAGACTGGCTTCTGCTGTACAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA	3025
Qy	1505	ACCTGCTTTCCACATTCGACGAGATGCTTTGTTTGCAGAGAAAAATGAAATGCTGATGTGAG	1564
Db	3026	ACCTGCTTTCCACATTCGACGAGATGCTTTGTTTGCAGAGAAAAATGAAATGCTGATGTGAG	3085
Qy	1565	TAGTACCAGATATATAACAATGAGGTGCTCCATCAACCCACTTTCTGAAGCTCAAGAGGAAAT	1624
Db	3086	TAGTATCGATATATAACAATGAGGTGCTCCATCAACCCACTTTCTGAAGCTCAAGAGGAAAT	3144
Qy	1625	CCAAAGCCCTAAAATAATTAATCTCAATATGCGAGAGATGCTCTTAAGAGAAAAATACATTGG	1684
Db	3145	CCAAAGCCCTAAAATAATTAATCTCAATATGCGAGAGATGCTCTTAAGAGAAAAATACATTGG	3204
Qy	1685	TTTTCAGGAAACATGCACAAAGAGCCAAAGTGAACACACAGTGTCAAATGAAGAGGAAGTGAA	1744
Db	3205	TTTTCA-GAA-CATGCACAAAGAGCCAAAGTGAACACACAGTGTCAAATGAAGAGGAAGTGAA	3263
Qy	1745	CACATGNTCAAANCGAACCAAGATNATGTGAAACAAACACACTGANCAGCAGGAGTCTCTA	1804
Db	3264	CACATGTATCAAAAACGAAACCAAGATNATGTGAAACAAACACACTGAAACAGCAGGAGTCTCTA	3323
Qy	1805	GATCAGAAATTTATTTCAACTACAAAGCAAAAAATATGTGGCTTCAAACAGCAATTAGTTTCAT	1864
Db	3324	GATCAGAAATTTATTTCAACTACAAAGCAAAAAATATGTGGCTTCAAACAGCAATTAGTTTCAT	3383
Qy	1865	GCACTAANGAAGCTGCACAAACAAAGCAAGATAACAAATTTGATNTTCATTTCTTTGAGAG	1924
Db	3384	GCACTATAA-GAAAGCTGCACAAACAAAGCAAGATAACAAATTTGATNTTCATTTCTTTGAGAG	3442
Qy	1925	GAAATATGC-NCATCATCTTCTTAAAGAGAAAAATGAGGAGATATTTNATTCNATAACCA	1983
Db	3443	GAAATATGCACATCATCTTCTTAAAGAGAAAAATGAGGAGATATTTNATTCNATAACCA	3502
Qy	1984	TTTTAAAAAACCCGATATATTTCAATATGCAAAAAAANAAAAA	2030
Db	3503	TTTTAAAAA-CCGATATATATCAATATGAAAAAGAGAAAGCAGAAACA	3548

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RESULT 15
US-10-076-622-474
; Sequence 474, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF BREAST CANCER
; FILE OF INVENTION: 210121.470C11
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 3865
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-474

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Query Match									
Best Local Similarity 95.5%; Score 1938.4; DB 15; Length 3865;									
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;									
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DB	1526	TCCTGTAAAGATGCTCTCTCAAGGCTAACTGGGAAATGAAGTTTCTATTCCAACTAA	1585						
QY	65	AGCCTTAAAGATGCTCTCTCAAGGCTAACTGGGAAATGAAGTTTCTATTCCAACTAA	124						
DB	1586	AGCCTTAAAGATGCTCTCTCAAGGCTAACTGGGAAATGAAGTTTCTATTCCAACTAA	1645						
QY	125	CTTCGAGCTCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAA	184						
DB	1646	CTTCGAGCTCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAA	1705						
QY	185	TGAACAAACATTTGAGAGCAGATGATATCTCCATCAGAAATCAAAAGAGCTATGA	244						
DB	1706	TGAACAAACATTTGAGAGCAGATGATATCTCCATCAGAAATCAAAAGAGCTATGA	1765						
QY	245	AGAAAGTTCTGGGATCTGAGAGTCTCTGTGAGACTGTTTCAAGAGAGATGTGTGTTT	304						
DB	1766	AGAAAGTTCTGGGATCTGAGAGTCTCTGTGAGACTGTTTCAAGAGAGATGTGTGTTT	1825						
QY	305	ACCAAGGCTACACATCAAAAGAAATAGATATAATGGAATTAAGAGAGCTCTCC	364						
DB	1826	ACCAAGGCTACACATCAAAAGAAATAGATATAATGGAATTAAGAGAGCTCTCC	1885						
QY	365	TGATAATGATGTTTCTGAAAGCTCCCTCGAGAGTGAAGTTTCTATTCCAACTAAAGC	424						
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QY	425	CTTAGAATGATGAGAGTGAAGTTTCAAGAGAGAGCTCCCGAGAGCCTATGCTG	484						
DB	1946	CTTAGAATGATGAGAGTGAAGTTTCAAGAGAGAGCTCCCGAGAGCCTATGCTG	2005						
QY	485	CGAGCCTGCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGATGA	544						
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QY	545	ACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGAGTTGAAGA	604						
DB	2066	ACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGAGTTGAAGA	2125						
QY	605	AAATTTCTGGGATCTGAGAGTCTCCGTGAGACTGTTTCAAGAGAGAGTGTGTGTACC	664						
DB	2126	AAATTTCTGGGATCTGAGAGTCTCCGTGAGACTGTTTCAAGAGAGAGTGTGTGTACC	2185						
QY	665	CAAGGCTACACATCAAAAGAAATGGATAAATAGTGGAAATTTAGAAATTTCAACTAG	724						
DB	2186	CAAGGCTACACATCAAAAGAAATGGATAAATAGTGGAAATTTAGAAATTTCAACTAG	2245						
QY	725	CCTATCAAAATCTTTGGATACAGTTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAGA	784						
DB	2246	CCTATCAAAATCTTTGGATACAGTTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAGA	2305						
QY	785	TCATGTGAAACCTGACAGGAAATGGAAATGAAATGAAATGAAATGTTGTACTGAA	844						
DB	2306	TCATGTGAAACCTGACAGGAAATGGAAATGAAATGAAATGAAATGTTGTACTGAA	2365						
QY	845	AAAGAAATCTGACAGAGCAAAAGAAATGAATTCAGTTAGAGACCAAAAGTTAAATG	904						
DB	2366	AAAGAAATCTGACAGAGCAAAAGAAATGAATTCAGTTAGAGACCAAAAGTTAAATG	2425						
QY	905	GGAAACAAAGAGCTCTGAGGTGAGATGATCTTTAAACCAAGAGAGAGAGAGAGAA	964						
DB	2426	GGAAACAAAGAGCTCTGAGGTGAGATGATCTTTAAACCAAGAGAGAGAGAGAGAA	2485						
QY	965	TGCGGATATTTAAATGAAATTTAGGAGAGAAATTTAGGAGAGAGAGAGAGAGATAG	1024						
DB	2486	TGCGGATATTTAAATGAAATTTAGGAGAGAAATTTAGGAGAGAGAGAGAGAGATAG	2545						

Search completed: May 7, 2004, 00:44:40
Job time : 863 secs

QY	1025	GAAGAGTTAGAAAGTGAAACCAACACTTTGAACAGGCTCTCAGATAACAAGATATAGAAAT	1084
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QY	1085	GAAGAGTTAGAAAGTTAAATTTGAATCAGGTTTCTCAGACTCATGAAATGAAATTTATCT	1144
DB	2606	GAAGAGTTAGAAAGTTAAATTTGAATCAGGTTTCTCAGACTCATGAAATGAAATTTATCT	2665
QY	1145	CTTACATGAAATTTGCATGTTGAAAGAGAAATTTGCCATGCTAAACCTGGAATAGCCAC	1204
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QY	1265	AGAAAGAAATGCTGAACCTTCAGATGACCTTAAACCTGAAAGAGAAATCATTAACCTAAAG	1324
DB	2786	AGAAAGAAATGCTGAACCTTCAGATGACCTTAAACCTGAAAGAGAAATCATTAACCTAAAG	2845
QY	1325	GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGATAGTGAACACAAATGCTCCTTC	1384
DB	2846	GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGATAGTGAACACAAATGCTCCTTC	2905
QY	1385	TAAATTTGAAGGAAACCAAGACAAAGAAATCTAGAGGACAGAAATTTGAATCACCATCC	1444
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QY	1445	TGAGCTGGCTCTGCTGTCAAGACCATGATCAAAATTTGTGACATCAAGAAAGTCAAGA	1504
DB	2966	TGAGCTGGCTCTGCTGTCAAGACCATGATCAAAATTTGTGACATCAAGAAAGTCAAGA	3025
QY	1505	ACCTGCTTCCCATTTGAGGAGATGCTTTGTTGCAAGAAATTTGAATTTGATGTGAG	1564
DB	3026	ACCTGCTTCCCATTTGAGGAGATGCTTTGTTGCAAGAAATTTGAATTTGATGTGAG	3085
QY	1565	TAGTACCGATATATAAATGAGTGTCCATCAACCACTTTCTGAAGCTCAAGGAAAT	1624
DB	3086	TAGTACCGATATATAAATGAGTGTCCATCAACCACTTTCTGAAGCTCAAGGAAAT	3144
QY	1625	CCAAAGCTTAAATTTAATCTCAATTTGAGGAGATGCTCTTAAGAGAAATACATTTGG	1684
DB	3145	CCAAAGCTTAAATTTAATCTCAATTTGAGGAGATGCTCTTAAGAGAAATACATTTGG	3204
QY	1685	TTTCAGGAAACATGCAAAAGAGACCAAGTGAACACACAGTGTCAAAATGAAGGAGCTGAA	1744
DB	3205	TTTCA-GAAGAGACCAAGAGACCAAGTGAACACACAGTGTCAAAATGAAGGAGCTGAA	3263
QY	1745	CACATGTTTCAAGCAAGATTAATGTTGAACACACACTGACAGCAGGAGTCTCTA	1804
DB	3264	CACATGTTTCAAGCAAGATTAATGTTGAACACACACTGACAGCAGGAGTCTCTA	3323
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DB	3324	GATCAGAAATTTTCAACTCAAAAGCAAAATATGTTGGCTTCAACAGCAATTTAGTTTCA	3383
QY	1865	GCATTAAGAAAGCTGACAAACAAAGCAAGATTAATTTGATTTTCTTTCTTTGAGAG	1924
DB	3384	GCATTAAGAAAGCTGACAAACAAAGCAAGATTAATTTGATTTTCTTTCTTTGAGAG	3442
QY	1925	GAAATGTC-NCATCATCTTTCTAAAGAGAAATTTGAGGAGATATTTTATACATTAACCA	1983
DB	3443	GAAATGTC-NCATCATCTTTCTAAAGAGAAATTTGAGGAGATATTTTATACATTAACCA	3502
QY	1984	TTTAAAGAGCTGATTTTCAATATGGAAGAAATTTGGAAGAAATTTGGAAGAAATTTGGA	2030
DB	3503	TTTAAAGAGCTGATTTTCAATATGGAAGAAATTTGGAAGAAATTTGGAAGAAATTTGGA	3548

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OM nucleic - nucleic search, using sw model

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(without alignments)
7460.598 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	1938.4	95.5	3288	4	US-09-834-759-490
3	1938.4	95.5	3865	4	US-09-620-405B-474
4	1938.4	95.5	3865	4	US-09-604-287A-474
5	1938.4	95.5	3865	4	US-09-834-759-474
6	1560.4	76.9	3681	4	US-09-620-405B-463
7	1560.4	76.9	3681	4	US-09-433-826B-463
8	1560.4	76.9	3681	4	US-09-604-287A-463
9	1560.4	76.9	3681	4	US-09-834-759-463
10	1558.8	76.8	2307	4	US-09-620-405B-468
11	1558.8	76.8	2307	4	US-09-433-826B-468
12	1558.8	76.8	2307	4	US-09-604-287A-468
13	1558.8	76.8	2307	4	US-09-834-759-468
14	1282.6	63.2	1337	4	US-09-620-405B-467
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16	1282.6	63.2	1337	4	US-09-604-287A-467
17	1282.6	63.2	1337	4	US-09-834-759-467
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21	1197.6	59.0	1681	4	US-09-433-826B-180
22	1197.6	59.0	1681	4	US-09-604-287A-180
23	1197.6	59.0	1681	4	US-09-285-480-180
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27	1116.2	55.0	1665	4	US-09-339-338-178

28	1116.2	55.0	1665	4	US-09-433-826B-178	Sequence 178, App
29	1116.2	55.0	1665	4	US-09-604-287A-178	Sequence 178, App
30	1116.2	55.0	1665	4	US-09-285-480-178	Sequence 178, App
31	1116.2	55.0	1665	4	US-09-834-759-178	Sequence 178, App
32	921	45.4	2232	4	US-09-620-405B-491	Sequence 491, App
33	921	45.4	2232	4	US-09-834-759-491	Sequence 491, App
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35	836	41.2	972	4	US-09-604-287A-482	Sequence 482, App
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37	836	41.2	1206	4	US-09-389-681-175	Sequence 175, App
38	836	41.2	1206	4	US-09-620-405B-175	Sequence 175, App
39	836	41.2	1206	4	US-09-339-338-175	Sequence 175, App
40	836	41.2	1206	4	US-09-433-826B-175	Sequence 175, App
41	836	41.2	1206	4	US-09-604-287A-175	Sequence 175, App
42	836	41.2	1206	4	US-09-285-480-175	Sequence 175, App
43	836	41.2	1206	4	US-09-834-759-175	Sequence 175, App
44	836	41.2	1233	4	US-09-620-405B-492	Sequence 492, App
45	836	41.2	1233	4	US-09-834-759-492	Sequence 492, App

ALIGNMENTS

RESULT 1
US-09-620-405B-490
; Sequence 490, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 490
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-490

Query Match	95.5%	Score	1938.4	DB	4	Length	3288
Best Local Similarity	98.5%	Pred. No.	0				
Matches	1997	Conservative	4	Mismatches	21	Indels	5
Gaps	5						
Qy	5	TGCCGTTAAAGATGGTCTCTGAGGCTACTCGGAATGAAAGTTCTATTCCAACTAA	64				
Db	1254	TCCTGTTAAAGATGGTCTCTGAGGCTACTCGGAATGAAAGTTCTATTCCAACTAA	1313				
Qy	65	AGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCCTCCCGAAGCCATCTGC	124				
Db	1314	AGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCCTCCCGAAGCCATCTGC	1373				
Qy	125	CTTCGACCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAGAGCCTTGGAAATGAAGAA	184				
Db	1374	CTTCGACCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAGAGCCTTGGAAATGAAGAA	1433				
Qy	185	TGAACAAACATTGAGACAGATGAGATACCTCCCATCAGATCCAAACAAAGGACTATGA	244				
Db	1434	TGAACAAACATTGAGACAGATGAGATACCTCCCATCAGATCCAAACAAAGGACTATGA	1493				
Qy	245	AGAAAGTCTTGGATCTCTGAGAGTCTCTGTGAGAGCTTTTCACAGAGGATGTGTGTTT	304				
Db	1494	AGAAAGTCTTGGATCTCTGAGAGTCTCTGTGAGAGCTTTTCACAGAGGATGTGTGTTT	1553				
Qy	305	ACCAAGGCTACATCAAAAAGAAATAGATAAAATTAATGGAATTAAGAGGCTCC	364				
Db							

1554	DB	ACC	AAGGCTRCRCATCAAAAAGAAATAAGATAAAATAATGGAAATTTAGAAGAGTCTCC	1613
365	QY	TG	ATAATGATGTTTTCTGAAGGCTCCCTCGAGAATGAAAGTTTTCTATTCCAACCTAAAGC	424
1614	DB	TG	ATAATGATGTTTTCTGAAGGCTCCCTCGAGAATGAAAGTTTTCTATTCCAACCTAAAGC	1673
425	QY	CT	TGAAATTTGATGGACATCCAAACTTTCAAGCAGAGCTCCCGAGAGGCGCATCTGCGCTT	484
1674	DB	CT	TGAAATTTGATGGACATCCAAACTTTCAAGCAGAGCTCCCGAGAGGCGCATCTGCGCTT	1733
485	QY	CG	AGCCTGCGCATTTGAAATGCAAAAGTCTCTTCCAAATAAAGCCTTTGGAAATGGAAGAATGA	544
1734	DB	CG	AGCCTGCGCATTTGAAATGCAAAAGTCTCTTCCAAATAAAGCCTTTGGAAATGGAAGAATGA	1793
545	QY	AC	CAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAAGAGGTTGAAGA	604
1794	DB	AC	CAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAAGAGGTTGAAGA	1853
605	QY	AA	ATTTCTGGGATTTCTGAGAGTCTCGTGAGACTGTTTCAAGAAGGATGTGTGTGTACC	664
1854	DB	AA	ATTTCTGGGATTTCTGAGAGTCTCGTGAGACTGTTTCAAGAAGGATGTGTGTGTACC	1913
665	QY	CA	AGGCTACACATCAAAAGAAATGATAAAATAAGTGGAAATTTAGAAAGATTTCAACTAG	724
1914	DB	CA	AGGCTACACATCAAAAGAAATGATAAAATAAGTGGAAATTTAGAAAGATTTCAACTAG	1973
725	QY	CC	TATCAAAATCTTGATACAGTTCACTTTGTGAAAGAGCAAGGAACTTCAAAAGA	784
1974	DB	CC	TATCAAAATCTTGATACAGTTCACTTTGTGAAAGAGCAAGGAACTTCAAAAGA	2033
785	QY	TC	ACTGTGAACAAGCTACAGGAAATTTGGAACAAATGAAAAGAAAGTTTTGTGTACTGAA	844
2034	DB	TC	ACTGTGAACAAGCTACAGGAAATTTGGAACAAATGAAAAGAAAGTTTTGTGTACTGAA	2093
845	QY	AA	AGAACTCTCAGAGCAAAAGAAATAAATCACAGTTAGAGAACCAAAAGTTAAATG	904
2094	DB	AA	AGAACTCTCAGAGCAAAAGAAATAAATCACAGTTAGAGAACCAAAAGTTAAATG	2153
905	QY	GG	ACAGAGCTCTGCACTGTGAGATTTGACTTTAAACCAAGAGAAAGAGAGAGAGAAA	964
2154	DB	GG	ACAGAGCTCTGCACTGTGAGATTTGACTTTAAACCAAGAGAAAGAGAGAGAGAAA	2213
965	QY	TG	CGATATTTAAATGAAAATTTAGGGAAGAAATTTAGNAGAAATCGAAGAGCAGATAG	1024
2214	DB	TG	CGATATTTAAATGAAAATTTAGGGAAGAAATTTAGNAGAAATCGAAGAGCAGATAG	2273
1025	QY	GA	AGGTTAGAGTGAACCAACCACTTTGAACAGGCTCTCAGAAATCAAGATATAGAAAT	1084
2274	DB	GA	AGGTTAGAGTGAACCAACCACTTTGAACAGGCTCTCAGAAATCAAGATATAGAAAT	2333
1085	QY	GA	AGGTTAGAGATTAATTTGAAATCAGGTTTCTCACACTCAAGAAATGAAATTTATCT	1144
2334	DB	GA	AGGTTAGAGATTAATTTGAAATCAGGTTTCTCACACTCAAGAAATGAAATTTATCT	2393
1145	QY	CT	TACATGAAAATTTGCATTTTGAAGAAAGGAAATTTGCCATGCTTAAACCTGAAATGCCAC	1204
2394	DB	CT	TACATGAAAATTTGCATTTTGAAGAAAGGAAATTTGCCATGCTTAAACCTGAAATGCCAC	2453
1205	QY	ACT	GAAACCAATACCAAGGAAAGGAAATTAATATCTTTGAGACATTAAGATTTTAA	1264
2454	DB	ACT	GAAACCAATACCAAGGAAAGGAAATTAATATCTTTGAGACATTAAGATTTTAA	2513
1265	QY	AG	AAAAAGATGCTGAACTTCAGATGACCTTAAACCTGAAAGAGGAATTCATTAACATAAG	1324
2514	DB	AG	AAAAAGATGCTGAACTTCAGATGACCTTAAACCTGAAAGAGGAATTCATTAACATAAG	2573
1325	QY	GG	CTCTCAATATATAGTGGGAGCTTTAAGTTCTCATAGCTGAGAACCAATGCTCACTTC	1384
2574	DB	GG	CTCTCAATATATAGTGGGAGCTTTAAGTTCTCATAGCTGAGAACCAATGCTCACTTC	2633
1385	QY	TAA	TTTGAAGGAAAAACAAGCAAGAAATTAAGGAGGAAATTTGAAATCACACCAATCC	1444
2634	DB	TAA	TTTGAAGGAAAAACAAGCAAGAAATTAAGGAGGAAATTTGAAATCACACCAATCC	2693

RESULT. T 2.

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US09-834-759-490
; Sequence 490, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jjiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FOR THE DIAGNOSIS OF BREAST
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 490
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-834-759-490

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Query Match	95.5%;	Score 1938.4;	DB 4;	Length 3288;
Best Local Similarity	98.5%;	Pred. No. 0;		
Matches 1997; Conservative	4;	Mismatches 21;	Indels 5;	Caps 5;

5 TGGCGTTAAACATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACATAA 64

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
 ; FILE REFERENCE: 210121.470C8
 ; CURRENT APPLICATION NUMBER: US/09/620,405B
 ; CURRENT FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 495
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 474
 ; LENGTH: 3865
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2448)...(2631)
 ; OTHER INFORMATION: 184 bp insert of B726P splice form
 US-09-620-405B-474

Query Match 95.5%; Score 1938.4; DB 4; Length 3865;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;
 QY 5 TGCCGTTAAAGATGCTCTTGAAGGCTAACTGGGAAATGAAGTTTCTATTCCAACTAA 64
 Db TCCTGTTAAAGATGCTCTTGAAGGCTAACTGGGAAATGAAGTTTCTATTCCAACTAA 1585
 QY 65 AGCCTTAGAATTGATGGACATGCAAACTTTCAAGCAGAGCCTCCGAGAGGCCATCTGC 124
 Db AGCCTTAGAATTGATGGACATGCAAACTTTCAAGCAGAGCCTCCGAGAGGCCATCTGC 1586
 QY 125 CTTGAGGCTGCTGATGAAATGCAAAAGTGTCTTCCAAATGAAGCTTGGAAATGAAGAA 184
 Db CTTGAGGCTGCTGATGAAATGCAAAAGTGTCTTCCAAATGAAGCTTGGAAATGAAGAA 1705
 QY 185 TGAACAAACATGAGAGCAGATGATATCTCCCATCAGAACTCCAAACAAAGGACTATGA 244
 Db TGAACAAACATGAGAGCAGATGATATCTCCCATCAGAACTCCAAACAAAGGACTATGA 1706
 QY 245 AGAAGTTCTTGGGATCTGAGCTCTGAGCTCTGAGAGTCTTTTCAAGAGGATGCTGTT 304
 Db AGAAGTTCTTGGGATCTGAGCTCTGAGAGTCTTTTCAAGAGGATGCTGTT 1766
 QY 305 ACCCAAGGCTACATCAAAAGAAATAGATAAAATAAATGAAATTTAGAAAGTCTCC 364
 Db ACCCAAGGCTACATCAAAAGAAATAGATAAAATAAATGAAATTTAGAAAGTCTCC 1825
 QY 365 TGATAATGATGTTTTCTGAGGCTCCCTGAGAGTGAAGTTCTATTCCAACTAAAGC' 424
 Db TGATAATGATGTTTTCTGAGGCTCCCTGAGAGTGAAGTTCTATTCCAACTAAAGC 1886
 QY 425 CTTAGAAATTGATGGACATGCAAACTTTCAAGCAGAGCCTCCGAGAGGCCATCTGCCTT 484
 Db CTTAGAAATTGATGGACATGCAAACTTTCAAGCAGAGCCTCCGAGAGGCCATCTGCCTT 1946
 QY 485 CGAGCTGCTGATGAAATGCAAAAGTCTGTTCCAAATGAAGCTTGGAAATGAAGATGA 544
 Db CGAGCTGCTGATGAAATGCAAAAGTCTGTTCCAAATGAAGCTTGGAAATGAAGATGA 2005
 QY 545 ACAAACTTGAAGCAGATCAGATGTTCCCTTCAAGATCAAAACAAAGAGAGTTGAAGA 604
 Db ACAAACTTGAAGCAGATCAGATGTTCCCTTCAAGATCAAAACAAAGAGAGTTGAAGA 2065
 QY 605 AAATCTTGGGATCTGAGAGTCTCCGAGAGTCTTTTCAAGAGGATGTTGTGTACC 664
 Db AAATCTTGGGATCTGAGAGTCTCCGAGAGTCTTTTCAAGAGGATGTTGTGTACC 2125
 QY 665 CAAGGCTACACATCAAAAGAAATGATGAATAAATAGTGGAAATTTAGAAAGATTTCAACTAG 724
 Db CAAGGCTACACATCAAAAGAAATGATGAATAAATAGTGGAAATTTAGAAAGATTTCAACTAG 2185
 QY 725 CCTATCAAAATCTTGGATACAGTTTCATTTCTGTGAAAGAGCAGGGAACCTTCAAAAGA 784
 Db CCTATCAAAATCTTGGATACAGTTTCATTTCTGTGAAAGAGCAGGGAACCTTCAAAAGA 2245
 QY 2246 CCTATCAAAATCTTGGATACAGTTTCATTTCTGTGAAAGAGCAGGGAACCTTCAAAAGA 2305

QY 785 TCACCTGTGAACAACGCTACAGGAAATCGAAACAATGAAAGAGATTTTCTGTACTGAA 844
 Db TCACCTGTGAACAACGCTACAGGAAATCGAAACAATGAAAGAGATTTTCTGTACTGAA 2306
 QY 845 AAAGAACTGTGAGAAAGCAAAAGAAATTAATACAGTTAGAGAACCAAAAAGTTAAATG 904
 Db AAAGAACTGTGAGAAAGCAAAAGAAATTAATACAGTTAGAGAACCAAAAAGTTAAATG 2366
 QY 905 GGAAACAAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 964
 Db GGAAACAAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 2425
 QY 2426 GGAAACAAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 2485
 Db GGAAACAAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 1024
 QY 2485 TGCCGATATATTAAATGAAAGAAATTTAGGAAAGAAATTCGAAAGAGAGAGAGAG 2545
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 QY 1025 GAAAGGTTAGAAATGAAACAACATTTGAAAGAGCTCTCAGATACAGATATAGATTA 1084
 Db GAAAGGTTAGAAATGAAACAACATTTGAAAGAGCTCTCAGATACAGATATAGATTA 2605
 QY 1085 GAAAGGTTAGAAATGAAACAACATTTGAAAGAGCTCTCAGATACAGATATAGATTA 1144
 Db GAAAGGTTAGAAATGAAACAACATTTGAAAGAGCTCTCAGATACAGATATAGATTA 2665
 QY 1145 CTTACATGAAATTCGATGTTGAAAGAGAAATTCGATGTTGAAAGAGCTCTCAGATAC 1204
 Db CTTACATGAAATTCGATGTTGAAAGAGAAATTCGATGTTGAAAGAGCTCTCAGATAC 2725
 QY 2666 CTTACATGAAATTCGATGTTGAAAGAGAAATTCGATGTTGAAAGAGCTCTCAGATAC 1264
 Db CTTACATGAAATTCGATGTTGAAAGAGAAATTCGATGTTGAAAGAGCTCTCAGATAC 2785
 QY 1205 ACTGAAACACCAATACCAAGGAAAGAAATTAATTAATTTGAGGACATTAAGATTTAAA 1324
 Db ACTGAAACACCAATACCAAGGAAAGAAATTAATTAATTTGAGGACATTAAGATTTAAA 1384
 QY 1265 AGAAAGAAATGCTGAATTCGATGTTGAAAGAGAAATTCGATGTTGAAAGAGCTCTCAGATAC 1444
 Db AGAAAGAAATGCTGAATTCGATGTTGAAAGAGAAATTCGATGTTGAAAGAGCTCTCAGATAC 2905
 QY 2786 AGAAAGAAATGCTGAATTCGATGTTGAAAGAGAAATTCGATGTTGAAAGAGCTCTCAGATAC 1444
 Db AGAAAGAAATGCTGAATTCGATGTTGAAAGAGAAATTCGATGTTGAAAGAGCTCTCAGATAC 2965
 QY 1325 GGCATCTCAATATAGTGGGACGCTTTAAAGTTCTGATAGTGAAGACACAATGCTCACATTC 1504
 Db GGCATCTCAATATAGTGGGACGCTTTAAAGTTCTGATAGTGAAGACACAATGCTCACATTC 3025
 QY 1385 TAAATGAAAGGAAAGCAAGACAAAGAAATTAATTAATTTGAGGACATTAAGATTTAAA 1564
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 QY 1445 TAGACTGGCTCTGCTGTGTAAGAGCAGATCAAAATTTGATGATCAAGAGAAAGTCAAGA 1624
 Db TAGACTGGCTCTGCTGTGTAAGAGCAGATCAAAATTTGATGATCAAGAGAAAGTCAAGA 3144
 QY 2966 TAGACTGGCTCTGCTGTGTAAGAGCAGATCAAAATTTGATGATCAAGAGAAAGTCAAGA 1684
 Db TAGACTGGCTCTGCTGTGTAAGAGCAGATCAAAATTTGATGATCAAGAGAAAGTCAAGA 3204
 QY 1505 ACCTGCTTTTCCATTTGAGGAGATGCTTTGTTTGAAGAGAAAGTGAATGTTGATGAG 1744
 Db ACCTGCTTTTCCATTTGAGGAGATGCTTTGTTTGAAGAGAAAGTGAATGTTGATGAG 3263
 QY 1565 TAGTCCGATATATACATGAGTGTCTCCATCAACCACTTTCTGAAGCTCAAGAGAAAT 1804
 Db TAGTCCGATATATACATGAGTGTCTCCATCAACCACTTTCTGAAGCTCAAGAGAAAT 3323
 QY 3086 TAGTA -CGATATATACATGAGTGTCTCCATCAACCACTTTCTGAAGCTCAAGAGAAAT 1864
 Db TAGTA -CGATATATACATGAGTGTCTCCATCAACCACTTTCTGAAGCTCAAGAGAAAT 3383
 QY 1625 CCNAAAGCCTAAATTTAATCTCAATTTATGAGGAGATGCTCTTAAGAGAAATACATTTGG 1924
 Db CCNAAAGCCTAAATTTAATCTCAATTTATGAGGAGATGCTCTTAAGAGAAATACATTTGG

Db 3384 GCACATAA-GAAAGCTGCAACAAAGCAAGATAACAATTGATATTCATTTCTTGAGAG 3442

Qy 1925 GAAATGTC-NCATCATCTCTTAAAGAGAGAAAATGAGGAGATATTNATTACNATAACCA 1983

Db 3443 GAAATGCAACATCATCTCTTAAAGAGAGAAAATGAGGAGATATTNATTACATACCA 3502

Qy 1984 TTTAAAAACCCGTATTTTCAATATGAAAANAAAAANAAAAA 2030

Db 3503 TTTAAAAA-CCGTATATATCATATGAAAAGAGAGAAAACGAAACA 3548

RESULT 4

US-09-604-287A-474

; Sequence 474, Application US/09604287A

; Patent No. 6586572

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Hepler, William T.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

; FILE REFERENCE: 210121.470C7

; CURRENT APPLICATION NUMBER: US/09/604,287A

; CURRENT FILING DATE: 2000-06-22

; NUMBER OF SEQ ID NOS: 489

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 474

; LENGTH: 3865

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (248)...(2631)

; OTHER INFORMATION: 184 bp insert of B726P splice form

US-09-604-287A-474

Query Match 95.5%; Score 1938.4; DB 4; Length 3865;

Best Local Similarity 98.5%; Pred No. 0;

Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;

Qy 5 TCCCGTTAAAGATGGTCTCTGAGCGTAACTGCGGAATGAAAGTTCTATTCOAACATAA 64

Db 1526 TCCGTGTTAAAGATGGTCTCTGAGCGTAACTGCGGAATGAAAGTTCTATTCOAACATAA 1585

Qy 65 AGCCTTAGAATTGATGGAGATGCAACTTTCAAAGCAGAGCTCCCGAGAGCCATCTGC 124

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Qy 125 CTTGAGGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTCAGAA 184

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Db 1706 TGAACAAACATTGAGAGAGATGAGTACTCCCATCAGATCCAAACAAAGGACTATGA 1765

Qy 245 AGAAAGTTCTGGGATCTGAGAGTCTCTGTGAGACTGTTTCAAGAGGATGTGTGTT 304

Db 1766 AGAAAGTTCTGGGATCTGAGAGTCTCTGTGAGACTGTTTCAAGAGGATGTGTGTT 1825

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Db 1826 ACCCAAGGCTACACATCAAAAGAAATAGATTAATTAATGAAAATTAGAGAGTCTCC 1885

Qy 365 TGATATGATGGTTTCTGAAAGCTCCCTGAGAGATGAAAGTTTCTATTCOAACATAAGC 424

Db 1886 TGATATGATGGTTTCTGAAAGCTCCCTGAGAGATGAAAGTTTCTATTCOAACATAAGC 1945

Qy 425 CTTAGAAATTGATGGAGATGCAAACTTTCAAAGCAGAGCTCCCGAGAGCCATCTGCCTT 484

Db 1946 CTTAGAAATTGATGGAGATGCAAACTTTCAAGCAGAGCCTCCCGAGAGCCATCTGCCTT 2005

Qy 485 CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTAAGAAATGA 544

Db 2006 CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTAAGAAATGA 2065

Qy 545 ACAAACATTGAGAGAGATGAGTCTCCCTTCAGATCAAAACAAAGAGAGGTTCAAGA 604

Db 2066 ACAAACATTGAGAGAGATGAGTCTCCCTTCAGATCAAAACAAAGAGAGGTTCAAGA 2125

Qy 605 AAATTCCTGGGATCTGAGAGTCTCCGTGAGACTGTTTCAAGAGAGGATGTGTGTATCC 664

Db 2126 AAATTCCTGGGATCTGAGAGTCTCCGTGAGACTGTTTCAAGAGAGGATGTGTGTATCC 2185

Qy 665 CAAGGCTACACATCAAAAGAAATGGAATAAGTGGAAATTAAGAGATTCAACTAG 724

Db 2186 CAAGGCTACACATCAAAAGAAATGGAATAAGTGGAAATTAAGAGATTCAACTAG 2245

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Db 2246 CCTATCAAAATCTCTGGATACAGTTCATTCCTTGTGAAAGCAGCAAGGAACTTCAAAAAGA 2305

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Db 3086 TAGTA-CGATATATAACAATGAGTGTCTCATCAACCACTTTCTGAAAGTCAAGGAAAT 3144
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Db 3145 CCAAGAGCCCTAAATAATTAATCTCAATATGCGAGAGATGCTCTTAAGAGAAATATACATTGG 3204
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Db 3264 CACATGNTTCAANCGNAGAGATGTAACAAACACACATGANCAGGAGAGTCTCTA 3323
Qy 1805 GATCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1864
Db 3324 GATCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3383
Qy 1865 GCATATTAAGAGAGCTGACAAACAAAGAGAGATGTAACAAATGATNTTCAATTTCTTGAGAG 1924
Db 3384 GCATATTAAGAGAGCTGACAAACAAAGAGAGATGTAACAAATGATNTTCAATTTCTTGAGAG 3442
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Db 3443 GAAATGTC-NCATCATCTTCTAAAGAGAGAAATGAGGAGATATTNTTATACNATAACCA 3502
Qy 1984 TTTTAAATCCCTATATTTCAATATGTAATGGAATGGAATGGAATGGAATGGAATGGAAT 2030
Db 3503 TTTTAAATCCCTATATTTCAATATGTAATGGAATGGAATGGAATGGAATGGAATGGAAT 3548

RESULT 5
US-09-834-759-474
; Sequence 474, Application US/09834759
; Patent No. 6580197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudi
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCES: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 474
; LENGTH: 3865
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2448)...(2631)
; OTHER INFORMATION: 184 bp insert of B726P splice form
US-09-834-759-474

Query Match 95.5%; Score 1938.4; DB 4; Length 3865;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;
Qy 5 TGCGTTAAAGATGGTCTTCTGAGGCTAACTGCGGAATGGAAGTTTCTATTCCAACTAA 64
Db 1526 TCCTGTAAAGATGGTCTTCTGAGGCTAACTGCGGAATGGAAGTTTCTATTCCAACTAA 1585
Qy 65 AGCCTTAGAATTGATGGACATGCAAACTTCAACAGAGAGCTCCCGAGAGGCAATCTGCG 124

Db 1586 AGCCTTAGAATTGATGGACATGCAAACTTCAACAGAGAGCTCCCGAGAGGCAATCTGCG 1645
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RESULT 6
US-09-620-405B-463
; Sequence 463. Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8

; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 463
; LENGTH: 3681
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-620-405B-463

Query Match 76.9%; Score 1560.4; DB 4; Length 3681;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1813; Conservative 4; Mismatches 21; Indels 189; Gaps 6;

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RESULT 7
US-09-433-826B-463
; Sequence 463, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqi
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433.826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 463
; LENGTH: 3681
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-463
Query Match 76.9%; Score 1560.4; DB 4; Length 3681;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1813; Conservative 4; Mismatches 21; Indels 189; Gaps 6;
QY 5 TCCGTTTAAAGATGTTCTTGAAGCTAACTGCGGAATGAAAGTTTCTTATCCAACTAA 64
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Db 3319 TTTAAAAAACCGTATATATATATGAAAAAATAAAAAA 3364

RESULT 8
US-09-604-287A-463
; Sequence 463, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 463
; LENGTH: 3681
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-463

Query Match 76.9%; Score 1560.4; DB 4; Length 3681;
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Qy 5 TCCCGTTAAAGATGCTTTCTGAAAGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAA 64
Db 1526 TCTGTAAAGATGCTTTCTGAAAGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAA 1585
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RESULT 10

US-09-620-405B-468
; Sequence 468, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuguo
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-468

Query Match 76.8%; Score 1558.8; DB 4; Length 2307;
Best Local Similarity 89.5%; Pred. No. 0;
Matches 1815; Conservative 0; Mismatches 23; Indels 189; Gaps 6;
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DB 1783 GATCAGAAATTTTCAACTCAAAAGCAAAATTAATGTTGGCTTCAACAGCAATTTAGTTTCA 1842
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DB 1843 GCACATTAANGAAGCTGCAACAAAGCAAGATTAATGATGTTTCTTTCTTGAGAG 1901
QY 1925 GAAATGTC-NCATCATCTTTCAAAAGAGAAATGAGGAGATATTTTATTACNATAACCA 1983

Db	1902	GAAATTCGAACATCATCTCCTCTAAAGAGAAAAATGAGGAGATATTTAATTACAATAACCA	1961
Qy	1984	TTTTAAAACCCTGTATTTTCAATATGCAAAAAAAAAAAAAAAAAAAAAA	2030
Db	1962	TITTAABBA-CCGTATATATCATATGAAAAGAGAAAGCAGAACA	2007
 RESULT 11 US-09-433-826B-468 ; Sequence 468, Application US/09433826B ; Patent No. 6579973 ; GENERAL INFORMATION: ; APPLICANT: Jiang, Yuqi ; APPLICANT: Dillon, Davin C. ; APPLICANT: Mitcham, Jennifer L. ; APPLICANT: Xu, Jiangchun ; APPLICANT: Harlocker, Susan L. ; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND ; FILE REFERENCE: 210121.470C4 ; CURRENT APPLICATION NUMBER: US/09/433,826B ; CURRENT FILING DATE: 1999-11-03 ; NUMBER OF SEQ ID NOS: 474 ; SOFTWARE: FastSeq for Windows Version 3.0 ; SEQ ID NO 468 ; LENGTH: 2307 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-433-826B-468			
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Db	229	AGCCTTAGAATTGATGGACATGCAACTTTCAAGACGAGCCTCCCAGAGGCCATCTGC	288
Qy	125	CTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCTTGGAATTGAAGAA	184
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Db	409	AGAAAGTCTTGGAATTCAGAGTCTCTGTGAGACTGTTTTCACAGAGGATGTGTGTTT	468
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QY 1805 GATCAGAAATTTTCAATGATCAAAAGCAAGAGATGATGAAACAAACACAGTGTCAATGAGGAAGCTGAA 1864
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QY 1984 TTTTAAAAACCCGTATATTTCAATATGAAAGAGAGAAATGAGGAGATATTTNATTAACAAACCA 2030
DB 1962 TTTTAAAAACCCGTATATTTCAATATGAAAGAGAGAAATGAGGAGATATTTNATTAACAAACCA 2007

RESULT 12
US-09-604-287A-468
; Sequence 468, Application US/09604287A
; Patent No. 5586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudi
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-468

Query Match 76.8%; Score 1558.8; DB 4; Length 2307;
Best Local Similarity 89.5%; Pred. No. 0;
Matches 1815; Conservative 0; Mismatches 23; Indels 189; Gaps 6;

QY 5 TGCGTTAAAGATGGTCTTCTGAAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAA 64
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DB 229 AGCCTTAGAATGTAGCATGCAAACTTTCAAGAGAGAGCTCCCGAGAGCATCTGC 288
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DB 829 CAAGCTTACATCAAAAGAGAAATGGAATTAATGGAATTTAGAGATTTCAATAG 888
QY 725 CCTATCAAAATCTTGGATGATGATGATGTTTCTTCTGAAAGAGAGAGGAACTTCAAAAGAA 784
DB 889 CCTATCAAAATCTTGGATGATGATGATGTTTCTTCTGAAAGAGAGAGGAACTTCAAAAGAA 948
QY 785 TCATCTGTAACAGCTTCAGAGAAATGGAATTAATGGAATTTAGAGATTTTGTCTACTGAA 844
DB 949 TCATCTGTAACAGCTTCAGAGAAATGGAATTAATGGAATTTAGAGATTTTGTCTACTGAA 1008
QY 845 AAAGAAATCTGTAACAGCTTCAGAGAAATGGAATTAATGGAATTTAGAGATTTTGTCTACTGAA 904
DB 1009 AAAGAAATCTGTAACAGCTTCAGAGAAATGGAATTAATGGAATTTAGAGATTTTGTCTACTGAA 1068
QY 905 GGAACAAAGAGCTCTGCAAGTGTGAGATTTGATTTTAAACCAAGAGAGAGAGAGAGAGAA 964
DB 1069 GGAACAAAGAGCTCTGCAAGTGTG----- 1090
QY 965 TGCGATATATTAATGAAATTTAGGAGAAATTTAGGAGAAATCGAAGAGAGAGATG 1024
DB 1091 ----- 1090
QY 1025 GAAAGAGTTAGAGAGTGAACAAACAACTTGAAACAGGCTCTCAGATATAGAAAT 1084
DB 1091 ----- 1090
QY 1085 GAAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCAGACTCATGAAATGAAATTTATCT 1144
DB 1091 -----AGGTTTCTCAGACTCATGAAATGAAATTTATCT 1124
QY 1145 CTTACATGAAATTTGCAATTTGAAAGAGGAAATTTGCCATGCTAAACTGGAATTTAGC 1204
DB 1125 CTTACATGAAATTTGCAATTTGAAAGAGGAAATTTGCCATGCTAAACTGGAATTTAGC 1184
QY 1205 ACTGAAACACCAATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1264
DB 1185 ACTGAAACACCAATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1244
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DB 1245 AGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1304
QY 1325 GGCATCTCAATATAGTGGCAGCTTTAAAGTTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAG 1384
DB 1305 GGCATCTCAATATAGTGGCAGCTTTAAAGTTTCTGATAGTGTGAGAGAGAGAGAGAGAGAGAG 1364

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1385 TAAATTGAAGGAAACAAAGCAAGAAATCTAGAGGCGAATTTGAATCACACCATCC 1444
 1365 TAAATTGAAGGAAACAAAGCAAGAAATCTAGAGGCGAATTTGAATCACACCATCC 1424
 1445 TAGACTGGCTTCTGCTGTACAGACCATGATCAAAATTTGTGACATCAAGAAAGAGTCAAGA 1504
 1425 TAGACTGGCTTCTGCTGTACAGACCATGATCAAAATTTGTGACATCAAGAAAGAGTCAAGA 1484
 1505 ACCTGCTTTCCACATTTGCGAGAGATGCTTGTTCGAAAGAAATGAATGTTGATGTGAG 1564
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 1545 TAGTA - CGATATATAACAGATGCTTCCATCAACACATTTCTGAAGCTCAAGAGGAAT 1603
 1625 CCNAGGCTTAAATTAATCTCAATATGAGAGATGCTTCTAAGAGAAATACATGG 1684
 1604 CCNAGGCTTAAATTAATCTCAATATGAGAGATGCTTCTAAGAGAAATACATGG 1663
 1685 TTTCCAGGAACATGCAAGAGAGCCAGCTGCAACACAGCTGCAAAATGAAGAGCTGAA 1744
 1664 TTTCA - GAACATGCAAGAGAGCCAGCTGCAACACAGCTGCAAAATGAAGAGCTGAA 1722
 1745 CACATGTTTCAAAGCAAGATNATGTGAACCAACACACTGANCAGAGAGTCTCTA 1804
 1723 CACATGTTTCAAAGCAAGATNATGTGAACCAACACACTGANCAGAGAGTCTCTA 1782
 1805 GATCAGAAATTTCAACTCAAGCAAGAAATATGCTGGCTTCAACAGCAATTTAGTTCAT 1864
 1783 GATCAGAAATTTCAACTCAAGCAAGAAATATGCTGGCTTCAACAGCAATTTAGTTCAT 1842
 1865 GCACATAANGAAGCTGCAACCAAGCAAGAAATGATNTTCAATTTCTTTCGAGAG 1924
 1843 GCACATA - GAAGCTGCAACCAAGCAAGAAATGATNTTCAATTTCTTTCGAGAG 1901
 1925 GAAATGC - NCATCATCTTTCAAGCAAGAAATGAGGAGATTTTATTTACNATAACCA 1983
 1902 GAAATGC - NCATCATCTTTCAAGCAAGAAATGAGGAGATTTTATTTACNATAACCA 1961
 1984 TTTTAAAAACCGGTATTTTCAATATGAAAAAAGAAAAA 2030
 1962 TTTTAAAAA - CCGTATATCATATGAAAAAGAAAGCAAGCA 2007

RESULT 13
 US-09-834-759-468
 ; Sequence 468, Application US/09834759
 ; Patent No. 6680197
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.470C9
 ; CURRENT FILING DATE: 2001-04-13
 ; NUMBER OF SEQ ID NOS: 547
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 468
 ; LENGTH: 2307
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-834-759-468

Query Match 76.8%; Score 1558.8; DB 4; Length 2307;
 Best Local Similarity 89.5%; Pred. No. 0;
 Matches 1815; Conservative 0; Mismatches 23; Indels 189; Gaps 6;

5 TCCTTTAAAGATGCTTCTCTGAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAA 64
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 229 AGCCTTAGAATTTGATGAGCATGCAAACTTTCAAAGAGAGCTCCCGAAGAGCCATCTGC 288
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 289 CTTTCAGGCTCCATTTGAATGCAAAAGCTCTGTTCCAAATAAAGCTTTGGAAATTCAGAA 348
 185 TGAACAAACATTTGAGAGAGATGAGATCTCCCATCAGAAATCCAAACAAAGAGCTATGA 244
 349 TGAACAAACATTTGAGAGAGATGAGATCTCCCATCAGAAATCCAAACAAAGAGCTATGA 408
 245 AGAAGATTTCTGGGATTTCTGAGAGTCTCTGAGAGCTTTTTCACAGAGAGGATGCTGTTT 304
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 305 ACCCAAGGCTACACATCAAAAGAAATAGATAAAATAAATGGAATAATTAGAAGAGTCTCC 364
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 365 TGATAATGATGTTTCTGAGGCTCCCTGAGAGATGAAAGTTTCTATTCACAACTAAAGC 424
 529 TGATAATGATGTTTCTGAGGCTCCCTGAGAGATGAAAGTTTCTATTCACAACTAAAGC 588
 425 CTTTAGAATTTGAGAGATGCAAACTTTCAAAGCAGAGCTCCCGAAGAGCCATCTGCTT 484
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 485 CGAGCCTCCATTTGAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATTTGAAGAATGA 544
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 709 ACAAACATTTGAGAGAGATGCAAGTCTCCCTTCAGAAATCAAACAAAGAGCTTCAAGA 768
 605 AAATTTCTGGGATTTCTGAGAGTCTCCGTCAGAGCTGTTTTCACAGAGAGTGTGTGTACC 664
 769 AAATTTCTGGGATTTCTGAGAGTCTCCGTCAGAGCTGTTTTCACAGAGAGTGTGTGTACC 828
 665 CAAGGCTACACATCAAAAGAAATGGAATAAATAGTGGAAATTAGAAGATTTCAACTAG 724
 829 CAAGGCTACACATCAAAAGAAATGGAATAAATAGTGGAAATTAGAAGATTTCAACTAG 888
 725 CCTATCAAAATCTTGGATACAGTTCATTTCTTGTGAAAGAGCAAGGGAATTTCAAAAGA 784
 889 CCTATCAAAATCTTGGATACAGTTCATTTCTTGTGAAAGAGCAAGGGAATTTCAAAAGA 948
 785 TCATCTGTAACAAAGTACAGGAAATGGAACAAATGAAAGAGCTTTTGTGTACTGAA 844
 949 TCATCTGTAACAAAGTACAGGAAATGGAACAAATGAAAGAGCTTTTGTGTACTGAA 1008
 845 AAAGAACTGTCAGAGCAAGAAATAAATCAACAGTTAGAGAAACAAAGAGTTAAATG 904
 1009 AAAGAACTGTCAGAGCAAGAAATAAATCAACAGTTAGAGAAACAAAGAGTTAAATG 1068
 905 GGAACAGAGCTCTGAGTGTGAGATGCTTTTAAACCAAGAGAGAGAGAGAGAGAA 964
 1069 GGAACAGAGCTCTGAGTGTGAGATGCTTTTAAACCAAGAGAGAGAGAGAGAGAA 1090
 965 TGCCGATATTAATTAAGAAAAATTTAGGGAAGAAATTTAGGGAAGAAATCGAAGAGCAGCATAG 1024
 1091 ----- 1090
 1025 GAAAGAGTTAGAGTGAACCAACACTTGAACAGGCTCTCAGAAATACAGATATAGAAAT 1084
 1091 ----- 1090

RESULT 14			
US 03-620-405B-467			
; Sequence 467, 9 application US/09620405B			
; GENERAL INFORMATION:			
; APPLICANT: Jigagag Yugid			
; APPLICANT: Dillan, Gavin C.			
; APPLICANT: Mirzbam, Jennifer I.			
QY	701	CAAGGCTACACATCAAAAAGAAATGATAAATAAGTGGAAAAATTAGAAGATTTCAACTAG	760
QY	725	CCTATCAAAAATCTTGGATACAGTTTCATTTCTTGTGAAGACGAAGGGAAGCTTCAAAAAGA	784
DB	761	CCATATCAAAAATCTTGGATACAGTTTCATTTCTTGTGAAGACGAAGGGAAGCTTCAAAAAGA	820
OV	785	TCAGTGTGAACAAACGTCACAGAAAAATGGAACAAATGAAAAAGAAAGTTTGTGTACTGAA	844

Db 821 TCACGTGACCAAGCTACAGAAATGGAACAAATGAAAGAGAGTTTGTGTACTGAA 880
Qy 845 AAAGAACTGTGACAGCAAAAGAAATGAAATCAAGTTAGAGAAACAAAGTTAAATG 904
Db 881 AAAGAACTGTGACAGCAAAAGAAATGAAATCAAGTTAGAGAAACAAAGTTAAATG 940
Qy 905 GGAACAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 964
Db 941 GGAACAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 1000
Qy 965 TGCCGATATATTAATGAAAGAAATAGGAGAGAAATAGGAGAGAAATCGAAGAGAGCATAG 1024
Db 1001 TGCCGATATATTAATGAAAGAAATAGGAGAGAAATAGGAGAGAAATCGAAGAGAGCATAG 1060
Qy 1025 GAAGAGTTAGAGTGAACCAACCACTGACAGGCTCTCAGATACAGATATAGAAAT 1084
Db 1061 GAAGAGTTAGAGTGAACCAACCACTGACAGGCTCTCAGATACAGATATAGAAAT 1120
Qy 1085 GAAGAGTTAGAGTGAACCAACCACTGACAGGTTCTCAGATACAGATATAGAAAT 1144
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Qy 1205 ACTGAACACCAATACAGAGAAAGAGAAATTAATATCTTTGAGGACATTAAGATTTTAA 1264
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Qy 1265 AGAAAGAGTCTGAACTTCAGATGACCC 1293
Db 1301 AGAAAGAGTCTGAACTTCAGATGACCC 1329

RESULT 15
US-09-433-826B-467
; Sequence 467, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yucui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433.826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 467
; LENGTH: 1337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-467

Query Match 63.2%; Score 1282.6; DB 4; Length 1337;
Best Local Similarity 99.7%; Pred. No. 9.5e-310;
Matches 1285; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 5 TGCCGTTAAAGATGCTCTTCTGAGGCTAACTCGGGAATGAAAGTTTCTATTCCAACTAA 64
Db 41 TCCTGTTAAAGATGCTCTTCTGAGGCTAACTCGGGAATGAAAGTTTCTATTCCAACTAA 100
Qy 65 AGCCTTAGAATGATGGAATGCAAACTTTCAAGAGAGAGCTCCGAGAGAGCCATCTGC 124
Db 101 AGCCTTAGAATGATGGAATGCAAACTTTCAAGAGAGAGCTCCGAGAGAGCCATCTGC 160
Qy 125 CTTGAGGCTGCAATGAAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATTTGAAGAA 184

Db 161 CTTGAGGCTGCCATTGAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATTTGAAGAA 220
Qy 185 TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGATCCAAACCAAGAGACTATGA 244
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Qy 425 CTTAGAATTTGATGACATGCAAACTTTTCAAGCAGAGCTCCCGAGAGAGCCATCTGCTT 484
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Qy 485 CGAGCTCCCATGGAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATTTGAAGATGA 544
Db 521 CGAGCTCCCATGGAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATTTGAAGATGA 580
Qy 545 ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAGAGAGTTGAAGA 604
Db 581 ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAGAGAGTTGAAGA 640
Qy 605 AAATTTCTTGGGATCTGAGAGTCTCCGAGAGACTGTTTTCACAGAGAGATGTGTGTACC 664
Db 641 AAATTTCTTGGGATCTGAGAGTCTCCGAGAGACTGTTTTCACAGAGAGATGTGTGTACC 700
Qy 665 CAAGGCTACATCAATCAAAAGAAATGATATAAATTAAGTGAAGAAATTAGAAGATTTCAACTAG 724
Db 701 CAAGGCTACATCAATCAAAAGAAATGATATAAATTAAGTGAAGAAATTAGAAGATTTCAACTAG 760
Qy 725 CCTATCAAAATCTTGGATCAGATCAGTCTTCTGTAAGAGCAAGGAGCTTCAAAAGAA 784
Db 761 CCTATCAAAATCTTGGATCAGATCAGTCTTCTGTAAGAGCAAGGAGCTTCAAAAGAA 820
Qy 785 TCACGTGTGAACCAACGTACAGGAAATGGAACAAATGAAAGAGAGTTTCTGTACTGAA 844
Db 821 TCACGTGTGAACCAACGTACAGGAAATGGAACAAATGAAAGAGAGTTTCTGTACTGAA 880
Qy 845 AAAGAACTGTGAGAGCAAAAGAAATTAATCAAGTTAGAGAACCAAAAGTTAAATG 904
Db 881 AAAGAACTGTGAGAGCAAAAGAAATTAATCAAGTTAGAGAACCAAAAGTTAAATG 940
Qy 905 GGAACAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 964
Db 941 GGAACAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 1000
Qy 965 TGCCGATATATTAATGAAAGAAATTAGGAGAGAAATAGGAGAGAAATCGAAGAGAGCATAG 1024
Db 1001 TGCCGATATATTAATGAAAGAAATTAGGAGAGAAATAGGAGAGAAATCGAAGAGAGCATAG 1060
Qy 1025 GAAGAGTTAGAGTGAACCAACCACTGACAGGCTCTCAGATACAGATATAGAAAT 1084
Db 1061 GAAGAGTTAGAGTGAACCAACCACTGACAGGCTCTCAGATACAGATATAGAAAT 1120
Qy 1085 GAAGAGTTAGAGTGAACCAACCACTGACAGGTTCTCAGATACAGATATAGAAAT 1144
Db 1121 GAAGAGTTAGAGTGAACCAACCACTGACAGGTTCTCAGATACAGATATAGAAAT 1180
Qy 1145 CTTACATGAAATTCGATGTTGAAAGAGAAATTCGATACAGATACAGATATAGAAAT 1204
Db 1181 CTTACATGAAATTCGATGTTGAAAGAGAAATTCGATACAGATACAGATATAGAAAT 1240
Qy 1205 ACTGAACACCAATACAGAGAAAGAGAAATTAATATCTTTGAGGACATTAAGATTTTAA 1264
Db 1241 ACTGAACACCAATACAGAGAAAGAGAAATTAATATCTTTGAGGACATTAAGATTTTAA 1300

Qy 1265 AGAAGAGATGCTGACTTCAGATGACCC 1293
Db 1301 AGAAGAGATGCTGACTTCAGATGACCC 1329

Search completed: May 7, 2004, 00:30:18
Job time : 163 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 17:01:24 ; Search time 793 Seconds
(without alignments)
10874.959 Million cell updates/sec

Title: US-09-451-739h-15

Perfect score: 2030
Sequence: 1 ctgctgcgtaagatggt.....Gaaataaaaaaanaaaaaa 2030

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 29Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2018	99.4	2030	4	Aah28489 Nucleotid
2	1940	95.6	4047	7	Abt33272 Human tum
3	1940	95.6	4458	6	Abt07694 Breast ca
4	1940	95.6	4458	7	Abt33271 Human tum
5	1940	95.6	4458	7	Acc50246 Breast ca
6	1938.4	95.5	3288	4	Aas47421 Human cdn
7	1938.4	95.5	3288	6	Abt33234 Human tum
8	1938.4	95.5	3288	7	Abt33234 Human tum
9	1938.4	95.5	3865	4	Aas47411 Human cdn
10	1938.4	95.5	3865	6	Abt33234 Human tum
11	1938.4	95.5	3865	7	Abt33234 Human tum
12	1938.4	95.5	3865	10	Ade44426 Human cdn
13	1927.2	94.9	3045	7	Abt33258 Human tum
14	1560.4	76.9	3681	4	Aaf17975 Human bre
15	1560.4	76.9	3681	4	Aaf17975 Human bre
16	1560.4	76.9	3681	6	Abt33218 Human tum
17	1560.4	76.9	3681	7	Abt33218 Human tum
18	1560.4	76.9	3681	10	Ade44415 Human cdn
19	1559.2	76.8	3681	4	Aas47405 Human cdn
20	1558.8	76.8	2307	4	Aaf17980 Human bre
21	1558.8	76.8	2307	4	Aaf17980 Human bre
22	1558.8	76.8	2307	4	Aas47410 Human cdn
23	1558.8	76.8	2307	6	Abt33234 Human tum

24 1558.8 76.8 2307 7 Abt33223
25 1558.8 76.8 2307 10 Ade44420
26 1557.2 76.7 2683 3 Aas59015
27 1557.2 76.7 2683 3 Aas59014
28 1439.8 70.9 2043 8 Adb83986
29 1282.6 63.2 1337 4 Aaf17979
30 1282.6 63.2 1337 4 Aaf17979
31 1282.6 63.2 1337 4 Aas47409
32 1282.6 63.2 1337 6 Aas64010
33 1282.6 63.2 1337 7 Abt33222
34 1282.6 63.2 1337 10 Ade44419
35 1212 59.7 3720 7 Abt33278
36 1197.6 59.0 1681 4 Aaf17693
37 1197.6 59.0 1681 4 Aaf17693
38 1197.6 59.0 1681 4 Aas47123
39 1197.6 59.0 1681 6 Abt08778
40 1197.6 59.0 1681 6 Abt33234
41 1197.6 59.0 1681 7 Abt32936
42 1197.6 59.0 1681 10 Ade44132
43 1116.2 55.0 1665 4 Aaf17692
44 1116.2 55.0 1665 4 Aaf17692
45 1116.2 55.0 1665 4 Aas47122

ALIGNMENTS

RESULT 1
AAH28489
ID AAH28489 standard; cDNA; 2030 BP.

XX AAH28489;

XX 17-SEP-2001 (first entry)

DE Nucleotide sequence of a human cancer associated antigen.

XX Cancer associated antigen; INGI1; tumour suppressor; cancer; vaccine; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 42..1580

XX /tag= a

XX /product= "cancer associated antigen"

XX WO200147959-A2.

XX 05-JUL-2001.

XX 29-NOV-2000; 2000WO-US042334.

XX 30-NOV-1999; 99US-00451739.

XX 24-OCT-2000; 2000US-00602362.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX (CORR) CORNELL RES FOUND INC.

XX Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;

XX WPI; 2001-441706/47.

XX P-PSDB; AAS47401.

XX Isolated cancer associated nucleic acid molecule identified by SEREX
(serological identification of antigens by recombinant expression
cloning) technique, useful in nucleic acid based therapies to treat
cancer.

XX Claim 1; Page 49-50; 62pp; English.

XX The present sequence encodes a human cancer associated antigen. The
sequence was identified using probes derived from the INGI Gene. The INGI

CC gene is a tumour suppressor candidate gene. The cancer associated antigen
 CC polynucleotides and polypeptides are useful for screening for the
 CC possible presence of a pathological condition in a subject such as
 CC cancer. The cancer associated antigen polypeptides are useful for
 CC producing vaccines
 XX

SQ Sequence 2030 BP; 827 A; 334 C; 397 G; 460 T; 0 U; 12 Other;

Query Match 99.4%; Score 2018; DB 4; Length 2030;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	CTCGTGGCGTTAAGATGCTCTCTGAGAGCTAACTCGGATGAAAGTTCTATTCGAA	60
QY	61	CTAAGCCTTAGAATGATGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAGCCAT	120
DB	61	CTAAGCCTTAGAATGATGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAGCCAT	120
QY	121	CTGCTTTGAGCCTGCCATTTGAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATTGA	180
DB	121	CTGCTTTGAGCCTGCCATTTGAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATTGA	180
QY	181	AGATGAACAAACATTCAGAGCAGATGAGATATCTCCCATCAGAACTCCAAACAAAGGACT	240
DB	181	AGATGAACAAACATTCAGAGCAGATGAGATATCTCCCATCAGAACTCCAAACAAAGGACT	240
QY	241	ATGAAGAAAGTTCTTGGATTTCTGAGAGTCTCTGTGAGAGCTGTTTCAAGAGAGTGTGT	300
DB	241	ATGAAGAAAGTTCTTGGATTTCTGAGAGTCTCTGTGAGAGCTGTTTCAAGAGAGTGTGT	300
QY	301	GTATTACCAAGGCTACACATCAAAAGAAATAGATATAATTAATGAAATTTAGAAGAGT	360
DB	301	GTATTACCAAGGCTACACATCAAAAGAAATAGATATAATTAATGAAATTTAGAAGAGT	360
QY	361	CTCTGTATATGATGCTTTCTGAAGCTCTCCGAGAGTCAAGTTCTPATTCCAACTA	420
DB	361	CTCTGTATATGATGCTTTCTGAAGCTCTCCGAGAGTCAAGTTCTPATTCCAACTA	420
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DB	421	AAGCCTTAGAATGATGACATGCAAACTTTCAAGCAGAGCCCTCCGAGAGCCATCTG	480
QY	481	CCTTTGGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTGA	540
DB	481	CCTTTGGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTGA	540
QY	541	ATGAACAAACATTCAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAGAGGTTG	600
DB	541	ATGAACAAACATTCAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAGAGGTTG	600
QY	601	AAGAAATTTCTTGGATTTCTGAGAGTCTCCGAGAGCTGTTTCAAGAGGATGTTGTG	660
DB	601	AAGAAATTTCTTGGATTTCTGAGAGTCTCCGAGAGCTGTTTCAAGAGGATGTTGTG	660
QY	661	TACCAAGGCTACACATCAAAAGAAATGATTAATTAAGTGGAAATTTAGAATTCAA	720
DB	661	TACCAAGGCTACACATCAAAAGAAATGATTAATTAAGTGGAAATTTAGAATTCAA	720
QY	721	CTAGCCTATCAAAATCTTGGATACAGTTCATTTCTTGTGAAAGCAAGGAACTTCAAA	780
DB	721	CTAGCCTATCAAAATCTTGGATACAGTTCATTTCTTGTGAAAGCAAGGAACTTCAAA	780
QY	781	AAGATCACTGTGAACAAAGTACAGAAATTTGGAACAAATGAAAGAAAGTTTGTGTAC	840
DB	781	AAGATCACTGTGAACAAAGTACAGAAATTTGGAACAAATGAAAGAAAGTTTGTGTAC	840
QY	841	TGAAAAAGAACTGTTCAGAGCAGAAAGAAATTAATTAATTAATTAATTAATTAATTA	900
DB	841	TGAAAAAGAACTGTTCAGAGCAGAAAGAAATTAATTAATTAATTAATTAATTAATTA	900
QY	901	AATGGGAACAGAGCTCTGAGAGTGTGAGATTGACTTTTAAACCAAGAGAGAGAGAA	960

DB	901	AATGGGAACAGAGCTCTGAGAGTGTGAGATTGACTTTTAAACCAAGAGAGAGAGAA	960
QY	961	GAAATGCCATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1020
DB	961	GAAATGCCATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1020
QY	1021	ATAGGAAGAGTTAGAGTGAACCAACACTTGAACAGGCTCTCAGAAATACAGATATAG	1080
DB	1021	ATAGGAAGAGTTAGAGTGAACCAACACTTGAACAGGCTCTCAGAAATACAGATATAG	1080
QY	1081	AATTGAAGAGTTAGAGTGAATTTGAATCAGGTTTCTCAGACTCATGAAATGAAATTT	1140
DB	1081	AATTGAAGAGTTAGAGTGAATTTGAATCAGGTTTCTCAGACTCATGAAATGAAATTT	1140
QY	1141	ATCTTTACATGAAATTTGATGTTGAAAGGAAATTTGCCATGCTTAAACTCGAAATAG	1200
DB	1141	ATCTTTACATGAAATTTGATGTTGAAAGGAAATTTGCCATGCTTAAACTCGAAATAG	1200
QY	1201	CCACACTGAAACACCAATACAGGAAAGGAAATTAATTAATTAATTAATTAATTAAT	1260
DB	1201	CCACACTGAAACACCAATACAGGAAAGGAAATTAATTAATTAATTAATTAATTAAT	1260
QY	1261	TAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTGAAAGAGGATCATTAACTA	1320
DB	1261	TAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTGAAAGAGGATCATTAACTA	1320
QY	1321	AAAGGAGTCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAAACCAATGCTCA	1380
DB	1321	AAAGGAGTCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAAACCAATGCTCA	1380
QY	1381	CTTCTTAAATTGAAGGAAAGAAACAAAGAAATTAATTAATTAATTAATTAATTAAT	1440
DB	1381	CTTCTTAAATTGAAGGAAAGAAACAAAGAAATTAATTAATTAATTAATTAATTAAT	1440
QY	1441	ATCTTAGAGTGGCTCTGCTGTACAGACCATGATCAATTTGTGACATCAAGAAAGATC	1500
DB	1441	ATCTTAGAGTGGCTCTGCTGTACAGACCATGATCAATTTGTGACATCAAGAAAGATC	1500
QY	1501	AAGAACTTCTTCCACATTCAGAGAGTGTGTTTTCGAAAGAAATTAATTAATTAAT	1560
DB	1501	AAGAACTTCTTCCACATTCAGAGAGTGTGTTTTCGAAAGAAATTAATTAATTAAT	1560
QY	1561	TGAGTAGTACCGATATTAACAAATGAGGTGCTCCATCAACACACTTCTGAAAGCTCAA	1620
DB	1561	TGAGTAGTACCGATATTAACAAATGAGGTGCTCCATCAACACACTTCTGAAAGCTCAA	1620
QY	1621	AAATCCANAAGCCTTAAATTAATTCATTAATTCAGAGAGTGTCTTAAGAGAAATACA	1680
DB	1621	AAATCCANAAGCCTTAAATTAATTCATTAATTCAGAGAGTGTCTTAAGAGAAATACA	1680
QY	1681	TTGGTTTCAGGAAACATGACAAAGAGACCAACGTTGAAACACAGTGTCAATTAAGAG	1740
DB	1681	TTGGTTTCAGGAAACATGACAAAGAGACCAACGTTGAAACACAGTGTCAATTAAGAG	1740
QY	1741	TGAACACATGTTTCAAAACGAAAGATTAATGTAACAAACACACTGAGAGAGGAGTC	1800
DB	1741	TGAACACATGTTTCAAAACGAAAGATTAATGTAACAAACACACTGAGAGAGGAGTC	1800
QY	1801	TTTAGATCAGAAATTTATTTCAACTCAAGCAAAATTAATTTGGCTTCAACAGCAATTA	1860
DB	1801	TTTAGATCAGAAATTTATTTCAACTCAAGCAAAATTAATTTGGCTTCAACAGCAATTA	1860
QY	1861	TCATGCAATTAAGAAAGCTGACAAACAAAGCAAGATTAATTAATTTGATTTTCTTTG	1920
DB	1861	TCATGCAATTAAGAAAGCTGACAAACAAAGCAAGATTAATTAATTTGATTTTCTTTG	1920
QY	1921	AGAGGAAATGNCATCATCTTCTTAAAGAGAAATTAATTAATTAATTAATTAATTA	1980
DB	1921	AGAGGAAATGNCATCATCTTCTTAAAGAGAAATTAATTAATTAATTAATTAATTA	1980
QY	1981	CAATTTAAAGAAACCCGATATATTTCAATATGGAAGAAAGAAAGAAAGAAAGAA	2030

Db 1981 CCATTTAAAAACCCGTATATTTCAATATGAAAAAANAAAAA 2030

RESULT 2

ID ABT33272

XX ABT33272 standard; DNA; 4047 BP.

XX AC ABT33272;

XX DT 15-MAY-2003 (first entry)

XX DE Human tumour-related DNA sequence - SEQ ID No 566.

XX DE Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;

XX KW tumour; breast cancer; cancer; immune response stimulation.

XX OS Homo sapiens.

XX PN WO200283956-A1.

XX PD 24-OCT-2002.

XX PF 15-APR-2002; 2002WO-US012378.

XX PR 13-APR-2001; 2001US-00834759.

XX PR 07-DEC-2001; 2001US-00007805.

XX PR 13-FEB-2002; 2002US-00076622.

XX PA (CORI-) CORIXA CORP.

XX PI Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;

XX PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;

XX PI Vedvick TS, McNeill PD, Durham M;

XX DR WPI; 2003-103376/09.

XX PT New polypeptide and polynucleotide useful for stimulating and/or

XX PT expanding T cells specific for a tumor protein and treating breast

XX PT cancer.

XX FS Example 12; Page 346-347; 375pp; English.

XX CC The invention comprises a method of stimulating and/or expanding T cells

XX CC specific for a tumor protein. The invention further comprises human

XX CC nucleic acids and proteins that are associated with tumors (e.g. breast

XX CC cancer). The method and sequences of the invention are useful for

XX CC stimulating and/or expanding T cells specific for a tumor protein,

XX CC detecting the presence of cancer, stimulating an immune response in a

XX CC patient and treating breast cancer. The present DNA sequence represents a

XX CC human tumour-related DNA sequence

SQ Sequence 4047 BP; 1563 A; 716 C; 850 G; 918 T; 0 U; 0 Other;

Query Match 95.6%; Score 1940; DB 7; Length 4047;

Best Local Similarity 98.7%; Pred. No. 0;

Matches 2001; Conservative 0; Mismatches (21) Indels 5; Gaps 5;

QY 5 TCCCGTTAAAGATGCTCTCTGAAGCTTAACCTGGGAATGAAGTTTCTATTCCTCAACTAA 64

DB 2016 TCCCTTAAAGATGCTCTCTGAAGCTTAACCTGGGAATGAAGTTTCTATTCCTCAACTAA 2075

QY 65 AGCCTTAGAATGATGACATGCAAACTTTCAAGCAGAGCTCCCGAAGAGCCATCTGC 124

DB 2076 AGCCTTAGAATGATGACATGCAAACTTTCAAGCAGAGCTCCCGAAGAGCCATCTGC 2135

QY 125 CTTTCAGAGCTGCTTGAAGTGAAGTCTTCCCAATGAAGCTTGGAAATGAAGAA 184

DB 2136 CTTTCAGAGCTGCTTGAAGTGAAGTCTTCCCAATGAAGCTTGGAAATGAAGAA 2195

QY 185 TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGGACTATGA 244

DB 2196 TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGGACTATGA 2255

QY 245 AGAAGATTCTTGGGATCTGAGAGTCTCTGTGAGACTGTTTTCACAGAGGATGTGTGTTT 304

DB 2256 AGAAGATTCTTGGGATCTGAGAGTCTCTGTGAGACTGTTTTCACAGAGGATGTGTGTTT 2315

QY 305 ACCCAAGGCTACACATCAAAAGAAATAGATAAATAATGGAATAATGGAAGATGTCTCC 364

DB 2316 ACCCAAGGCTACACATCAAAAGAAATAGATAAATAATGGAATAATGGAAGATGTCTCC 2375

QY 365 TGATAATGATGTTTCTGAAAGGCTCCCTGAGAGTGAAGTTTCTTATTCCTCAATGAAGC 424

DB 2376 TGATAATGATGTTTCTGAAAGGCTCCCTGAGAGTGAAGTTTCTTATTCCTCAATGAAGC 2435

QY 425 CTTAGAAATGATGACATGCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGCTT 484

DB 2436 CTTAGAAATGATGACATGCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGCTT 2495

QY 485 CGAGCTCCCATTTGAAATGCAAAAGTCTGTTCCTCAAAATAAAGCCTTGGAAATGAAGATGA 544

DB 2496 CGAGCTCCCATTTGAAATGCAAAAGTCTGTTCCTCAAAATAAAGCCTTGGAAATGAAGATGA 2555

QY 545 ACAAACATTGAGAGCAGATCAGATGTTTCCCTTCAGAAATCAAAACAAAGAGGTTGAGA 604

DB 2556 ACAAACATTGAGAGCAGATCAGATGTTTCCCTTCAGAAATCAAAACAAAGAGGTTGAGA 2615

QY 605 AAATTTCTTGGGATCTGAGAGTCTCCGAGAGTCTTTCACAGAGGATGTGTGTAC 664

DB 2616 AAATTTCTTGGGATCTGAGAGTCTCCGAGAGTCTTTCACAGAGGATGTGTGTAC 2675

QY 665 CAAGCTACACATCAAAAGAAATGGAATAAATAAGTGAAGAAATAGAGATTCACATAG 724

DB 2676 CAAGCTACACATCAAAAGAAATGGAATAAATAAGTGAAGAAATAGAGATTCACATAG 2735

QY 725 CCTATCAAAATCTTGGATCAGATTCATCTTGTGAAGAGCAAGGGAACCTCAAAAGA 784

DB 2736 CCTATCAAAATCTTGGATCAGATTCATCTTGTGAAGAGCAAGGGAACCTCAAAAGA 2795

QY 785 TCACCTGTGAACAACTGACAGGAAATGCAACAAATGAAAGAAAGTTTGTGTACTGAA 844

DB 2796 TCACCTGTGAACAACTGACAGGAAATGCAACAAATGAAAGAAAGTTTGTGTACTGAA 2855

QY 845 AAAGAACTGTGAGAGCAAAAGAAATTAATTCAGTTGAGACCAACCAAGTTTAAATG 904

DB 2856 AAAGAACTGTGAGAGCAAAAGAAATTAATTCAGTTGAGACCAACCAAGTTTAAATG 2915

QY 905 GGAAACAAGAGCTCTGAGATTCAGATTCGATTTAAACCAAGAGAGAGAGAGAGAA 964

DB 2916 GGAAACAAGAGCTCTGAGATTCAGATTCGATTTAAACCAAGAGAGAGAGAGAGAA 2975

QY 965 TCCCGATATATTAATGAAATTAAGGAGAAATAGGAGAAATCGAGAGCAGCATAG 1024

DB 2976 TCCCGATATATTAATGAAATTAAGGAGAAATAGGAGAAATCGAGAGCAGCATAG 3035

QY 1025 GAAAGAGTTAGAGTGAACCAACCACTTGAACAGGCTCTCAGAAATCAAGATATAGAATT 1084

DB 3036 GAAAGAGTTAGAGTGAACCAACCACTTGAACAGGCTCTCAGAAATCAAGATATAGAATT 3095

QY 1085 GAAGAGTGAAGAGTAAATTTGAATCAGGTTTCTCAGATCTATGAAATGAAATATATCT 1144

DB 3096 GAAGAGTGAAGAGTAAATTTGAATCAGGTTTCTCAGATCTATGAAATGAAATATATCT 3155

QY 1145 CTTTACATGAAATTTGATGTTTCAAAAGGAAATTCGCAATGCTTAAACTGGAAATAGCCAC 1204

DB 3156 CTTTACATGAAATTTGATGTTTCAAAAGGAAATTCGCAATGCTTAAACTGGAAATAGCCAC 3215

QY 1205 ACTTGAACCACTACCCAGGAAAGAAATTAATTAATCTTTGAGGACATTAAGATTTTAA 1264

DB 3216 ACTTGAACCACTACCCAGGAAAGAAATTAATTAATCTTTGAGGACATTAAGATTTTAA 3275

QY 1265 AGAAGAGATGCTGAACTTCAGATGACCTTAACTGAAAGAGGAAATCAATTAACCTTAAAG 1324

DB 3276 AGAAGAGATGCTGAACTTCAGATGACCTTAACTGAAAGAGGAAATCAATTAACCTTAAAG 3335

QY 1325 GGCACTCTCAATATAGTGGGAGCTTAAAGTTCTGTAGTGTGAGAAACAATGCTCATCTTC 1384

Db 3336 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGACACAACTGCTCACITC 3395
QY 1385 TAAATTGAAGAAACACAGACAAAGAAATACCTAGAGGAGAAATTTGAATCACCACATCC 1444
Db 3396 TAAATTGAAGAAACACAGACAAAGAAATACCTAGAGGAGAAATTTGAATCACCACATCC 3455
QY 1445 TAGACTGGCTTCTGCTGTACAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 1504
Db 3456 TAGACTGGCTTCTGCTGTACAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 3515
QY 1505 ACTGCTTTCCATTTGCAGGAGATGCTTTGTCAGAGAAATGAATTTGATGTGAG 1564
Db 3516 ACTGCTTTCCATTTGCAGGAGATGCTTTGTCAGAGAAATGAATTTGATGTGAG 3575
QY 1565 TAGTACCGATATATAAATGAGTGTCTCCATCAACACCTTTCTGAAGCTCAAGAGAAAT 1624
Db 3576 TAGTA-CGATATATAAATGAGTGTCTCCATCAACACCTTTCTGAAGCTCAAGAGAAAT 3634
QY 1625 CCNAAAGCTTAAATTTAATCTCAATTTATGTCAGGAGATGCTTAAAGAAATACATTTGG 1684
Db 3635 CCNAAAGCTTAAATTTAATCTCAATTTATGTCAGGAGATGCTTAAAGAAATACATTTGG 3694
QY 1685 TTTCAAGAAATGTCACAAAGAGACCAACGTCGAAACACAGTGTCAAAATGAAGAAAGTGA 1744
Db 3695 TTTCA-GAATGTCACAAAGAGACCAACGTCGAAACACAGTGTCAAAATGAAGAAAGTGA 3753
QY 1745 CACATGNTCAANCGAACCAAGATNATGTGAACAAACACTGACAGAGAGTGTCTTA 1804
Db 3754 CACATGNTCAANCGAACCAAGATNATGTGAACAAACACTGACAGAGAGTGTCTTA 3813
QY 1805 GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTGGCTTCAACAGCAATTTAGTTCA 1864
Db 3814 GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTGGCTTCAACAGCAATTTAGTTCA 3873
QY 1865 GCACATANGAAGCTGACAAACAAAGCAAGATTAACAAATTTGATTTTCTTGAGAG 1924
Db 3874 GCACATAA-GAAAGCTGACAAACAAAGCAAGATTAACAAATTTGATTTTCTTGAGAG 3932
QY 1925 GAAATGTCACATCTTCTTAAAGAGAAATATGAGAGATATTTNATTACNATAACCA 1983
Db 3933 GAAATGTCACATCTTCTTAAAGAGAAATATGAGAGATATTTNATTACNATAACCA 3992
QY 1984 TTTAAAAACCCGATATTTCAATATGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 2030
Db 3993 TTTAAAAACCCGATATTTCAATATGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 4038

RESULT 3
ID ABT07694 standard; DNA; 4458 BP.
AC ABT07694;
XX
DT 14-NOV-2002 (first entry)
XX
DE Breast cancer-associated gene sequence 2.
XX
XX Gene; ds; breast cancer; breast cancer-associated gene sequence;
KW drug development; pharmacogenetics; biosensor development.
XX
OS Unidentified.
XX
FN WO200259377-R2.
XX
XX 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-US002242.
XX
XX 24-JAN-2001; 2001US-0263965P.
PR 02-FEB-2001; 2001US-0265928P.
PR 09-APR-2001; 2001US-00829472.
PR 09-APR-2001; 2001US-0282696P.
PR

PR 04-MAY-2001; 2001US-0288590P.
PR 29-MAY-2001; 2001US-0294443P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Mack DH, Gish KC, Afar D;
XX
XX WPI; 2002-583738/62.
DR N-PSDB; ABJ05537.
XX
PT Detecting a breast cancer-associated transcript in a patient's cell,
PT useful for diagnosing breast cancer, comprises contacting a biological
PT sample with a polynucleotide that selectively hybridizes with breast
PT cancer nucleic acids.
XX
PS Claim 9; Page 347-348; 41app; English.
XX
CC The invention comprises a method of detecting a breast cancer-associated
CC transcript in a cell from a patient. The method of the invention involves
CC contacting a biological sample from the patient with a nucleotide that
CC hybridizes to one of the 69 breast cancer-associated gene sequences shown
CC in the specification. The method of the invention is useful in the
CC diagnosis or prognosis of breast cancer, and for detecting genes that are
CC up or down-regulated in breast cancer cells. Genes identified by the
CC method of the invention can be used in diagnostic purposes and also as
CC targets for screening for therapeutic compounds that modulate breast
CC cancer (e.g. hormones or antibodies). Identification of genes that are
CC over or under expressed in breast cancer can additionally provide high-
CC resolution, high-sensitivity datasets which can be used in the areas of
CC diagnostics, therapeutics, drug development, pharmacogenetics, protein
CC structure and biosensor development. DNA sequences ABT07693 - ABT07761
XX represent the 69 breast cancer-associated gene sequences of the invention
SQ Sequence 4458 BP; 1698 A; 812 C; 931 G; 1017 T; 0 U; 0 Other;
Query Match 95.6%; Score 1940; DB 6; Length 4458;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;
QY 5 TGCCTGTTAAAGATGCTTCTCTGAAGGCTAACTGCGAATGAAAGTTTCTATTCCAACTAA 64
Db 2091 TCCTGTTAAAGATGCTTCTCTGAAGGCTAACTGCGAATGAAAGTTTCTATTCCAACTAA 2150
QY 65 AGCCTTAGAATGTAGACATGCAAACTTTCAAGAGAGAGCTCCGAGAGGCACTGTC 124
Db 2151 AGCCTTAGAATGTAGACATGCAAACTTTCAAGAGAGAGCTCCGAGAGGCACTGTC 2210
QY 125 CTTGAGGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGAATTTGAAGAA 184
Db 2211 CTTGAGGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGAATTTGAAGAA 2270
QY 185 TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGATCCCAACAAAGAGGACTATGA 244
Db 2271 TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGATCCCAACAAAGAGGACTATGA 2330
QY 245 AGAAAGTTCTTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTCACAGAGGATGTGTGTTT 304
Db 2331 AGAAAGTTCTTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTCACAGAGGATGTGTGTTT 2390
QY 305 ACCCAAGGCTACATCAATCAAAAGAAATAGATATAAATAAATGAAAAATAGAGAGTCTCC 364
Db 2391 ACCCAAGGCTACATCAATCAAAAGAAATAGATATAAATAAATGAAAAATAGAGAGTCTCC 2450
QY 365 TGATAATGATGTTTCTGAAAGGCTCCCTGAGAGTGAAGTTTCTATTCCAACTAAAGC 424
Db 2451 TGATAATGATGTTTCTGAAAGGCTCCCTGAGAGTGAAGTTTCTATTCCAACTAAAGC 2510
QY 425 CTTAGAATTTGATGGAATGCAAACTTTCAAGAGAGGCTCCCGAGAGGCACTGTCCTT 484
Db 2511 CTTAGAATTTGATGGAATGCAAACTTTCAAGAGAGGCTCCCGAGAGGCACTGTCCTT 2570
QY 485 CGAGGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGAATTTGAAGATGA 544

Qy	1625	CCNAAAGCCCTAA	AAATTAATCTCAAT	TATGCGAGGATGCTCTAAGAGAAATACATGG	1684
Db	3710	CCAAAAGCCCTAA	AAATTAATCTCAAT	TATGCGAGGATGCTCTAAGAGAAATACATGG	3769
Qy	1685	TTTCAGGAACATG	CCACAAAGACCAAC	CGTGAAACACACAGTGTCAAAATGAAGGAAGCTGAA	1744
Db	3770	TTTCA-GAACATG	CCACAAAGACCAAC	CGTGAAACACACAGTGTCAAAATGAAGGAAGCTGAA	3828
Qy	1745	CACATGNTCAAN	CGAACCAAGATNAT	GTGAAACAAACACACTGANCAGCAGAGTCTCTA	1804
Db	3829	CACATGTATCAA	AACCAAGATAT	GTGAAACAAACACACTGAAACAGCAGAGTCTCTA	3888
Qy	1805	GATCAGAAATTA	TTTCAACTCAAC	AGCAAAATATGTGGCTTCAACAGCAATTAGTTTCAT	1864
Db	3889	GATCAGAAATTA	TTTCAACTCAAC	AGCAAAATATGTGGCTTCAACAGCAATTAGTTTCAT	3948
Qy	1865	GCACATAANGAA	AGCTGACACAA	AGCAAGATATCAATGATNTTCATTTCTTGAGAG	1924
Db	3949	GCACATAA-GAA	AGCTGACACAA	AGCAAGATATCAATGATNTTCATTTCTTGAGAG	4007
Qy	1925	GAATAATGC-NC	ATCANTCTTCTA	AAAGAGAAATATGAGGAGATATTTNATTAACNATAACCA	1983
Db	4008	GAATAATGCAC	ATCANTCTTCTA	AAAGAGAAATATGAGGAGATATTTNATTAACNATAACCA	4067
Qy	1984	TTTAAAAAACC	CGTATATTTCA	ATATGAAAAAANAAAAA 2030	
Db	4068	TTTAAAAA-CC	GATATATCAAT	ATGAAAAAGAGAAAGCAAAACA 4113	
RESULT 4					
ABT33271					
ID	ABT33271	standard; DNA; 4458 BP.			
AC	ABT33271;				
XX	15-MAY-2003	(first entry)			
DE	Human tumour-related DNA sequence - SEQ ID No 564.				
KW	Human; ss; vaccine; gene therapy; T cell stimulation; T cell expansion;				
OS	tumour; breast cancer; cancer; immune response stimulation; PCR; primer.				
PN	Homo sapiens.				
PD	WO200283956-A1.				
PF	24-OCT-2002.				
PR	15-APR-2002; 2002WO-US012378.				
PR	13-APR-2001; 2001US-00834759.				
PR	07-DEC-2001; 2001US-00007805.				
PR	13-FEB-2002; 2002US-00076622.				
PA	(CORI-) CORIXA CORP.				
PI	Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;				
PI	Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;				
PI	Vedvick TS, McNeill PD, Durham M;				
DR	WPI; 2003-103376/09.				
PT	New polypeptide and polynucleotide useful for stimulating and/or				
PT	expanding T cells specific for a tumor protein and treating breast				
PS	Example 9; Page 340-341; 375pp; English.				
CC	The invention comprises a method of stimulating and/or expanding T cells				
CC	specific for a tumour protein. The invention further comprises human				
CC	nucleic acids and proteins that are associated with tumours (e.g. breast				
CC	cancer). The method and sequences of the invention are useful for				

CC stimulating and/or expanding T cells specific for a tumour protein,
CC detecting the presence of cancer, stimulating an immune response in a
CC patient and treating breast cancer. The present DNA sequence represents a
CC human tumour-related PCR primer
XX
SQ Sequence 4458 BP; 1698 A; 812 C; 931 G; 1017 T; 0 U; 0 Other;
Query Match 95.6%; Score 1940; DB 7; Length 4458;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;
QY 5 TGCGGTTAAAGATGGTCTCTGAGGCTAACTCGGGAATGAAAGTTTCTATTCCAACTAA 64
Db 2091 TCCTGTTAAAGATGGTCTCTGAGGCTAACTCGGGAATGAAAGTTTCTATTCCAACTAA 2150
QY 65 AGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGCCATCTGC 124
Db 2151 AGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGCCATCTGC 2210
QY 125 CTTGAGCCTGCCATTGAAATGCAAAAGTCTGTTCMAATAAAGCCTTGGAAATGAAAGAA 184
Db 2211 CTTGAGCCTGCCATTGAAATGCAAAAGTCTGTTCMAATAAAGCCTTGGAAATGAAAGAA 2270
QY 185 TGAACAAACATTGAGAGCAGATGATCTCCCATCAGATCCAAACAAAGGACTATGA 244
Db 2271 TGAACAAACATTGAGAGCAGATGATCTCCCATCAGATCCAAACAAAGGACTATGA 2330
QY 245 AGAAAGTCTTGGATTCTGAGATCTCTGTGAGATCTGTTTACAGAGATGTGTGTTT 304
Db 2331 AGAAAGTCTTGGATTCTGAGATCTCTGTGAGATCTGTTTACAGAGATGTGTGTTT 2390
QY 305 ACCCAGGCTACATCAAAAGAAATAGATAAATAATGGAATAATTAGAAGAGTCTCC 364
Db 2391 ACCCAGGCTACATCAAAAGAAATAGATAAATAATGGAATAATTAGAAGAGTCTCC 2450
QY 365 TGATAATGATGGTCTTCTGAAGGCTCCCTGAGAGTGAAGTCTTCTATTCCAACTAAAGC 424
Db 2451 TGATAATGATGGTCTTCTGAAGGCTCCCTGAGAGTGAAGTCTTCTATTCCAACTAAAGC 2510
QY 425 CTTAGAAATTGATGNCATGCAAACTTTCAAAGCAGAGCCTCCGAGAGCAATCTGCCTT 484
Db 2511 CTTAGAAATTGATGNCATGCAAACTTTCAAAGCAGAGCCTCCGAGAGCAATCTGCCTT 2570
QY 485 CGAGCCTGCCATTGAAATGCAAAAGTCTGTTTCCAAATAAAGCCTTGGAAATGGAAGATGA 544
Db 2571 CGAGCCTGCCATTGAAATGCAAAAGTCTGTTTCCAAATAAAGCCTTGGAAATGGAAGATGA 2630
QY 545 ACAACATTGAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAGAGGTTGAAGA 604
Db 2631 ACAACATTGAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAGAGGTTGAAGA 2690
QY 605 AAATCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTACAGAGAGGATGTGTGTACC 664
Db 2691 AAATCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTACAGAGAGGATGTGTGTACC 2750
QY 665 CAAGGCTACATCAAAAGAAATGGATAAATAAGTGGAAATTTAGAGATTCACTAG 724
Db 2751 CAAGGCTACATCAAAAGAAATGGATAAATAAGTGGAAATTTAGAGATTCACTAG 2810
QY 725 CTTATCAAAATCTTGGATACAGTTCATTCTTGTGAAGAGCAAGGAACTTCAAAAGA 784
Db 2811 CTTATCAAAATCTTGGATACAGTTCATTCTTGTGAAGAGCAAGGAACTTCAAAAGA 2870
QY 785 TCCTGTGAACAGCTACAGGAAATGGAACAAATGAAAGAGTTTGTGTACTGAA 844
Db 2871 TCCTGTGAACAGCTACAGGAAATGGAACAAATGAAAGAGTTTGTGTACTGAA 2930
QY 845 AAGAACTGTGACAGCAAAAGAAATAAATCAGAGTTAGAGAACCAAAAGTTTAAATG 904
Db 2931 AAGAACTGTGACAGCAAAAGAAATAAATCAGAGTTAGAGAACCAAAAGTTTAAATG 2990
QY 905 GGAACAGAGCTCTGAGTGTGAGATGTGCTTTAAACCAAGAGAGAGAGAGAA 964

Db 2991 GGAACAGAGCTCTGAGTGTGAGATGTGCTTTAAACCAAGAGAGAGAGAGAA 3050
QY 965 TGCCGATATATTAAATGAAAAAATTAGGGAAGAAATTAGGAAGAAATCGAAGAGCAGATAG 1024
Db 3051 TGCCGATATATTAAATGAAAAAATTAGGGAAGAAATTAGGAAGAAATCGAAGAGCAGATAG 3110
QY 1025 GAAAGAGTTAGAGTGAACCAAACTTTGAACAGGCTCTCAGAAATCAGATATAGAAAT 1084
Db 3111 GAAAGAGTTAGAGTGAACCAAACTTTGAACAGGCTCTCAGAAATCAGATATAGAAAT 3170
QY 1085 GAAGAGTGTAGAAGTAATTTGAATCAGGTTTCTCAGCTCATGAAATGAAATTTATCT 1144
Db 3171 GAAGAGTGTAGAAGTAATTTGAATCAGGTTTCTCAGCTCATGAAATGAAATTTATCT 3230
QY 1145 CTTACATGAAATTTGCAATTTGAAAGGAAATTTGCCATGCTAAACTGGAATAGCCAC 1204
Db 3231 CTTACATGAAATTTGCAATTTGAAAGGAAATTTGCCATGCTAAACTGGAATAGCCAC 3290
QY 1205 ACTGAAACCAATACACAGGAAAGGAAATAAATCTTTGAGGACATTAAGATTTTAAA 1264
Db 3291 ACTGAAACCAATACACAGGAAAGGAAATAAATCTTTGAGGACATTAAGATTTTAAA 3350
QY 1265 AGAAAGAAATCTGAACTTCAGATGAGCCTTAAACTGAAAGAGGAAATCAATTAACATAAAG 1324
Db 3351 AGAAAGAAATCTGAACTTCAGATGAGCCTTAAACTGAAAGAGGAAATCAATTAACATAAAG 3410
QY 1325 GGCATCTCAATATAGTGGGCAAGCTTAAAGTTCTGATAGCTGAGAACCAATGCTCATCTC 1384
Db 3411 GGCATCTCAATATAGTGGGCAAGCTTAAAGTTCTGATAGCTGAGAACCAATGCTCATCTC 3470
QY 1385 TAAATGAAGGAAAAAACAGACAAAGAAATCTAGAGCGAGATTTGAATCAGACCATCTCC 1444
Db 3471 TAAATGAAGGAAAAAACAGACAAAGAAATCTAGAGCGAGATTTGAATCAGACCATCTCC 3530
QY 1445 TAGACTGCTCTGCTGTACAGACCATGATCAAAATTTGATGACATCAAGAAAAAGTCAAGA 1504
Db 3531 TAGACTGCTCTGCTGTACAGACCATGATCAAAATTTGATGACATCAAGAAAAAGTCAAGA 3590
QY 1505 ACCTGCTTCCACATGTCAGAGATGCTTGTTCGAAAGAAAAATGAATGTTGATGTGAG 1564
Db 3591 ACCTGCTTCCACATGTCAGAGATGCTTGTTCGAAAGAAAAATGAATGTTGATGTGAG 3650
QY 1565 TAGTACCGATATATAACCAATGAGGTCTCCATCAACCACTTTCTGAAAGCTCAAGGAAAT 1624
Db 3651 TAGTACCGATATATAACCAATGAGGTCTCCATCAACCACTTTCTGAAAGCTCAAGGAAAT 3709
QY 1625 CCNAAAGCCTAAAAATTAATCTCAATATGAGAGGATGCTCTAAGAGAAAAATCATTTGG 1684
Db 3710 CCNAAAGCCTAAAAATTAATCTCAATATGAGAGGATGCTCTAAGAGAAAAATCATTTGG 3769
QY 1685 TTTTCAGAACTGCAAAAGAGACCAACGTAAGAACACACAGTGTCAAAATGAAGGAACTGAA 1744
Db 3770 TTTTCAGAACTGCAAAAGAGACCAACGTAAGAACACACAGTGTCAAAATGAAGGAACTGAA 3828
QY 1745 CACATGTTNTCAANCGAACCAAGATNATGTGAACAAACACACTGTGANCAGAGGATCTCTA 1804
Db 3829 CACATGTTNTCAANCGAACCAAGATNATGTGAACAAACACACTGTGANCAGAGGATCTCTA 3888
QY 1805 GATCAGAAATTTTCAACTACAAAGCAAAATATGTGCTTCAACAGCAATTTAGTTTCAAT 1864
Db 3889 GATCAGAAATTTTCAACTACAAAGCAAAATATGTGCTTCAACAGCAATTTAGTTTCAAT 3948
QY 1865 GCACATAANGAAGCTGACACAAAGAGCAAGATAAATTTGATNTTCAATNTTCTTGAGAG 1924
Db 3949 GCACATAANGAAGCTGACACAAAGAGCAAGATAAATTTGATNTTCAATNTTCTTGAGAG 4007
QY 1925 GAAATATGC-NCATCATCTTCTAAAGAGAAATGAGGAGATATTNATTCNATATACCA 1983
Db 4008 GAAATATGC-NCATCATCTTCTAAAGAGAAATGAGGAGATATTNATTCNATATACCA 4067
QY 1984 TTTTAAAAAACCCCTATATTTCATATATGAAAAAATAAAAAAATAAAAAA 2030
Db 4068 TTTTAAAAAACCCCTATATATATATGAAAAAATAAAAAAATAAAAAA 4113

RESULT 5
ACC50246
ID ACC50246 standard; cDNA; 4458 BP.
XX
AC ACC50246;
XX
DT 12-JUN-2003 (first entry)
XX
DE Breast cancer associated cDNA sequence SEQ ID NO:333.
XX
KW Human; breast cancer; cytostatic; gene therapy; gene, ss.
XX
OS Homo sapiens.
XX
PN W02003004989-A2.
XX
XX 16-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-US019669.
XX
XX 21-JUN-2001; 2001US-0299887P.
XX
XX 27-JUN-2001; 2001US-0301572P.
XX
XX 18-JUL-2001; 2001US-0306501P.
XX
XX 25-SEP-2001; 2001US-0325002P.
XX
XX 05-MAR-2002; 2002US-0362585P.
XX
XX 14-MAY-2002; 2002US-0380391P.
XX
XX (MILL-) MILLENIUM PHARM INC.
XX
XX Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
XX Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
XX Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;
XX
XX WPI: 2003-210381/20.
XX
XX P-PSDB; ABR47548.
XX
XX
XX Breast cancer diagnosis or treatment by comparing the level of expression
XX of a marker in a patient sample with that in the control non-breast
XX cancer sample.
XX
XX Claim 1; SEQ ID NO 333; 128pp; English.
XX
XX The present invention describes a method for assessing whether a patient
XX is afflicted with breast cancer. The method comprises comparing the level
XX of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
XX ABR47386 to ABR47632) in a patient sample and the normal level of
XX expression of the marker in a control non-breast cancer sample, where a
XX significant increase in the level of expression of the marker in the
XX patient sample and the normal level is an indication that the patient is
XX afflicted with breast cancer. The breast cancer associated sequences from
XX the present invention have cytostatic activities and can be used in gene
XX therapy. The method is useful for diagnosing and treating breast cancer.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 4458 BP; 1698 A; 812 C; 931 G; 1017 T; 0 U; 0 Other;
XX
XX Query Match 95.6%; Score 1940; DB 7; Length 4458;
XX Best Local Similarity 98.7%; Pred. No. 0;
XX Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;
XX
XX 5 TCCCGTTAAAGTCTCTTCTGGAAGGCTAACTCGGGAATGAAGTCTTCTATTCCTCAACTAA 64
XX
XX 2091 TCCTGTTAAAGATGGTCTCTCTGGAAGGCTAACTCGGGAATGAAGTCTTCTATTCCTCAACTAA 2150
XX
XX 65 AGCCTTAGAATGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGCCCATCTGC 124
XX
XX 2151 AGCCTTAGAATGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGCCCATCTGC 2210
XX
XX 125 CTTCAGCCTGCTGATGAAATGCAAAAGTCTGTTCCCAATAAAGCCTTGGNATGAAGA 184

Db	2211	CTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAA	2270
Qy	185	TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGAGCTATGA	244
Db	2271	TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGAGCTATGA	2330
Qy	245	AGAAAGTTCTTTGGGATCTGAGAGTCTCTGTGAGACTGTTTTCACAGAAAGATGTGTGTT	304
Db	2331	AGAAAGTTCTTTGGGATCTGAGAGTCTCTGTGAGACTGTTTTCACAGAAAGATGTGTGTT	2390
Qy	305	ACCAAGGCTACACATCAAAAGAAATAGATAAAATAAATGAAATGAAATGAAAGATGTCTCC	364
Db	2391	ACCAAGGCTACACATCAAAAGAAATAGATAAAATAAATGAAATGAAATGAAAGATGTCTCC	2450
Qy	365	TCATAATGATGTTTCTGAGAGGCTCCCTGCAGAAATGAAAGTCTTCTATTCCAACTAAAGC	424
Db	2451	TGATAATGATGTTTCTGAGAGGCTCCCTGCAGAAATGAAAGTCTTCTATTCCAACTAAAGC	2510
Qy	425	CTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGCCATCTGCCTT	484
Db	2511	CTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGCCATCTGCCTT	2570
Qy	485	CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTTGAAGAATGA	544
Db	2571	CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTTGAAGAATGA	2630
Qy	545	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAGAGGTTGAAGA	604
Db	2631	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAGAGGTTGAAGA	2690
Qy	605	AAATCTCTGGGATCTGAGAGTCTCCGTGAGACTGTTTCAGAGAGAGTGTGTGTACC	664
Db	2691	AAATCTCTGGGATCTGAGAGTCTCCGTGAGACTGTTTCAGAGAGAGTGTGTGTACC	2750
Qy	665	CAAGGCTACACATCAAAAGAAATGGATAAAATAAGTGGAAATTTAGAAGATTTCAACTAG	724
Db	2751	CAAGGCTACACATCAAAAGAAATGGATAAAATAAGTGGAAATTTAGAAGATTTCAACTAG	2810
Qy	725	CTATCAAAATCTTGGATACAGTTCATCTTGTGAAGAGCAGAGGAGTTCCTCAAGAGA	784
Db	2811	CTATCAAAATCTTGGATACAGTTCATCTTGTGAAGAGCAGAGGAGTTCCTCAAGAGA	2870
Qy	785	TCACCTGTGAACCACTCAGCAAAATGGAACAAATGGAACAAATGGAACAAATGGAACAA	844
Db	2871	TCACCTGTGAACCACTCAGCAAAATGGAACAAATGGAACAAATGGAACAAATGGAACAA	2930
Qy	845	AAAGAACTGTGAGAGCAAAAGAAATAAATCAAGTTAGAGAACCCAAAGTAAATG	904
Db	2931	AAAGAACTGTGAGAGCAAAAGAAATAAATCAAGTTAGAGAACCCAAAGTAAATG	2990
Qy	905	GGAAACAGAGCTCTGCAGTGTGAGATTCACCTTTAAACCAAGAGAGAGAGAGAGAA	964
Db	2991	GGAAACAGAGCTCTGCAGTGTGAGATTCACCTTTAAACCAAGAGAGAGAGAGAGAGAA	3050
Qy	965	TGCCGATATATTAAATGAAAAATTTAGGGAAGAATTTAGGAAGAATTCGAAGAGCAGATAG	1024
Db	3051	TGCCGATATATTAAATGAAAAATTTAGGGAAGAATTTAGGAAGAATTCGAAGAGCAGATAG	3110
Qy	1025	GAAAGATTAGAGTGAACCAACCACTTGAACAGCTCTCAGATACAGATATAGATTT	1084
Db	3111	GAAAGATTAGAGTGAACCAACCACTTGAACAGCTCTCAGATACAGATATAGATTT	3170
Qy	1085	GAAAGATTAGAGTGAACCAACCACTTGAACAGCTCTCAGATACAGATATAGATTT	1144
Db	3171	GAAAGATTAGAGTGAACCAACCACTTGAACAGCTCTCAGATACAGATATAGATTT	3230
Qy	1145	CTTACATGAAATTTGATGTTGAAAAGAAATTTGCCATGTCTAAACCTGGAATAGCCAC	1204
Db	3231	CTTACATGAAATTTGATGTTGAAAAGAAATTTGCCATGTCTAAACCTGGAATAGCCAC	3290
Qy	1205	ACTGAAACCAACCAATCCAGGAAAGGAAATTAATACCTTTGAGGACATTTAGATTTTAA	1264

Db	1614	TGATAATGATGGTTTTTCTGAAAGGCTCCCTGCAGATGAAGTTTCTATTCCAACTAAAGC	1673
Qy	425	CTTTAGAAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAGAGCCATCTGCCTT	484
Db	1674	CTTTAGAAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAGAGCCATCTGCCTT	1733
Qy	485	CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCAAATAAAAGCCTTGGAAATTGAAGAATGA	544
Db	1734	CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCAAATAAAAGCCTTGGAAATTGAAGAATGA	1793
Qy	545	ACAAACATTGAGAGCAGATCAGATGTGTCCCTTCAGAAATCAAAACAAAAGAAGGTTGAAGA	604
Db	1794	ACAAACATTGAGAGCAGATCAGATGTGTCCCTTCAGAAATCAAAACAAAAGAAGGTTGAAGA	1853
Qy	605	AAATTCTTGGGATTTCTCAGAGTCTCCGTGAGACTGTTTTCACAGAAGGATGTGTGTGTACC	664
Db	1854	AAATTCTTGGGATTTCTCAGAGTCTCCGTGAGACTGTTTTCACAGAAGGATGTGTGTGTACC	1913
Qy	665	CAAGGCTACACATCAAAAGAAATGGAATAAAATAAGTGGAAATTAGAGATTTCAACTAG	724
Db	1914	CAAGGCTACACATCAAAAGAAATGGAATAAAATAAGTGGAAATTAGAGATTTCAACTAG	1973
Qy	725	CCTATCAAAAATCTTGGATACAGTTCATTTCTTGTGAAAGCAAGGGAATTTCAAAAAGA	784
Db	1974	CCTATCAAAAATCTTGGATACAGTTCATTTCTTGTGAAAGCAAGGGAATTTCAAAAAGA	2033
Qy	785	TCACTGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAGTTTTTGTGTACTGA	844
Db	2034	TCACTGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAGTTTTTGTGTACTGA	2093
Qy	845	AAAGAACTGTCAAGACCAAGAAATAAATCACAGTTAGAGAAACCAAAAAGTTAAATG	904
Db	2094	AAAGAACTGTCAAGACCAAGAAATAAATCACAGTTAGAGAAACCAAAAAGTTAAATG	2153
Qy	905	GGAAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAAGAGAGAGAGAGAAA	964
Db	2154	GGAAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAAGAGAGAGAGAGAAA	2213
Qy	965	TGCCGATATATTAATGAAABAAATTAGGGAAGAAATTAGGAAGAAATCGAAGACAGCATAG	1024
Db	2214	TGCCGATATATTAATGAAABAAATTAGGGAAGAAATTAGGAAGAAATCGAAGACAGCATAG	2273
Qy	1025	GAAAGAGTTAGAAGTGAACAACAACCTTGAAACAGGCTCTCAGAAATCAAGATATAGAATT	1084
Db	2274	GAAAGAGTTAGAAGTGAACAACAACCTTGAAACAGGCTCTCAGAAATCAAGATATAGAATT	2333
Qy	1085	GAAGAGTGTAGAAAGTAAATTGAATCAGGTTTCTCACACTCATGAAATGAAATTTATCT	1144
Db	2334	GAAGAGTGTAGAAAGTAAATTGAATCAGGTTTCTCACACTCATGAAATGAAATTTATCT	2393
Qy	1145	CTTACATGAAAAATTCATGTTGAAAAAGGAAATTCGCATCTAAAACTGAAAAATGCCAC	1204
Db	2394	CTTACATGAAAAATTCATGTTGAAAAAGGAAATTCGCATCTAAAACTGAAAAATGCCAC	2453
Qy	1205	ACTGAAPACCAATACCAAGGAAAGGAAATTAATTAATCTTTGAGGACATTAAGATTTTAA	1264
Db	2454	ACTGAAPACCAATACCAAGGAAAGGAAATTAATTAATCTTTGAGGACATTAAGATTTTAA	2513
Qy	1265	AGAAAAAGATCTCGAATTCAGATGACCCCTAAAACTGAAAGAGGAATTCATTAATCAAAAAG	1324
Db	2514	AGAAAAAGATCTCGAATTCAGATGACCCCTAAAACTGAAAGAGGAATTCATTAATCAAAAAG	2573
Qy	1325	GGCATCTCAATATATAGTGGCAGCTTAAAGTTCTGATAGCTGAGAAACAATGTCTCACTTC	1384
Db	2574	GGCATCTCAATATATAGTGGCAGCTTAAAGTTCTGATAGCTGAGAAACAATGTCTCACTTC	2633
Qy	1385	TAAATTGAAGGAAAAACAAGCAAGAAATACTAGAGCGAAAAATTCGAATCACACCATCC	1444
Db	2634	TAAATTGAAGGAAAAACAAGCAAGAAATACTAGAGCGAAAAATTCGAATCACACCATCC	2693
Qy	1445	TAGACTGGCTTCTGCTGTACAAGACCATGATCAAAATTGTGTGATCAAGAAAAAGTCAAGA	1504

Db	2694	TAGACTGGCTTCGTGTACAAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA	2753
Qy	1505	ACCTGCTTTTCCACATTCGACAGGAGATGCTTTGTTTGCACAAAGAAAAATGAATGTTGATGTGAG	1564
Db	2754	ACCTGCTTTTCCACATTCGACAGGAGATGCTTTGTTTGCACAAAGAAAAATGAATGTTGATGTGAG	2813
Qy	1565	TAGTACCGATATATAACATGATGAGGTGCTCCATCAACCACTTTCTCGAAGCTCAAAAGGAAAT	1624
Db	2814	TAGTA-CGATATATATAACATGATGAGGTGCTCCATCAACCACTTTCTCGAAGCTCAAAAGGAAAT	2872
Qy	1625	CCANAAAGCCTTAAATAATTAATCTCAATATGTCAGGAGATGCTCTTAAGAGAAAAATACATTGG	1684
Db	2873	CCANAAAGCCTTAAATAATTAATCTCAATATGTCAGGAGATGCTCTTAAGAGAAAAATACATTGG	2932
Qy	1685	TTTCAGGAACATGCACAAAGAGACCAACGCTGGAACACAGTGTGCAATGAAGGAAAGCTGAA	1744
Db	2933	TTTCA-GAACATGCACAAAGAGACCAACGCTGGAACACAGTGTGCAATGAAGGAAAGCTGAA	2991
Qy	1745	CACATGNTCAAAACGAAACAAAGATATATGTGAACAAACACACTGANCAGCAGGAGTCTCTA	1804
Db	2992	CACATGTATCAAAACGAAACAAAGATATATGTGAACAAACACACTGANCAGCAGGAGTCTCTA	3051
Qy	1805	GATCAGAAATATTTCACTCAACCTCAAAAGCAAAATATGTGCTTCAACAGCAATTAGTTCTAT	1864
Db	3052	GATCAGAAATATTTCACTCAACCTCAAAAGCAAAATATGTGCTTCAACAGCAATTAGTTCTAT	3111
Qy	1865	GCACATAAGAAAGCTTGACAAACAAAGCAAGATAACAATTTGATTTTCTTTTGAGAG	1924
Db	3112	GCACATRA-GAAAGCTTGACAAACAAAGCAAGATAACAATTTGATTTTCTTTTGAGAG	3170
Qy	1925	GAAATGTC-NCATCATCTTCTTAAAGAGAAAAATGAGGAGATATTTTATACNATTAACCA	1983
Db	3171	GAAATGCAACATCATCTTCTTAAAGAGAAAAATGAGGAGATATTTTATACNATTAACCA	3230
Qy	1984	TTTAAAAACCCGCTATATTTCAATATGGAAGAAAAAANAAAAA 2030	
Db	3231	TTTAAAAACCCGCTATATTTCAATATGGAAGAAAAAANAAAAA 3276	
RESULT 7			
AB	ABS64022	standard; DNA, 3288 BP.	
XX	AC	ABS64022;	
XX	DT	15-NOV-2002 (first entry)	
XX	DE	Human breast tumour polynucleotide #471.	
XX	KW	Human; breast tumour protein; gene; ds; breast cancer; cytostatic;	
XX	OS	vaccine.	
XX	PN	Homo sapiens.	
XX	PD	US2002085998-A1.	
XX	PF	04-JUL-2002.	
XX	PR	13-APR-2001; 2001US-00834759.	
XX	PR	28-DEC-1998; 98US-00222575.	
XX	PR	02-APR-1999; 99US-00285480.	
XX	PR	23-JUN-1999; 99US-00393338.	
XX	PR	02-SEP-1998; 99US-00389681.	
XX	PR	03-NOV-1999; 99US-00433826.	
XX	PR	17-APR-2000; 2000US-00551621.	
XX	PR	08-JUN-2000; 2000US-00590751.	
XX	PR	22-JUN-2000; 2000US-00604287.	
XX	PR	20-JUL-2000; 2000US-00620405.	
PA	(CORI-) CORIXA CORP.		
PI	Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;		

PI	Henderson RA;	
XX	WPI; 2002-635657/68.	
DR	P-PSDB; ABG78924.	
XX		
PT	Novel breast cancer polynucleotides and polypeptides encoded by the	
PT	polynucleotides, useful for detecting the presence of breast cancer in a	
PT	patient, and in pharmaceutical compositions, for treating breast cancer.	
XX		
PS	Disclosure; Page 219-221; 247pp; English.	
XX		
CC	The invention relates to an isolated breast tumour polynucleotide and the	
CC	polypeptide it encodes. The polynucleotide and polypeptide are useful for	
CC	detecting the presence of breast cancer in a patient, and in	
CC	pharmaceutical compositions for treating breast cancer. The sequences are	
CC	useful for stimulating an immune response in a patient and can therefore	
CC	be used in production of vaccines. The sequences are also useful for	
CC	detecting the presence of a cancer in a patient, by obtaining a	
CC	biological sample from the patient, contacting the biological sample with	
CC	a composition of the invention and detecting the amount of polynucleotide	
CC	that hybridizes to the sample. This sequence represents a human breast	
CC	tumour polynucleotide of the invention	
XX		
SQ	Sequence 3288 BP; 1293 A; 564 C; 664 G; 761 T; 0 U; 6 Other;	
	Query Match 95.5%; Score 1938.4; DB 6; Length 3288;	
	Best Local Similarity 98.5%; Pred. No. 0;	
	Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;	
QY	5 TGCGTGTAAAGATGGTCTCTGAAGGCTAACTGGGAATGAAAGTTTCTATTCCAACTAA 64	
DB	1254 TCCTGTTAAAGATGGTCTCTGAAGGCTAACTGGGAATGAAAGTTTCTATTCCAACTAA 1313	
QY	65 AGCCTTAGAATTGATGACATGCAAACTTTCAAGAGAGAGCCTCCGAGAGGCATCTGC 124	
DB	1314 AGCCTTAGAATTGATGACATGCAAACTTTCAAGAGAGAGCCTCCGAGAGGCATCTGC 1373	
QY	125 CTTGAGGCTGCCATTGGAATGCAAAAGTCTGTTCCAAATAAAGCCTTGAAATTGAAGAA 184	
DB	1374 CTTGAGGCTGCCATTGGAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAA 1433	
QY	185 TGAACAAACATTGAGAGCAGATGATACCTCCATCAGAAATCCAAACAAAGGACTATGA 244	
DB	1434 TGAACAAACATTGAGAGCAGATGATACCTCCATCAGAAATCCAAACAAAGGACTATGA 1493	
QY	245 AGAAAGTTCTTGGGATCTCTGAGAGTCTCTGTGAGACTGTTTTCAGAGAGGATGTGTTT 304	
DB	1494 AGAAAGTTCTTGGGATCTCTGAGAGTCTCTGTGAGACTGTTTTCAGAGAGGATGTGTTT 1553	
QY	305 ACCCAAGGCTACACATCAAAAAGAAATAGATATAAATAAATGGAATAATTAGAGAGTCTCC 364	
DB	1554 ACCCAAGGCTACACATCAAAAAGAAATAGATATAAATAAATGGAATAATTAGAGAGTCTCC 1613	
QY	365 TGATAATGATGTTTCTGAGGCTCCCTGAGAGTGAAGTTTCTATTCCAACTAAGC 424	
DB	1614 TGATAATGATGTTTCTGAGGCTCCCTGAGAGTGAAGTTTCTATTCCAACTAAGC 1673	
QY	425 CTTAGAAATTGATGACATGCAAACTTTTCAAGAGAGAGCCTCCGAGAGGCATCTGCCTT 484	
DB	1674 CTTAGAAATTGATGACATGCAAACTTTTCAAGAGAGAGCCTCCGAGAGGCATCTGCCTT 1733	
QY	485 CGAGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGATGA 544	
DB	1734 CGAGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGATGA 1793	
QY	545 ACAACATTGAGAGCAGATCAGATGTTCCCTTTCAGAAATCAAAAACAAAGAGGTTGAAGA 604	
DB	1794 ACAACATTGAGAGCAGATCAGATGTTCCCTTTCAGAAATCAAAAACAAAGAGGTTGAAGA 1853	
QY	605 AAATCTTGGGATCTCGAGTCTCCGTGAGACTGTTTTCAGAGAGGATGTGTGTACC 664	
DB	1854 AAATCTTGGGATCTCGAGTCTCCGTGAGACTGTTTTCAGAGAGGATGTGTGTACC 1913	

QY	665 CAAGGCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAAATTAGAGATTCAACTAG 724	
DB	1914 CAAGGCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAAATTAGAGATTCAACTAG 1973	
QY	725 CCTATCAAAATCTTGGATACAGTTCAATCTTGTGAAAGAGCAAGGAACTTCAAAAAGA 784	
DB	1974 CCTATCAAAATCTTGGATACAGTTCAATCTTGTGAAAGAGCAAGGAACTTCAAAAAGA 2033	
QY	785 TCACCTGTGAACAACCTACAGGAAAAATGGAAACAAATGAAAAAGAAAGTTTGTGTACTGAA 844	
DB	2034 TCACCTGTGAACAACCTACAGGAAAAATGGAAACAAATGAAAAAGAAAGTTTGTGTACTGAA 2093	
QY	845 AAAGAACTGTGAGAGCAAAAGAAATAAATACAGTTAGAGAACCAAAAAGCTTAAATG 904	
DB	2094 AAAGAACTGTGAGAGCAAAAGAAATAAATACAGTTAGAGAACCAAAAAGCTTAAATG 2153	
QY	905 GGAACCAAGAGCTCTGCACTGTGAGATTGACCTTTAAACCAAGAGAGAGAGAGAGAGAA 964	
DB	2154 GGAACCAAGAGCTCTGCACTGTGAGATTGACCTTTAAACCAAGAGAGAGAGAGAGAA 2213	
QY	965 TGCCGATATATAATGAAAAATTTAGGGAAGAAATTAGGAAGAAATCGAAGAGCGAGTAG 1024	
DB	2214 TGCCGATATATAATGAAAAATTTAGGGAAGAAATTAGGAAGAAATCGAAGAGCGAGTAG 2273	
QY	1025 GAAAGAGTTAGAGTGAAACCAACCACTTGAACAGGCTCTCAGAAATCAAGATATAGAAAT 1084	
DB	2274 GAAAGAGTTAGAGTGAAACCAACCACTTGAACAGGCTCTCAGAAATCAAGATATAGAAAT 2333	
QY	1085 GAAGAGCTAGAAAATTAATTTGAAATCAGGTTTCTCACAATCAAGAAATGAATTTATCT 1144	
DB	2334 GAAGAGCTAGAAAATTAATTTGAAATCAGGTTTCTCACAATCAAGAAATGAATTTATCT 2393	
QY	1145 CTTACATCAAAATTCGATGTTGAAAAAGGAAATTCCTAAATCTGAAAAATGAGCCAC 1204	
DB	2394 CTTACATCAAAATTCGATGTTGAAAAAGGAAATTCCTAAATCTGAAAAATGAGCCAC 2453	
QY	1205 ACTGAAACCAACCACTACAGGAAAAAGGAAATAAATATCTTTGAGCACTTAAGATTAAAA 1264	
DB	2454 ACTGAAACCAACCACTACAGGAAAAAGGAAATAAATATCTTTGAGCACTTAAGATTAAAA 2513	
QY	1265 AGAAAGAAATGCTGAATCTCAGATGACCCCTAAATCTGAAGAGAGAAATCATTAATCTAAAG 1324	
DB	2514 AGAAAGAAATGCTGAATCTCAGATGACCCCTAAATCTGAAGAGAGAAATCATTAATCTAAAG 2573	
QY	1325 GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGATAGCTGAGAACCAATGCTCACTTC 1384	
DB	2574 GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGATAGCTGAGAACCAATGCTCACTTC 2633	
QY	1385 TAAATGAAGGAAACCAAGACAAAGAAATCTAGAGGCGAGAAATGGAATCACCACTCC 1444	
DB	2634 TAAATGAAGGAAACCAAGACAAAGAAATCTAGAGGCGAGAAATGGAATCACCACTCC 2693	
QY	1445 TAGACTGGCTTCTGCTGTACAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 1504	
DB	2694 TAGACTGGCTTCTGCTGTACAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 2753	
QY	1505 ACTGCTTTCCACATTTGAGAGATGCTGTTTGCAGAAAGAAATGAATGTTGATGTGAG 1564	
DB	2754 ACTGCTTTCCACATTTGAGAGATGCTGTTTGCAGAAAGAAATGAATGTTGATGTGAG 2813	
QY	1565 TAGTACCGATATATAAATGAGGTCCTCAATCAACCACTTTCTGAAGCTCAAGAGAAAT 1624	
DB	2814 TAGTACCGATATATAAATGAGGTCCTCAATCAACCACTTTCTGAAGCTCAAGAGAAAT 2872	
QY	1625 CCANAAGCCTTAAATTTCTCAATTTATGCGAGAGATGCTCTAGAGAAATCATTTGG 1684	
DB	2873 CCANAAGCCTTAAATTTCTCAATTTATGCGAGAGATGCTCTAGAGAAATCATTTGG 2932	
QY	1685 TTTTCAGGAACTGCAAAAAGAGACCAACCTGTAACCACTGTCATTAATGAAGAGAGCTGAA 1744	
DB	2933 TTTTCAGGAACTGCAAAAAGAGACCAACCTGTAACCACTGTCATTAATGAAGAGAGCTGAA 2991	
QY	1745 CACATGTTCAAAACGAAACAAGATNATGTGAACAAACACACTGANCAGCAGAGTCTCTA 1804	

Db	2992	CATCATGTATCAAAACGAACCAAGTAATGTGAACAAACACACTGAACGACGAGTCTCTA	3051
QY	1805	GATCAGAAATTAATTTCAACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCA	1864
Db	3052	GATCAGAAATTAATTTCAACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCA	3111
QY	1865	GCACATAAGAAAGCTGACAAACAAAAGCAAGATAACAATTTGATNTTCATNTTCTTGAGAG	1924
Db	3112	GCACATAA-GAAAGCTGACAAACAAAAGCAAGATAACAATTTGATNTTCATNTTCTTGAGAG	3170
QY	1925	GAATAATGC-NCATCATCTCTCTAAAGAGAAAAATGAGGAGATATTTTATTACNATAACCA	1983
Db	3171	GAATAATGCACATCACTCTCTAAAGAGAAAAATGAGGAGATATTTTATTACNATAACCA	3230
QY	1984	TTTAAAAAACCCGTATATTTCAATATGAAAAAANAANAANA 2030	
Db	3231	TTTAAAAA-CCGTATATATCAATATGAAAAAGAGAAAGCAGAAACA 3276	
RESULT 8			
ABT33234			
ID	ABT33234	standard; DNA; 3288 BP.	
XX	AC	ABT33234;	
XX	AC		
DT	15-MAY-2003	(first entry)	
XX			
DE	Human tumour-related DNA sequence - SEQ ID No 490.		
XX			
KW	Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;		
KW	tumour; breast cancer; cancer; immune response stimulation.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200283956-A1.		
PD			
XX	24-OCT-2002.		
XX	15-APR-2002; 2002WO-USQ12378.		
XX			
PR	13-APR-2001; 2001US-00834759.		
PR	07-DEC-2001; 2001US-00007805.		
PR	13-FEB-2002; 2002US-00076622.		
XX			
XX	(CORI-) CORIXA CORP.		
PA			
PI	Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;		
PI	Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;		
PI	Vedvick TS, McNeill PD, Durham M;		
XX			
DR	WPI; 2003-103376/09.		
XX			
PT	New polypeptide and polynucleotide useful for stimulating and/or		
PT	expanding T cells specific for a tumor protein and treating breast		
PT	cancer.		
XX			
PS	Disclosure; Page 307-308; 375pp; English.		
XX			
CC	The invention comprises a method of stimulating and/or expanding T cells		
CC	specific for a tumour protein. The invention further comprises human		
CC	nucleic acids and proteins that are associated with tumours (e.g. breast		
CC	cancer). The method and sequences of the invention are useful for		
CC	stimulating and/or expanding T cells specific for a tumour protein,		
CC	detecting the presence of cancer, stimulating an immune response in a		
CC	patient and treating breast cancer. The present DNA sequence represents a		
CC	human tumour-related DNA sequence		
XX			
SQ	Sequence 3288 BP; 1293 A; 564 C; 664 G; 761 T; 0 U; 6 Other;		
Query Match	95.5%; Score 1938.4; DB 7; Length 3288;		
Best Local Similarity	98.5%; Pred. No. 0;		
Matches 1997; Conservative	4; Mismatches 21; Indels 5; Gaps 5;		

DE	Human cDNA encoding breast cancer protein B726P alternative splice form.	
XX	Human; ss; breast cancer protein; tumour; cancer; cytostatic;	
KW	gene therapy.	
XX	Homo sapiens.	
OS	WO200179286-A2.	
PN	25-OCT-2001.	
PD	12-APR-2001; 2001WO-US012164.	
PF	17-APR-2000; 2000US-00551621.	
XX	08-JUN-2000; 2000US-00590751.	
PR	22-JUN-2000; 2000US-00604287.	
PR	20-JUL-2000; 2000US-00620405.	
XX	(CORI-) CORIXA CORP.	
PA	Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;	
XX	WPI; 2001-611721/70.	
PI	P-PSDB; AAU33351.	
XX	Breast Tumor Proteins and nucleic acids useful for the prevention,	
XX	diagnosis and treatment of breast cancer.	
XX	Claim 1; Page 280-281; 297pp; English.	
PS	The invention relates to isolated breast tumour proteins and nucleic	
XX	acids that encode them, including immunogenic fragments of the proteins.	
XX	Also included are expression vectors expressing the proteins, transformed	
CC	cells and antibodies raised against the proteins or an antigen presenting	
CC	cell expressing the protein. The proteins and nucleic acids may be used	
CC	in the prevention, diagnosis and treatment of diseases associated with	
CC	inappropriate breast tumour protein expression, i.e. breast tumours and	
CC	breast cancer e.g by gene therapy. The nucleic acids and their	
CC	complements may also be used as DNA probes in diagnostic assays to detect	
CC	and quantitate the presence of similar nucleic acids in samples, and	
CC	therefore which patients may be in need of restorative therapy. The	
CC	proteins, nucleic acids and antibodies may be used in assays to identify	
CC	modulators (e.g. antagonists) of breast tumour protein expression and	
CC	activity. The antibodies and antagonists may also be used to down	
CC	regulate expression and activity. The antibodies may also be used as	
CC	diagnostic agents for detecting the presence of the proteins in samples	
CC	(e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immuno-	
CC	purification diagnostic techniques. The present sequence is a cDNA from a	
CC	breast tumour cDNA library isolated by subtractive hybridisation against	
CC	a normal breast cDNA library and encodes a breast tumour protein of the	
CC	invention. The present sequence is also a splice variant	
XX	Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;	
SQ	Query Match 95.5%; Score 1938.4; DB 4; Length 3865;	
	Best Local Similarity 98.5%; Pred. No. 0;	
	Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;	
QY	5 TGCCCTTAAGATGGTCTTCTGAAGCGTAACCTGCGGAATGAAAGTTCTATTCCAACTAA 64	
Db	1526 TCCTGTTAAAGATGGTCTTCTGAAGCGTAACCTGCGGAATGAAAGTTCTATTCCAACTAA 1585	
QY	65 AGCCTTAGAATTGATGGACATGCAACTTCAAGACAGAGCTCCCGAGAGAGCCATCTGC 124	
Db	1586 AGCCTTAGAATTGATGGACATGCAACTTCAAGACAGAGCTCCCGAGAGAGCCATCTGC 1645	
QY	125 CTTGAGAGCTGCCATTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 184	
Db	1646 CTTGAGAGCTGCCATTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1705	
QY	185 TGAACAAAATTTGAGAGCAGATGAGATCTCCATCAGATCCCAACAAAAGGACTATGA 244	
Db	1706 TGAACAAAATTTGAGAGCAGATGAGATCTCCATCAGATCCCAACAAAAGGACTATGA 1765	

RESULT 9
AAS47411
ID AAS47411 standard; cDNA; 3865 BP.
XX
AC
AAS47411;
XX
DT
18-DEC-2001 (first entry)
XX

245 AGAAGTTCTTGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCACAGAGGATGTGTGTTT 304
Db
1766 AGAAGTTCTTGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCACAGAGGATGTGTGTTT 1825
Qy
305 ACCAAGGCTACACATCAAAAAGAAATAGATAAATAAATGGAATTTAGAGAGTCTCC 364
Db
1826 ACCAAGGCTACACATCAAAAAGAAATAGATAAATAAATGGAATTTAGAGAGTCTCC 1885
Qy
365 TGATATGATGGTTTCTGAGGCTCCCTCAGAAATGAAAGTTTCTATTCCAACTAAAGC 424
Db
1886 TGATATGATGGTTTCTGAGGCTCCCTCAGAAATGAAAGTTTCTATTCCAACTAAAGC 1945
Qy
425 CTTAGAAATTGATGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAAGCCATCTCCCTT 484
Db
1946 CTTAGAAATTGATGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAAGCCATCTCCCTT 2005
Qy
485 CGAGCCTGCCATTGAATGCAAAAGTCTGTTCCAAATTAAGCCTTGGAAATGGAAGTGA 544
Db
2006 CGAGCCTGCCATTGAATGCAAAAGTCTGTTCCAAATTAAGCCTTGGAAATGGAAGTGA 2065
Qy
545 ACAAACTTGAAGCAGATCAGATGTTCCCTTTCAGAAATCAAAACAAAAGAGGTTGAAGA 604
Db
2066 ACAAACTTGAAGCAGATCAGATGTTCCCTTTCAGAAATCAAAACAAAAGAGGTTGAAGA 2125
Qy
605 AAATCTTGGATTTCTGAGAGTCTCCGTGAGACTGTTTTCAGAGAGGATGTGTGTACC 664
Db
2126 AAATCTTGGATTTCTGAGAGTCTCCGTGAGACTGTTTTCAGAGAGGATGTGTGTACC 2185
Qy
665 CAAGGCTACACATCAAAAAGAAATGGAATAAATTAAGTGGAAATTTAGAAATCAACTAG 724
Db
2186 CAAGGCTACACATCAAAAAGAAATGGAATAAATTAAGTGGAAATTTAGAAATCAACTAG 2245
Qy
725 CCTATCAAAAATCTTGGATACAGTTTCATCTTGTGAAAGAGCAAGGGAATCTCAAAAGA 784
Db
2246 CCTATCAAAAATCTTGGATACAGTTTCATCTTGTGAAAGAGCAAGGGAATCTCAAAAGA 2305
Qy
785 TCATCTGCAACACGTCAGAGAAATGGAACAAATGAAAGAGAGTTTGTGTACTGAA 844
Db
2306 TCATCTGCAACACGTCAGAGAAATGGAACAAATGGAAGAGAGTTTGTGTACTGAA 2365
Qy
845 AARGAACTGTCAGAGCAAAAGAAATTAATATCACGTTAGAGAACCAAAAAGTTAAATG 904
Db
2366 AARGAACTGTCAGAGCAAAAGAAATTAATATCACGTTAGAGAACCAAAAAGTTAAATG 2425
Qy
905 GGAACAGAGCTCTGAGTGTGAGATTGACCTTTAAACCAAGAGAGAGAGAGAGAA 964
Db
2426 GGAACAGAGCTCTGAGTGTGAGATTGACCTTTAAACCAAGAGAGAGAGAGAGAA 2485
Qy
965 TGCCGATATATTAATGAAAAATTTAGGGAAGAATTAGGAAGATCGAAGAGCAGCATAG 1024
Db
2486 TGCCGATATATTAATGAAAAATTTAGGGAAGAATTAGGAAGATCGAAGAGCAGCATAG 2545
Qy
1025 GAAGAGTTAGAGTGAACACAACTTGAACAGGCTCTCAGATACAGATATAGATTT 1084
Db
2546 GAAGAGTTAGAGTGAACACAACTTGAACAGGCTCTCAGATACAGATATAGATTT 2605
Qy
1085 GAAGAGTTAGAGTGAATTTGAATCAGGTTTCTCACACTCATGAAAAATGAAATTTATCT 1144
Db
2606 GAAGAGTTAGAGTGAATTTGAATCAGGTTTCTCACACTCATGAAAAATGAAATTTATCT 2665
Qy
1145 CTTACATGAAAATTTGATGTTGAAAAGGAAATTTGCCATGCTAAACTGGAATAGCCAC 1204
Db
2666 CTTACATGAAAATTTGATGTTGAAAAGGAAATTTGCCATGCTAAACTGGAATAGCCAC 2725
Qy
1205 ACTGAAACACCAATACCAAGGAAAGGAAATTAATATCTTTGAGGACATTAAGATTTTAAA 1264
Db
2726 ACTGAAACACCAATACCAAGGAAAGGAAATTAATATCTTTGAGGACATTAAGATTTTAAA 2785
Qy
1265 AGAAAAGATGCTGAATCTGAGTACCCCTTAAACTGAAAGAGGAATCATTAACATAAG 1324
Db
2786 AGAAAAGATGCTGAATCTGAGTACCCCTTAAACTGAAAGAGGAATCATTAACATAAG 2845

1325 GGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATAGCTGAGAACAAATGTCTACTTC 1384
Db
2846 GGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATAGCTGAGAACAAATGTCTACTTC 2905
Qy
1385 TAAATTTGAAGAAAAACAGACAAAGAAATCTAGAGCGAGAAATTTGAATCACACCATCC 1444
Db
2906 TAAATTTGAAGAAAAACAGACAAAGAAATCTAGAGCGAGAAATTTGAATCACACCATCC 2965
Qy
1445 TAGACTGGCTTCTGCTGTACAAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 1504
Db
2966 TAGACTGGCTTCTGCTGTACAAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 3025
Qy
1505 ACCTGCTTTCCACATTTGAGAGAGATGCTTTTTCAAAGAAAAATGATCTGATGTGAG 1564
Db
3026 ACCTGCTTTCCACATTTGAGAGAGATGCTTTTTCAAAGAAAAATGATCTGATGTGAG 3085
Qy
1565 TAGTACCGATATATAAACAATGAGGTGCTTCCATCAACCACTTTCTGAAAGCTCAAGAGAAAT 1624
Db
3086 TAGTA-CGATATATAAACAATGAGGTGCTTCCATCAACCACTTTCTGAAAGCTCAAGAGAAAT 3144
Qy
1625 CCANAGCCTAAAAATTAATCTCAATTTATGAGAGAGATGCTTCTTAAGAGAAAAATACATTGG 1684
Db
3145 CCANAGCCTAAAAATTAATCTCAATTTATGCMGAGATGCTTCTTAAGAGAAAAATACATTGG 3204
Qy
1685 TTTCAAGGAACATGCAAAAGAGACCAACCTGAAACACAGTGTCAATGAAAGAAAGCTGAA 1744
Db
3205 TTTCA-GAACATGCAAAAGAGACCAACCTGAAACACAGTGTCAATGAAAGAAAGCTGAA 3263
Qy
1745 CACATGTTNCAANGAACCAAGATNATGTGAAACAAACACACTGANCAGCAGAGTCTCTA 1804
Db
3264 CACATGTTNCAANGAACCAAGATNATGTGAAACAAACACACTGANCAGCAGAGTCTCTA 3323
Qy
1805 GATCAAGAAATTTTCAACTACAAAGCAAAATATGTGGCTTCAACAGCAATTTAGTTTCA 1864
Db
3324 GATCAAGAAATTTTCAACTACAAAGCAAAATATGTGGCTTCAACAGCAATTTAGTTTCA 3383
Qy
1865 GCACATNANGAAAGCTGACACAAAGCAAGATNATGAAATTTCAATTTCTTGTGAGAG 1924
Db
3384 GCACATAA-GAAAGCTGACACAAAGCAAGATNATGAAATTTCAATTTCTTGTGAGAG 3442
Qy
1925 GAAATGTC-NCATCATCTTCTAAAGAGAAAAATGAGGAGATTTTATTTACNATAACCA 1983
Db
3443 GAAATGCAACATCATCTTCTAAAGAGAAAAATGAGGAGATTTTATTTACATTAACCA 3502
Qy
1984 TTTAAAAAACCCGTTATTTTCAATATGAAAAAANAAAAA 2030
Db
3503 TTTAAAAAAC-CCGTATATCAATATGAAAAAAGAAAGACAGAAACA 3548

RESULT 10
ABS64012
ID ABS64012 standard; cdNA; 3865 BP.
XX
AC ABS64012;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human breast tumour polynucleotide #464.
XX
KW Human; breast tumour protein; gene; ss; breast cancer; cytostatic;
XX
OS Homo sapiens.
XX
PN US2002085998-A1.
XX
PD 04-JUL-2002.
XX
PP 13-APR-2001; 2001US-00834759.
XX
PR 28-DEC-1998; 98US-00222575.
PR 02-APR-1999; 99US-00285480.
PR 23-JUN-1999; 99US-00393338.

PR 02-SEP-1999; 99US-00389681.
 PR 03-NOV-1999; 99US-00433826.
 PR 17-APR-2000; 2000US-00551621.
 PR 08-JUN-2000; 2000US-00590751.
 PR 22-JUN-2000; 2000US-00604287.
 PR 20-JUL-2000; 2000US-00620405.
 XX (CORI-) CORIXA CORP.
 FA
 XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
 PI Henderson RA;
 PI
 XX WPI; 2002-635657/68.
 DR P-PSDB; ABG78918.
 DR
 XX
 PT Novel breast cancer polynucleotides and polypeptides encoded by the
 PT polynucleotides, useful for detecting the presence of breast cancer in a
 PT patient, and in pharmaceutical compositions, for treating breast cancer.
 XX
 XX Claim 1; Page 207-208; 247pp; English.
 XX
 CC The invention relates to an isolated breast tumour polynucleotide and the
 CC polypeptide it encodes. The polynucleotide and polypeptide are useful for
 CC detecting the presence of breast cancer in a patient, and in
 CC pharmaceutical compositions for treating breast cancer. The sequences are
 CC useful for stimulating an immune response in a patient and can therefore
 CC be used in production of vaccines. The sequences are also useful for
 CC detecting the presence of a cancer in a patient, by obtaining a
 CC biological sample from the patient, contacting the biological sample with
 CC a composition of the invention and detecting the amount of polynucleotide
 CC that hybridizes to the sample. This sequence represents a human breast
 CC tumour polynucleotide of the invention
 XX
 SQ Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;
 Query Match 95.5%; Score 1938.4; DB 6; Length 3865;
 Best Local Similarity 98.5%; Pred No 0;
 Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;
 5 TGCCTTAAAGATGGTCTTCTGAAGGCTAACTCGGAATGAAAGTTCTATTCCAACTAA 1585
 1526 TCCTGTTAAAGATGGTCTTCTGAAGGCTAACTCGGAATGAAAGTTCTATTCCAACTAA 1585
 65 AGCTTAAAGATGGTCTTCTGAAGGCTAACTCGGAATGAAAGTTCTATTCCAACTAA 164
 1586 AGCTTAAAGATGGTCTTCTGAAGGCTAACTCGGAATGAAAGTTCTATTCCAACTAA 1645
 125 CTTGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATGAAAGCCTTGGAAATGGAAGAA 184
 1646 CTTGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATGAAAGCCTTGGAAATGGAAGAA 1705
 185 TGAACAAACATTGAGACAGATGAGATCTCCCATGAGATCCAAACAAAGGACTATGA 244
 1706 TGAACAAACATTGAGACAGATGAGATCTCCCATGAGATCCAAACAAAGGACTATGA 1765
 245 AGAAAGTCTTGGGATCTCGAGAGTCTCTGTGAGCTGTTTCCAGAGAGGATGTTGTTT 304
 1766 AGAAAGTCTTGGGATCTCGAGAGTCTCTGTGAGCTGTTTCCAGAGAGGATGTTGTTT 1825
 305 ACCAAGGCTACATCAAAAGAAATAGATAAATAAATGGAATAATGGAAGGCTCC 364
 1826 ACCAAGGCTACATCAAAAGAAATAGATAAATAAATGGAATAATGGAAGGCTCC 1885
 365 TGATAATGATGGTCTTCTGAAGGCTCCCTGAGAGTCTCTGAGATGTTTCCAACTAAAGC 424
 1886 TGAATAATGATGGTCTTCTGAAGGCTCCCTGAGAGTCTCTGAGATGTTTCCAACTAAAGC 1945
 425 CTTGAAATGATGAGATGCAAACTTTCAAGCAGAGAGCTCCCGAGAGGCTATCGCCTT 484
 1946 CTTGAAATGATGAGATGCAAACTTTCAAGCAGAGAGCTCCCGAGAGGCTATCGCCTT 2005
 485 CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATGAAAGCCTTGGAAATGGAAGATGA 544

2006 CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATGAAAGCCTTGGAAATGGAAGATGA 2065
 545 ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGATGTAACAAACAAAGAGGTTGAAGA 604
 2066 ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGATGTAACAAACAAAGAGGTTGAAGA 2125
 605 AAATTTCTTGGGATCTCGAGAGTCTCGGTGAGACTGTTTTCACAGAGGATGTTGTGTACC 664
 2126 AAATTTCTTGGGATCTCGAGAGTCTCGGTGAGACTGTTTTCACAGAGGATGTTGTGTACC 2185
 665 CAAGGCTACACATCAAAAGAAATGATAAATAAGTGGAAATTAGAGATTCACACTAG 724
 2186 CAAGGCTACACATCAAAAGAAATGATAAATAAGTGGAAATTAGAGATTCACACTAG 2245
 725 CCTATCAAAATCTTGGATACAGTTCATTTCTGTAAGAGCAAGGAACTTCAAAAGA 784
 2246 CCTATCAAAATCTTGGATACAGTTCATTTCTGTAAGAGCAAGGAACTTCAAAAGA 2305
 785 TCACGTGGAACAACGTTACAGGAAATGGAACAAATGGAAGAACTTGTGTACTGAA 844
 2306 TCACGTGGAACAACGTTACAGGAAATGGAACAAATGGAAGAACTTGTGTACTGAA 2365
 845 AAGAAACTCTCAGAGCAAAAGAAATGGAACAAATGGAAGAACTTGTGTACTGAA 904
 2366 AAGAAACTCTCAGAGCAAAAGAAATGGAACAAATGGAAGAACTTGTGTACTGAA 2425
 905 GGAACAAAGAGTCTCGAGTGTGAGTCTTAAACCAAGAGAGAGAGAGAGAGAGAGAGAG 964
 2426 GGAACAAAGAGTCTCGAGTGTGAGTCTTAAACCAAGAGAGAGAGAGAGAGAGAGAGAG 2485
 965 TGCCGATATATTAATGAAAGAAATGGAAGAAATGGAAGAACTTGTGTACTGAA 1024
 2486 TGCCGATATATTAATGAAAGAAATGGAAGAACTTGTGTACTGAA 2545
 1025 GAAAGGTTGAGAGTGAAGCAACAACTTGAAGAGGCTCTCAGAGATCAAGATATAGATTT 1084
 2546 GAAAGGTTGAGAGTGAAGCAACAACTTGAAGAGGCTCTCAGAGATCAAGATATAGATTT 2605
 1085 GAAAGGTTGAGAGTGAAGCAACAACTTGAAGAGGCTCTCAGAGATCAAGATATAGATTT 1144
 2606 GAAAGGTTGAGAGTGAAGCAACAACTTGAAGAGGCTCTCAGAGATCAAGATATAGATTT 2665
 1145 CTTACATGAAATTCATGTTGAAAGAGGAAATGCGCATGCTAAACTGGAAGATAGCCAC 1204
 2666 CTTACATGAAATTCATGTTGAAAGAGGAAATGCGCATGCTAAACTGGAAGATAGCCAC 2725
 1205 ACTGAAACCAACATACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1264
 2726 ACTGAAACCAACATACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2785
 1265 AGAAAGAAATCTGAACTTCAAGATGAGCCTGAAAGAGGAAATCAATTAACCTAAAG 1324
 2786 AGAAAGAAATCTGAACTTCAAGATGAGCCTGAAAGAGGAAATCAATTAACCTAAAG 2845
 1325 GGCATCTCAATATAGTGGGAGCTTAAAGTCTGATAGCTGAGAGACATGCTCACTTC 1384
 2846 GGCATCTCAATATAGTGGGAGCTTAAAGTCTGATAGCTGAGAGACATGCTCACTTC 2905
 1385 TAAATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1444
 2906 TAAATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2965
 1445 TAGACTGCTTCTGCTGTACAGACCATGATCAAAATTTGTGACATCAAGAGAGAGAGAGAG 1504
 2966 TAGACTGCTTCTGCTGTACAGACCATGATCAAAATTTGTGACATCAAGAGAGAGAGAGAG 3025
 1505 ACCTGCTTTCCACATTTGAGAGAGATGCTGTTTTCGAAAGAGAGAGAGAGAGAGAGAG 1564
 3026 ACCTGCTTTCCACATTTGAGAGAGATGCTGTTTTCGAAAGAGAGAGAGAGAGAGAGAG 3085
 1565 TAGTACCGATATTAACAAATGAGGCTGCTCCATCAACCACTTTCTGAGAGCTCAAGAGAGAT 1624
 3086 TAGTA -CGATATATAACAAATGAGGCTGCTCCATCAACCACTTTCTGAGAGCTCAAGAGAGAT 3144

Dd	2426	GGAAACAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAAGAGAGAAAGAAA	2488
Qy	965	TGCCGATATATTAAATGAAAAATTAGGGAAGAAATTTAGGAAGAAATCGAAGAGCAGCATAG	1024
Dd	2486	TGCCGATATATTAAATGAAAAATTAGGGAAGAAATTTAGGAAGAAATCGAAGAGCAGCATAG	2545
Qy	1025	GAAGAGATTAGAGTGAAGACAACTGCAACAGGCTCTCAGAAATCAAGATATAGAAAT	1084
Dd	2546	GAAGAGATTAGAGTGAAGACAACTGCAACAGGCTCTCAGAAATCAAGATATAGAAAT	2605
Qy	1085	GAAGAGTGTAGAAAGTAATTTGAATCAGSTTTCTCACTCATGAAAAATGAAATTTATCT	1144
Dd	2606	GAAGAGTGTAGAAAGTAATTTGAATCAGSTTTCTCACTCATGAAAAATGAAATTTATCT	2665
Qy	1145	CTTTACATGAAAAATTGCATGTTGAAAAAGGAAATTTGCCATGCTAAAACTGGAATAGCCAC	1204
Dd	2666	CTTTACATGAAAAATTGCATGTTGAAAAAGGAAATTTGCCATGCTAAAACTGGAATAGCCAC	2725
Qy	1205	ACTGAAACCAATACACAGAAAGGAAATAAATACTTTTGAGGACATTAAGATTTTAAA	1264
Dd	2726	ACTGAAACCAATACACAGAAAGGAAATAAATACTTTTGAGGACATTAAGATTTTAAA	2785
Qy	1265	AGAAAAAATGCTGAACTTCAGATGACCCATAAATCTGAAAGAGGAATCATTAACATAAAG	1324
Dd	2786	AGAAAAAATGCTGAACTTCAGATGACCCATAAATCTGAAAGAGGAATCATTAACATAAAG	2845
Qy	1325	GGCATCTCAATATAGTGGGAGCTTAAAGTTCGTATAGCTGAGAACACAATGCTCACTTC	1384
Dd	2846	GGCATCTCAATATAGTGGGAGCTTAAAGTTCGTATAGCTGAGAACACAATGCTCACTTC	2905
Qy	1385	TAAATTGAAAGGAAAAACAAGACAAAGAAATTACTAGAGGCGAGAAATTCGAATCACACCATCC	1444
Dd	2906	TAAATTGAAAGGAAAAACAAGACAAAGAAATTACTAGAGGCGAGAAATTCGAATCACACCATCC	2965
Qy	1445	TAGACTGGCTTCGTCTACAGACCATGATCAAAATTTGCATCAAGAAAAAGTCAAGA	1504
Dd	2966	TAGACTGGCTTCGTCTACAGACCATGATCAAAATTTGCATCAAGAAAAAGTCAAGA	3025
Qy	1505	ACCTGCTTTCCACATTCAGAGAGATGCTTGTTGCAAGAAAAAATGAATGTTGATGTGAG	1564
Dd	3026	ACCTGCTTTCCACATTCAGAGAGATGCTTGTTGCAAGAAAAAATGAATGTTGATGTGAG	3085
Qy	1565	TAGTACCGATATATAAACAATGAGTGTCTCATCAACCACTTCTGAGGCTCAAGGAAAT	1624
Dd	3086	TAGTACCGATATATAAACAATGAGTGTCTCATCAACCACTTCTGAGGCTCAAGGAAAT	3144
Qy	1625	CCANAAGCCTAAAAATTAATCTCAATTTATGCAGAGATGCTCTTAAGAGAAAAATACATTGG	1684
Dd	3145	CCANAAGCCTAAAAATTAATCTCAATTTATGCAGAGATGCTCTTAAGAGAAAAATACATTGG	3204
Qy	1685	TTTTCAGAACATGACACAAAGAGCCACGTTGAACACAGTGTCAATGAGGAGCTGAA	1744
Dd	3205	TTTTCA-GAATATACAAAGAGACCAACGTTGAACACAGTGTCAATGAGGAGCTGAA	3263
Qy	1745	CACATGNTCAAACGAAACAGATNATGTGAACAAACACACTGANCAGAGGAGTCTCTA	1804
Dd	3264	CACATGNTCAAACGAAACAGATNATGTGAACAAACACACTGANCAGAGGAGTCTCTA	3323
Qy	1805	GATCAGAAATTTATTTCACTACAAAGCAAAATATGTGGCTTCAACAGCAATTAGTTTAT	1864
Dd	3324	GATCAGAAATTTATTTCACTACAAAGCAAAATATGTGGCTTCAACAGCAATTAGTTTAT	3383
Qy	1865	GCACATAANGAAGCTGACACAAAGCAAGATAACAAATTTGATNTTCTTTGAGAG	1924
Dd	3384	GCACATAA-GAAAGCTGACACAAAGCAAGATAACAAATTTGATNTTCTTTGAGAG	3442
Qy	1925	GAAATGTC-NCATCATCTTCTTAAAGAGAAAAATGAGGAGATATTTNATACNATAACCA	1983
Dd	3443	GAAATGCAACATCATCTTCTTAAAGAGAAAAATGAGGAGATATTTNATACNATAACCA	3502
Qy	1984	TTTTAAAAACCCGTATATTTTCAATATGAAAAAANAAAAA	2030
Dd	3503	TTTTAAAAA-CCGTATATATCAATATGAAAAAGAAAGACAGAAACA	3548

RESULT 12	
ADE44426	
ID ADE44426 standard; cDNA; 3865 BP.	
XX AC	
AC ADE44426;	
XX 29-JAN-2004 (first entry)	
DT XX	
XX Human cDNA associated with breast cancer #464.	
DE XX	
XX human; ss; gene; breast tumour; cancer; vaccine; T cell stimulator;	
KW KW	T cell expander.
OS OS	Homo sapiens.
XX US2003104366-A1.	
EV XX	
PD 05-JUN-2003.	
XX 17-APR-2000; 2000US-00551621.	
FF 28-DEC-1998; 98US-00222575.	
XX 02-APR-1999; 99US-00285480.	
PR 23-JUN-1999; 99US-00339338.	
PR 02-SEP-1999; 99US-00389681.	
ER 03-NOV-1999; 99US-00433826.	
XX (JIAN/) JIANG Y.	
PA (DILL/) DILLON D C.	
PA (MITC/) MITCHAM J L.	
PA (XUJJ/) XU J.	
PA (HARL/) HARLOCKER S L.	
XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL;	
EI WPI; 2004-020270/02.	
XX P-PSDB; ADE44427.	
DR Novel isolated polypeptide comprising immunogenic portion of breast tumor	
PT protein or its variant, useful for formulating vaccines for inhibiting	
ET cancer development in a patient.	
XX Claim 5; SEQ ID NO 474; 217pp; English.	
PS The invention relates to an isolated polypeptide comprising at least an	
XX immunogenic portion of a breast tumour protein. The polynucleotide, its	
CC polypeptide, its antibody, a pharmaceutical composition comprising the	
CC fusion protein or the polynucleotide encoding it, a vaccine comprising	
CC the fusion protein or the polynucleotide encoding it, an isolated T cell	
CC population comprising T cells specific for a breast tumour protein, and a	
CC method for removing tumour cells from a biological sample is useful for	
CC inhibiting the development of a cancer in a patient. The polypeptide is	
CC useful for stimulating and/or expanding T cells specific for a breast	
CC tumour protein. Stimulating and/or expanding T cells specific for a	
CC breast tumour protein is useful for inhibiting the development of a	
CC cancer in a patient. The method additionally involves the step of cloning	
CC at least one proliferated cell and then administering the cloned T cells	
CC to the patient. The present sequence represents a cDNA associated with	
XX breast cancer.	
XX Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;	
SQ Best Local 95.5%; Score 1938.4; DB 10; Length 3865;	
Query Match Similarity 98.5%; Pred. No. 0;	
Best Local Similarity 98.5%; Pred. No. 0;	
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;	
QY 5 TGCGGTAAAGATGGCTTCTTGGAAGGCTTAAGTCGGGAATGAAGTTCTATTCCAATAA 64	
Db 1526 TCCTGTTAAAGATGGCTTCTTGGAAGGCTTAAGTCGGGAATGAAGTTCTATTCCAATAA 158	
OY 65 AGCCTTAGAATTGATGGACATGCACAACTTTCAAAGCAGAGCCTCCCAGAGAGCATCTGC 124	

Db 2448 ----- 2447
QY 1025 GAAAGAGTTAGAAAGTGAACAACTTGAACAGGCTCTCAGATACAGATATAGAATT 1084
Db 2448 ----- 2447
QY 1085 GAAGAGTGTAGAAAGTAATTGAACTTCTCAGCTTCTCAGCTGAAATGAAATTAATCT 1144
Db 2448 ----- 2447
QY 1145 CTTACATGAAATTTGCATGTTGAAAGGAAATTTGCCATGCTTAAACTGAAATAGCCAC 1204
Db 2482 CTTACATGAAATTTGCATGTTGAAAGGAAATTTGCCATGCTTAAACTGAAATAGCCAC 2541
QY 1205 ACTGAAACACCAATACAGAGAAAGAAATTAATTAATTTGAGGACATTAAGATTTTAA 1264
Db 2542 ACTGAAACACCAATACAGAGAAAGAAATTAATTAATTTGAGGACATTAAGATTTTAA 2601
QY 1265 AGAAAGAAATGCTGAACTTCAGATGACCTTAAACTGAAAGAGAAATTAATTAATTAAG 1324
Db 2602 AGAAAGAAATGCTGAACTTCAGATGACCTTAAACTGAAAGAGAAATTAATTAATTAAG 2661
QY 1325 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACCAATGCTCACTTC 1384
Db 2662 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACCAATGCTCACTTC 2721
QY 1385 TAAATTGAAGGAAACAAAGCAAAAGAAATTAATTAAGGAGGAGAAATTAATTAATTAAG 1444
Db 2722 TAAATTGAAGGAAACAAAGCAAAAGAAATTAATTAAGGAGGAGAAATTAATTAATTAAG 2781
QY 1445 TAGACTGGCTTCTGCTGTAAGACCAATGATCAAAATTTGACATCAAGAAAGTCAAGA 1504
Db 2782 TAGACTGGCTTCTGCTGTAAGACCAATGATCAAAATTTGACATCAAGAAAGTCAAGA 2841
QY 1505 ACCTGCTTTCACATTCAGAGAGATGCTTTGCAAGAAAGAAATTAATTAATTAAGTGG 1564
Db 2842 ACCTGCTTTCACATTCAGAGAGATGCTTTGCAAGAAAGAAATTAATTAATTAAGTGG 2901
QY 1565 TAGTACCGATATATACAAATGAGTGTCTCCATCAACCACTTCTGAGCTCAAGGAAAT 1624
Db 2902 TAGTA-CGATATATACAAATGAGTGTCTCCATCAACCACTTCTGAGCTCAAGGAAAT 2960
QY 1625 CCNAAAGCTTAAATTAATCTCAATTAATGACGAGATGCTTAAGAGAAATTAATTAAGTGG 1684
Db 2961 CCNAAAGCTTAAATTAATCTCAATTAATGACGAGATGCTTAAGAGAAATTAATTAAGTGG 3020
QY 1685 TTTGAGGAAATGCAAGAGAGACCAAGCTGAAACACAGTGTCAAAATGAAGGAGCTGAA 1744
Db 3021 TTTGCA-GAATGCAAGAGAGACCAAGCTGAAACACAGTGTCAAAATGAAGGAGCTGAA 3079
QY 1745 CACATGTTTCAAGACAGATGATGTAACAAACACACTGACAGGAGGAGTCTCTA 1804
Db 3080 CACATGTTTCAAGACAGATGATGTAACAAACACACTGACAGGAGGAGTCTCTA 3139
QY 1805 GATCAGAAATTAATTTCAACTACAAAGCAAAATATGCTTCAACAGCAATTAATTCAT 1864
Db 3140 GATCAGAAATTAATTTCAACTACAAAGCAAAATATGCTTCAACAGCAATTAATTCAT 3199
QY 1865 GCACATRANGAAGCTGACACAAAGCAAGATCAATTAATTAATTTCTTCTGAGAG 1924
Db 3200 GCACATAA-GAAGAGCTGACACAAAGCAAGATCAATTAATTAATTTCTTCTGAGAG 3258
QY 1925 GAAATGTC-NCATCATCTTCTTAAAGGAGAAATGAGGAGATATTTNATTACNATAACCA 1983
Db 3259 GAAATGTCACATCATCTCTTAAAGGAGAAATGAGGAGATATTTNATTACNATAACCA 3318
QY 1984 TTTTAAAGCCGTTATTTCAATATGAAATTAATTAATTAATTAATTAATTAATTAATTA 2030
Db 3319 TTTTAAAGCCGTTATTTCAATATGAAATTAATTAATTAATTAATTAATTAATTAATTA 3364

RESULT 15
AAI67218

ID AAI67218 standard; cDNA; 3681 BP.
XX AC AAI67218;
XX DT 11-FEB-2002 (first entry)
XX DE B726P splice variant encoding cDNA.
XX KW Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
XX KW cancer; B726P; ss.
XX OS Homo sapiens.
XX PN W0200175171-A2.
XX PD 11-OCT-2001.
XX PF 02-APR-2001; 2001WO-US010631.
XX PR 03-APR-2000; 2000US-0194241P.
XX PR 20-JUL-2000; 2000US-0219862P.
XX PR 27-JUL-2000; 2000US-0221300P.
XX PR 18-DEC-2000; 2000US-0256592P.
XX PA (CORI-) CORIXA CORP.
XX PI Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;
XX DR P-PSDB; AAG65983.
XX DR WPI; 2001-626449/72.
XX PT Identifying tissue (tumor)-specific polynucleotides overexpressed in
XX PT tissue of interest as compared to control tissue, for detecting cancer
XX PT cells in patient, comprises DNA microarray analysis or quantitative
XX PT polymerase chain reaction.
XX PS Claim 4; Page 104-105; 127pp; English.
XX CC The invention relates to identifying tissue-specific polynucleotides (P)
XX CC that involves performing a genetic subtraction to identify pool of (P)
XX CC from tissue of interest (TI), performing DNA microarray analysis to
XX CC identify first subset of polynucleotides (SP1) at least 2-fold over
XX CC expressed in TI, and performing quantitative polymerase chain reaction
XX CC (PCR) analysis on SP1 to identify second subset of (P). The method is
XX CC useful for determining the presence or absence of a cancer cell in a
XX CC patient, monitoring the progression of cancer in a patient using a
XX CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
XX CC urine or a tumour biopsy sample. The methods are useful for determining
XX CC the presence or absence of or monitoring progression of prostate, breast,
XX CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
XX CC gastric, kidney, bladder, pancreatic or endometrial cancer. Sequences
XX CC AAI67218-223 represent determined cDNA sequences of splice variants of
XX CC B726P
SQ Sequence 3681 BP; 1411 A; 680 C; 758 G; 826 T; 0 U; 6 Other;
Query Match 76.9%; Score 1560.4; DB 4; Length 3681;
Best Local Similarity 89.4%; Pred. No. 6.7e-312;
Matches 1813; Conservative 4; Mismatches 21; Indels 189; Gaps 6;
QY 5 TCCCGTTAAAGATGCTCTTCTGAGGCTTAAGTGGGATGAAGTTCTTATTCACACTAA 64
Db 1526 TCTGTAAAGATGCTCTTCTGAGGCTTAAGTGGGATGAAGTTCTTATTCACACTAA 1595
QY 65 AGCCTTAGAATTTGATGGACATGCAAACTTTCAGAGCAGAGCTCCGAGAGCCATCTGC 124
Db 1586 AGCCTTAGAATTTGATGGACATGCAAACTTTCAGAGCAGAGCTCCGAGAGCCATCTGC 1645
QY 125 CTTGAGGCTGCCATTTGAAATGCAAAAGTCTGTTTCCAAATTAAGCTTGGATTGAAGAA 184
Db 1646 CTTGAGGCTGCCATTTGAAATGCAAAAGTCTGTTTCCAAATTAAGCTTGGATTGAAGAA 1705
QY 185 TGAACAAACATTTGAGAGCAGATGAGATACTCCCATCAGAAATCCAAACAAAGGACTATGA 244

2602	AGAAAGAATGCTGAAC	TTCAGATGACCCTTAAAAC	TGAAAGAGAAATCA	TAACTAATAAG	2661
1325	GGCATCTCAATATAGTGGCAGCTTAAAGTTCT	GATAGCTGAGAACAAATGC	TTCAC	TTCC	1384
2662	GGCATCTCAATATAGTGGCAGCTTAAAGTTCT	GATAGCTGAGAACAAATGC	TTCAC	TTCC	2721
1395	TAAATTGAAGGAAAAACAAGCAAAGAAACTAGAGCGCAGAAATG	GAATCACACCATCC	1444		
2722	TAAATTGAAGGAAAAACAAGCAAAGAAACTAGAGCGCAGAAATG	GAATCACACCATCC	2781		
1445	TAGACTGGCTCTGCTGTACAGAGCAATGATCAAAATTTGTG	CATCAAGAAAAAGTCAAGA	1504		
2782	TAGACTGGCTCTGCTGTACAGAGCAATGATCAAAATTTGTG	CATCAAGAAAAAGTCAAGA	2841		
1505	ACCTGCTTTCCACATTCGACGAGATGCTTGTTGCCAAGAA	AAATGTAATGTTGATGTCAG	1564		
2842	ACCTGCTTTCCACATTCGACGAGATGCTTGTTGCCAAGAA	AAATGTAATGTTGATGTCAG	2901		
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1625	CCANAAGCTTAAAAATTTAATCTCAATTTATGACGAGATGCTCTA	AGAGAAATACATGG	1684		
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3021	TTTTCA-GAACATGCACAAAGAGACCAACGTCGAAACACAGTGT	CAATGAAGGAAGCTGAA	3079		
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3080	CACATGTTTCAANCGAACAGATTAATGTGAACAAACACATGNC	ACGAGTCTCTA	3139		
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1865	GCACATAANGAAAGCTGCAACAAAGCAAGATAACAATTTGATNTT	CAITWTCTTGAGAG	1924		
3200	GCACATAA-GAAAGCTGCAACAAAGCAAGATAACAATTTGATNTT	CAITWTCTTGAGAG	3258		
1925	GAAATATGC-NCATCATCTTCTTAAAAAGAAAAAATGAGGAGAT	TATTTNATTACNATAACCA	1983		
3259	GAAATATGCACATCATCTTCTTAAAAAGAAAAAATGAGGAGAT	TATTTNATTACNATAACCA	3318		
1984	TTTTAAAAAACCGTATATTTCAATATGGA	AAAAAAAAAAAAAAAA	2030		
3319	TTTTAAAAAA-CGGTATATATCAATATGA	AAAGAGAAAGCAAAACA	3364		

QY 965 TGCCGATATATTAAATGAAAAATTAGCGAAGATTAGCAAGATCGAAGACGAGCATAG 1024.

antigens, the antigens per se, and uses thereof

JOURNAL Patent: WO 0147959-A 15 05-JUL-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL
SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation
(US)

FEATURES

source

Location/Qualifiers
1..2030
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 99.4%; Score 2018; DB 6; Length 2030;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2030; Conservative 0

QY 1 CTCGTGCCGTTAAAGATGTCCTCTGAAGCTTAACCTGCGAATGAAGTTTCTATTCCAA 60
DB 1 CTCGTGCCGTTAAAGATGTCCTCTGAAGCTTAACCTGCGAATGAAGTTTCTATTCCAA 60

QY 61 CTAAGCGCTTAGAATTGATGGACATCAAACTTTCAAGCAGAGCCTCCGAGAGCCAT 120
DB 61 CTAAGCGCTTAGAATTGATGGACATCAAACTTTCAAGCAGAGCCTCCGAGAGCCAT 120

QY 121 CTGCGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGA 180
DB 121 CTGCGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGA 180

QY 181 AGAATGAACAACTTTAGAGCAGATGAGATATCCCATCAGATCCAAACAAAGGACT 240
DB 181 AGAATGAACAACTTTAGAGCAGATGAGATATCCCATCAGATCCAAACAAAGGACT 240

QY 241 ATGAAGAAAGTTCTTGGATTCTGAGAGTCTCTGTGAGACTGTTTCAAGAGGATGTGT 300
DB 241 ATGAAGAAAGTTCTTGGATTCTGAGAGTCTCTGTGAGACTGTTTCAAGAGGATGTGT 300

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DB 361 CTCCTGATATGATGTTTCTGAAGGCTCCCTGCAGATGAAAGTTTCTATTCCAACTA 420

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DB 841 TGAAAAAGAACTGTGAGAGCAAAAGAAATTAATACAGTTAGAGAACCAAAAAGTTA 900

QY 901 AATGGGAAACAAAGCTCTCGAGTGTGAGATTGACATTTAAACCAAGAGAGAGAGAGAA 960

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DB 1141 ATCTCTTACATGAAAAATTTGATTTGAAAGAAATTTGCCATCTGTTAAACTGGAATATAG 1200

QY 1201 CCACACTGAAACCACTATACAGGAAAGGAAATTAATACTTTGAGGACATTAAGATTT 1260

DB 1201 CCACACTGAAACCACTATACAGGAAAGGAAATTAATACTTTGAGGACATTAAGATTT 1260

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DB 1261 TAAAGAAAAAGAAATGCTGAACTTCAGATGACCTTAAACTGAAAGAGGAAATCATTAACTA 1320

QY 1321 AAGGGCATCTCATATATAGTGGCAGCTTAAAGTTCTGTAGCTGAGAACACAACTGCTCA 1380

DB 1321 AAGGGCATCTCATATATAGTGGCAGCTTAAAGTTCTGTAGCTGAGAACACAACTGCTCA 1380

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QY 1801 TCTAGATCAGAAATTTATTCTAACTAAGGAAAAATATGTCGCTTCAACAGCAATTAGT 1860

DB 1801 TCTAGATCAGAAATTTATTCTAACTAAGGAAAAATATGTCGCTTCAACAGCAATTAGT 1860

QY 1861 TCATCCATTAAGAAAGCTGACAAAGCAAGATAAATTAATTTGATNTTCATTNTCTTG 1920

DB 1861 TCATCCATTAAGAAAGCTGACAAAGCAAGATAAATTAATTTGATNTTCATTNTCTTG 1920

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Qy 1981 CMTTAAAAACCCGCTATATTTCAATATGGAAGAAAAAANAANAANA 2030

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RESULT 2

AX829110

LOCUS AX829110 4458 bp DNA linear PAT 12-DEC-2003

DEFINITION Sequence 3 from Patent WO02059377.

ACCESSION AX829110

VERSION AX829110.1 GI:39838904

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Mack,D.H., Gish,K.C. and Afar,D.

TITLE Methods for diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer

JOURNAL Patent: WO 02059377-A 3 01-AUG-2002;

EOS Biotechnology, Inc. (US)

FEATURES

source

1. 4458

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 95.68; Score 1940; DB 57 Length 4458;

Best Local Similarity 98.78; Pred. No. 0;

Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;

Qy 5 TGCGTTAAAGATGGTCTTCTGAAGGCTAACTCGGAATGAAAGTTTCTATTCCAACTAA 64

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Qy 65 AGCCTTAGAATTGATGACATGCAAACTTTCAAGAGAGCCCTCCGAGAGCCATCTGC 124

Db 2151 AGCCTTAGAATTGATGACATGCAAACTTTCAAGAGAGCCCTCCGAGAGCCATCTGC 2210

Qy 125 CTTGAGCGCTGCCATTGAATGCAAAAGTCTGTTCCAAATGAAAGCTTTGGAATTGAAGAA 184

Db 2211 CTTGAGCGCTGCCATTGAATGCAAAAGTCTGTTCCAAATGAAAGCTTTGGAATTGAAGAA 2270

Qy 185 TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGATCCAAACAAAGAGCACTATGA 244

Db 2271 TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGATCCAAACAAAGAGCACTATGA 2330

Qy 245 AGAAAGTTCTTGGATTCTGAGAGTCTCTGTGAGACTGTTCACAGAGGATGTGTGTTT 304

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Db 2391 ACCGAGGCTACATCAAAAAGAAATAGATAAAATTAATGGAATTTAGAGAGTCTCC 2450

Qy 365 TGATAATCATGTTTCTGAGAGTCTCCCTGAGAGTGAAGTTTCTATTCCAACTAAAGC 424

Db 2451 TGATAATCATGTTTCTGAGAGTCTCCCTGAGAGTGAAGTTTCTATTCCAACTAAAGC 2510

Qy 425 CTTAGAATTGATGGAATGCAAACTTTCAAAGCAGAGCTCCCGAGAGGCCATCTGCCTT 484

Db 2511 CTTAGAATTGATGGAATGCAAACTTTCAAAGCAGAGCTCCCGAGAGGCCATCTGCCTT 2570

Qy 485 CGAGCTGCCATTTGAATGCAAAAGTCTGTTCCAAATGAAAGCTTTGGAATTGAAGATGA 544

Db 2571 CGAGCTGCCATTTGAATGCAAAAGTCTGTTCCAAATGAAAGCTTTGGAATTGAAGATGA 2630

Qy 545 ACAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 604

Db 2631 ACAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGTTGAAGA 2690

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Db 2871 TCACCTGGAACAAGCTACAGGAAATGGAACAAATGGAAGAAAGCTTTGTGTACTGAA 2930

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Db 2931 AAAGAAACTGTGAGAGCAAAAGAAATATAAATCACAGTTTAGAGAAACCAAAAGTTTAAATG 2990

Qy 905 GGAACAAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAGAAA 964

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Db 3051 TGCCGATATATTAATGAAAAAATTAGGGAAGAAATAGGAAGAAATCGAAGCAGCATAG 3110

Qy 1025 GAAAGAGTTAGAGTGAAACAACTTTGAAGAGGAAATGCCATGCTAATAACAGATATAGNATT 1084

Db 3111 GAAAGAGTTAGAGTGAAACAACTTTGAAGAGGAAATGCCATGCTAATAACAGATATAGNATT 3170

Qy 1085 GAAGAGTGTACAAAGTAAATTTGAATCAGTTTCTCACACTCATGAAATCAAAATATATCT 1144

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RESULT 3
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LOCUS Homo sapiens breast cancer antigen NY-BR-1 mRNA, complete cds.
DEFINITION AF269087
ACCESSION AF269087
VERSION AF269087.1 GI:13469728
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4458)
Jager, D., Stockert, E., Gure, A.O., Scanlan, M.J., Karbach, J., Jager, E., Knuth, A., Old, L.J. and Chen, Y.T.
Identification of a tissue-specific putative transcription factor in breast tissue by serological screening of a breast cancer library
Cancer Res. 61 (5), 2055-2061 (2001)
MEDLINE 21174979
PUBMED 11280766
REFERENCE 2 (bases 1 to 4458)
Jager, D., Stockert, E., Gure, A.O., Scanlan, M.J., Karbach, J., Jager, E., Knuth, A., Old, L.J. and Chen, Y.T.
AUTHORS
Direct Submission
TITLE Submitted (18-May-2000) Pathology, Cornell Medical Center, 1300 York Avenue, New York, NY 10021, USA
JOURNAL Location/Qualifiers
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DEFINITION Sequence 490 from patent US 6528054.
ACCESSION AR283467
VERSION AR283467.1 GI:29720294
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 3288)
AUTHORS Jiang, Y., Dillon, D. C., Mitcham, J. L., Xu, J., Harlocker, S. L. and Hepler, W. T.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: US 6528054-A 490 04-MAR-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 98.5%; Pred. No. 0;
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;
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DEFINITION	Sequence 490 from Patent WO0179286.		
ACCESSION	AX303170		
VERSION	AX303170.1	GI:17383660	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.		
JOURNAL	Compositions and methods for the therapy and diagnosis of breast cancer		
FEATURES	Patent: WO 0179286-A 490 25-OCT-2001;		
source	CORIXA CORPORATION (US)		
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Best Local Similarity	98.5%; Pred. No. 0;		
Matches 1997;	Conservative 4; Mismatches 21; Indels 5; Gaps 5;		
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1984	QY	TTTTAAAAAACCGTATATTTTCAATATGAAAAAANAANAANAANAANAANAANAANAANAANA	2030
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RESULT 6
AR283457 LOCUS linear PAT 10-APR-2003
DEFINITION Sequence 474 from patent US 6528054.
ACCESSION AR283457
VERSION AR283457.1 GI:29720284
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3865)
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: US 6528054-A 474 04-MAR-2003;
FEATURES source 1..3865
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 95.5%; Score 1938.4; DB 6; Length 3865;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;

QY 5 TGCGGTTAAAGATGSGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTTCCAACTAA 64
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RESULT 7
AR351426
LOCUS AR351426 3855 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 474 from patent US 6586572.
ACCESSION AR351426
VERSION AR351426.1 GI:33753105
KEYWORDS Unknown.

ORGANISM Unknown.
REFERENCE 1. (bases 1 to 3865)
AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and Repler, W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: US 6586572-A 474 01-JUL-2003;
FEATURES Location/Qualifiers
source 1..3865
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 95.5%; Score 1938.4; DB 6; Length 3865;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;

Qy 5 TGGCGTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAGTTTCTATTCCCACTAA 64
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RESULT 9
AR283451 AR283451 3681 bp DNA linear PAT 10-APR-2003
LOCUS
DEFINITION Sequence 463 from patent US 6528054.
ACCESSION AR283451
VERSION AR283451.1 GI:29720278
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3681)
AUTHORS Jiang,Y.; Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.F.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: US 6528054-A 463 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..3681
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 76.9%; Score 1560.4; DB 6; Length 3681;
Best Local Similarity 89.4%; Pred. No. 7.2e-275;
Matches 1813; Conservative 4; Mismatches 21; Indels 189; Gaps 6;
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SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 3681)		
AUTHORS	Yuqiu,J., Dillon,D.C., Mitcham,J.L., Xu,J. and Harlocker,S.L.		
TITLE	Compositions for the treatment and diagnosis of breast cancer and methods for their use		
JOURNAL	Patent: US 6579973-A 463 17-JUN-2003;		
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Query Match 76.9%; Score 1560.4; DB 6; Length 3681;			
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 ACCESSION AR351420
 VERSION AR351420.1 GI:33753099
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 3681)

AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and Hepler, W.T.
 TITLE Compositions and methods for the therapy and diagnosis of breast cancer
 JOURNAL Patent: US 6586572-A 463 01-JUL-2003;
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ORIGIN

Query Match 76.9%; Score 1560.4; DB 6; Length 3681;
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AUTHORS		
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JOURNAL		
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Query Match	76.94;	Score 1560.4; DB 6; Length 3681;
Best Local Similarity	89.4%;	Pred. No. 7.2e-275;
Matches 1813;	Conservative 4;	Mismatches 21; Indels 189; Gaps 6;
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QY 1625 CCANAAGCCTAAATTAATCTCAATATATGAGGAGATGCTCTTAAAGAGAAATATACATTGG 1684
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Db 3080 CACATGTTCAAAACGACCAAGATNATGTGAACAAACACACTGACAGCAGGAGCTCTCTA 3139
QY 1805 GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTGGCTTCAACAGCAATTTAGTTTCA 1864
Db 3140 GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTGGCTTCAACAGCAATTTAGTTTCA 3199
QY 1865 GCACATGANGAAGCTGACACAAAGCAAGATACAAATTAATGATNTTCATTTCTTGAGAG 1924
Db 3200 GCACATGANGAAGCTGACACAAAGCAAGATACAAATTAATGATNTTCATTTCTTGAGAG 3258
QY 1925 GAAATGTC-NCATCATCTTTTAAAGAGAAATATGAGAGATATTTTATTCATTAACCA 1983
Db 3259 GAAATGTC-NCATCATCTTTTAAAGAGAAATATGAGAGATATTTTATTCATTAACCA 3318
QY 1984 TTTTAAACCAACCGTATATTTCAATATGAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2030
Db 3319 TTTTAAACCAACCGTATATTTCAATATGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 3364

RESULT 13
AX303143 3681 bp DNA linear PAT 30-NOV-2001
LOCUS AX303143
DEFINITION Sequence 463 from Patent WO0179286.
ACCESSION AX303143
VERSION AX303143.1 GI:17383644
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and Hepler, W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0179286-A 463 25-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..3681
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 76.9%; Score 1560.4; DB 6; Length 3681;
Best Local Similarity 89.4%; Pred. No. 7.2e-275;
Matches 1813; Conservative 4; Mismatches 21; Indels 189; Gaps 6;
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QY 65 AGCTTTAGAAATGATGACATGCAAACTTTTAAAGCAGAGCTCCGAGAGAGCTATCTGC 124
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289	CTTCGAGCTGCTGATTTGAATTCAAAAGTCTGTTCCAAATAAAGCTTTGGAATTTGAAGAA	348	Db	ACTGAAACACCAATACACGAGAAAGAAATTAATCTTTGAGGACATTTAAGATTTTAA	1244
185	TGAACCAACATTTGAGAGCAGATGAGATCTCCATCAGATCCAAACCAAGAGGACTATGA	244	Qy	AGAAAAGATGCTGAACTTCAGATGACCTCAAACTGAAAAGAGGAATCATTAACATAAAG	1324
349	TGAACCAACATTTGAGAGCAGATGAGATCTCCATCAGATCCAAACCAAGAGGACTATGA	408	Db	AGAAAAGATGCTGAACTTCAGATGACCTCAAACTGAAAAGAGGAATCATTAACATAAAG	1304
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305	ACCAAGGCTACACATCAAAAGAAATAGATTAATTAATGAAATTTAGAGAGTCTCC	364	Qy	TAAATTTGAAGGAAAAACAAGCAAAATATCTAGAGGAGCAAAATTTGAATCACCATCC	1444
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365	TGATATGATGTTTCTCAAGCTCCCTGAGAGTCTGTTTCAAGCTTAAAGTCTTCTTCAACTTAAAGC	424	Qy	TAGACTGGCTTCTGCTGTCAAGACCATGATCAAAATTTGTGACATCAAGAAAGTCAAGA	1504
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425	CTTGAATTTGATGAGATGCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGCCTT	484	Qy	ACCTGCTTTCCATTTGAGAGTCTGCTTCAAGAGCAAAATTAATCTTCAAGAGAAAT	1564
589	CTTGAATTTGATGAGATGCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGCCTT	648	Db	ACCTGCTTTCCATTTGAGAGTCTGCTTCAAGAGCAAAATTAATCTTCAAGAGAAAT	1544
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829	CAAGGCTACACATCAAAAGAAATGATTAATTAAGTGGAAATTTAGAGATTTCACTAG	888	Db	CACATGTTCAAAACGAGAGATGTAACAAACACACTGANCAGCAGGAGTCTCTA	1782
725	CCTATCAAAATCTTGATACAGTTCTTCTGTAAGAGCAGGAGCTTCAAAAGA	784	Qy	GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTTGGCTTCAACAGCAATTAGTTCT	1864
889	CCTATCAAAATCTTGATACAGTTCTTCTGTAAGAGCAGGAGCTTCAAAAGA	948	Db	GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTTGGCTTCAACAGCAATTAGTTCT	1842
785	TCATCTGTAACACGTACAGGAAATGGAACAAATGAAAGAAAGTCTGTTGTAAGTAA	844	Qy	GCACATTAANGAGCTGACAAACAAAGCAAAATGTAAGTGAATTTCAATTTCTTGAGAG	1924
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845	AAAGAACTGTCAGAGCAAAAGAAATTAATTAAGTGAAGCAAAAGAGTAAATG	904	Qy	GAATATGCAACATCATCTCTTAAAGGAGAAATGAGGAGATTTTAATTAACATAACCA	1983
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905	GGAAACAGAGCTGTCAGAGTGTGAGTTGACTTTTAAACCAAGAGAGAGAGAGAGAAA	964	Qy	TTTAAAAACCCGTATATTTTCAATATGTAATGTAATGTAATTTCTTTCTTGAGAG	2030
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965	TGCGATATATTAATGAAAAATTTAGGAGAAATTTAGGAGAAATCGAGAGCAGATAG	1024	Qy	AR344224	
1091	-----	1090	Db	Sequence 468 from patent US 6579973.	
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			Db	Source	Unknown.
			Qy	Organism	Unclassified.

RESULT 15
AR344224
LOCUS
DEFINITION
SEQUENCE 468 from patent US 6579973.
ACCESSION
AR344224
VERSION
AR344224.1
GI:33740124
KEYWORDS
Unknown.
SOURCE
Organism
Unclassified.

REFERENCE	1 (bases 1 to 2307)	
AUTHORS	Yugu, J., Dillon, D.C., Mitcham, J.L., Xu, J. and Harlocker, S.L.	
TITLE	Compositions for the treatment and diagnosis of breast cancer and methods for their use	
JOURNAL	Patent: US 6579973-A 468 17-JUN-2003;	
FEATURES	Location/Qualifiers	
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Best Local Similarity	89.5%; Pred. No. 1.6e-274;	
Matches 1815; Conservative	0; Mismatches 23; Indels 189; Gaps 6;	
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Qy	185 TGAACAAACATTGAGCAGATGATGATCTCCATCAGATCCAAACAAAGAGGACTATGA	244
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Search completed: May 6, 2004, 21:03:15
Job time : 7892 secs

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Run on: May 6, 2004, 13:47:23 ; Search time 3855 Seconds (without alignments)
3966.131 Million cell updates/sec

Title: US-09-451-739H-16
Perfect score: 2599
Sequence: 1 MKVSIPTKALELMDMQTFKA.....IAGDACLOKMNVDVSTDI 512

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+ pzn.model -DEV=xlh
-Q/cgn2 1/USPTO.spool/US09451739/runat_05052004.101644.18701/app_query.fasta.1.711
-DB=EST -QPMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLCN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
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2: em_esthum:*
3: em_estin:*
4: em_estmu:*
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7: em_estro:*
8: em_hic:*
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20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
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27: em_gss_vrl:*
28: gb_gss1:*

OM protein - nucleic search, using frame_plus_p2n model

Result No.	Score	Query Match	Length	DB ID	Description
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2	809	31.1	490	9	AI951118
3	771	29.7	565	10	AW373574
4	717	27.6	630	10	BE177744
5	716.5	27.6	344.3	11	BC028407
6	646	24.9	3794	11	BC036210
7	540.5	20.8	596	13	BQ429618
8	520	20.0	443	10	BF746270
9	520	20.0	443	10	BF746340
10	458	17.6	904	12	BG539426
11	437.5	16.8	862	12	BG431116
12	433.5	16.7	821	12	BG622779
13	431.5	16.6	684	14	CA394381
14	427.5	16.4	683	14	CF181571
15	416.5	16.0	638	13	BU678550
16	389.5	15.0	1105	13	BQ071543
17	385	14.8	546	10	BE929777
18	375.5	14.4	519	9	AL711745
19	365.5	14.1	700	14	CB527418
20	354.5	13.6	751	14	CD000265
21	351.5	13.5	574	14	CB298280
22	351.5	13.5	630	14	CB298279
23	346.5	13.3	774	14	CA324174
24	340.5	13.1	633	10	AW976709
25	340.5	13.1	642	10	AW976715
26	329.5	12.7	504	10	BF512258
27	305.5	11.8	644	13	BU680626
28	305	11.7	692	10	BE284531
29	292.5	11.3	388	10	BE939777
30	291	11.2	669	29	AG068976
31	288.5	11.1	738	10	BE748456
32	287	11.0	462	10	BF840427
33	286.5	11.0	603	13	EX478214
34	280.5	10.8	858	14	CD244895
35	278.5	10.7	597	14	CB228494
36	274.5	10.6	1014	13	BQ26802
37	274	10.5	368	28	AQ280806
38	271	10.4	386	10	AW614036
39	270.5	10.4	521	10	BF895056
40	269.5	10.4	483	12	BI035374
41	265.5	10.2	886	13	BQ437838
42	261.5	10.1	2417	11	EC028960
43	258	9.9	699	10	BB614443
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ALIGNMENTS

RESULT 1
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DEFINITION RC5-BN0192-010900-025-E09 BN0192 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF328582
VERSION BF328582.1 GI:11299317
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 574)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC5&t2=RC5-BN0192-010900-025-E09&t3=2000-09-01&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 25
 High quality sequence stop: 525.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="BN0192"
 /notes="Organ: breast normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 ORIGIN
 Alignment Scores:
 Pred. No.: 4,74e-73 Length: 574
 Score: 870.00 Matches: 173
 Percent Similarity: 97.22% Conservative: 2
 Best Local Similarity: 96.11% Mismatches: 4
 Query Match: 33.47% Indels: 1
 DB: 10 Gaps: 0
 US-09-451-739H-16 (1-512) x BF328582 (1-574)
 QY 52 LeuArgAlaAspGluLeuLeuProSerGluSerGlnLysAspTyrGluGluSer 71
 Db 37 TTGAGACAGATGATGATCTCCCATCAGATCCAAAGAGACTATGAGAAAGTTCT 96
 QY 72 TTPAspSer-GluSerLeuGlnLysValSerGlnLysValSerGlnLysValSer 91
 Db 97 TGGGGGGCGTGAGAGTCTCTGTGAGACTGTTTACAGAGAGTGTGTGTACCCAGGC 156
 QY 91 aThrHisGlnLysGlnLysLeuLeuLeuLeuGlnLysValSerProAspAsnAs 111
 Db 157 TACCGCGTCAAAAGAAATAGATATAAAATAATGGAATTTAGAGAGTCTCTGATATGA 216
 QY 111 pGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeuGlu 131
 Db 217 TGGTTTCTGAAGGCTCCCTGACAGATGAAAGTTTCTTCCAACTAAGCCCTAGAAAT 276
 QY 131 uMetAspVetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGluProAl 151
 Db 277 GATGGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAGCCATCTCCCTTCGAGCCGTC 336
 QY 151 aileGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLe 171

Db 337 CATTGAATGCAGAAAGTCTGTTCCAAATAAAGCCTTGAATGAAGATGAACAAACATT 396
 QY 171 uArgAlaAspGlnMetPheProSerGluSerGlnLysValGluGluAsnSerTr 191
 Db 397 GAGAGCATGATGATGTTCCCTTCAGATCAAAACAAAGAGGTTGAAGAAATCTTG 456
 QY 191 pAspSerGluSerLeuArgGluThrValSerGlnLysValSerGlnLysValSer 211
 Db 457 TGATTCGAGAGTCTCCGTGAGACTGTTTCACAGAGGATGTTGTGTACCCAGGCTAC 516
 QY 211 rHisGlnLysGluMetAspLysIleSerGlnLysLeuGluAspSerThrSerLeuSer 230
 Db 517 ACATCAAAAGATATGATTAATAATAGTGAATAATAGAGATTCACTGGCCTATCA 574
 RESULT 2
 AI9511118/c 490 bp mRNA linear EST 09-MAR-2000
 LOCUS wx63905.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2548376 3',
 DEFINITION mRNA sequence.
 ACCESSION AI9511118 GI:5743428
 VERSION AI9511118.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 490)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
 Technologies, Inc. CDNA Library Arrayed By: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing By: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
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 Seq primer: -400P from Gibco
 High quality sequence stop: 423.
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 /tissue_type="four pooled high-grade tumors, including two
 primary tumors and two metastatic to ovary"
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 /clone_lib="NCI_CGAP_Br18"
 /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies."
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.63e-67 Length: 490
 Score: 809.00 Matches: 157
 Percent Similarity: 97.55% Conservative: 2
 Best Local Similarity: 96.32% Mismatches: 4
 Query Match: 31.13% Indels: 0
 DB: 9 Gaps: 0
 US-09-451-739H-16 (1-512) x AI9511118 (1-490)
 QY 94 GlnLysGluLeuAspLysIleAsnGlnLysLeuGluSerProAspAsnAspGlyPhe 113
 Db 489 CAAAAGAAATAGATTAATAATAATGGAATTTAGAGAGTCTCCCTGATTAATGATGTTT 430

QY	114	LeuLyAalaProCysArgMetLysValSerIleProThrTlysAlaLeuGluLeuMetAsp	133
Dd	429	CTGAAGGCCTCCCTGCAGAATGAAAGTTTCATTCCAACATAAAGCCTTAGAAATGATGGAC	370
QY	134	MetGlnThrPhelysAlaGluProProGluLysProSerAlaphedGluProAlalleGlu	153
Dd	369	ATCCAAACTTTCAAAGCAGACGCTCCCGAAGGCCATCTGCCTTCGAGCGCTGCANTGAA	310
QY	154	MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla	173
Dd	309	ATCCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAAGTAACAACCAATTCGAGCA	250
QY	174	AspGlnMetPheProSerGluSerLysGlnLysLysValGluGluAsnSerTrpAspSer	193
Dd	249	GATCAGATGTTCCCTTCAGAAATCAAAACAAGAACGTTGAAGAAATTTCTTGGGATTC	190
QY	194	GluSerLeuArgGluThrValSerGlnLysAspValCysValProLysAlaThrHisGln	213
Dd	189	GAGAGTCTCCGTGAGACTGTGTTACAGAAGATGTGTGTGTACCAGGCTCACATCAA	130
QY	214	LysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeuSerLysLysLeu	233
Dd	129	AAAGAAATGATAAATAAAGTGGAAAAATTAGAAGATTCAACTGACCTTACAAAAATCTTG	70
QY	234	AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg	253
Dd	69	GATACAGTTCATTCTTCTGGAAGAACCAAGGGAACCTTCAAAAAGACCCCTGTGACCCACGT	10
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Dd	9	TCAGGAAAA	1
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LOCUS	AW373574	QV4-BT0534-281299-053-a01 BT0534 Homo sapiens cDNA, mRNA sequence.	
DEFINITION	AW373574		
ACCESSION	AW373574		
VERSION	AW373574.1	GI:6878228	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 565)		
JOURNAL	HCBP http://www.ludwig.org.br/ORESTES.		
COMMENT	The FAPESP/LICR Human Cancer Genome Project Unpublished (1999) Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV4&t2=QV4-BT0534- 281299-053-a01&t3=1999-12-28&t4=1) Seq primer: puc 18 forward High quality sequence stop: 565. Location/Qualifiers 1..565		
FEATURES			
SOURCE			

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=4r2=RC1-HT0598-140
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High quality sequence start: 24
High quality sequence stop: 569.

FEATURES

Location/Qualifiers
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/clone_stage="Adult"
/clone_lib="HT0598"
/notes="Organ: head neck; Vector: puc18; Site 1: Smal;
Site 2: SnaI; A mini-library was made by cloning products
derived from ORESSES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:
Pred No.: 2,41e-58 Length: 650
Score: 717.00 Matches: 148
Percent Similarity: 83.67% Conservative: 16
Best Local Similarity: 75.51% Mismatches: 24
Query Match: 27.59% Indels: 8
DB: 10 Gaps: 1

US-09-451-739H-16 (1-512) x BE177744 (1-650)

QY 497 AlaCysLeuGlnArgLysMetAsnValSerThrAspLeu 512
DB 92 GTCCTTTGCAAGGAATATGATGTTGATGAGTAATACATATATA 45

RESULT 5

BC028407
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)

Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 3443)

REFERENCE

AUTHORS

Strausberg, R.D., Collins, F.S., Wagner, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Udwin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

23388257

12477932

2 (bases 1 to 3443)

REFERENCE

AUTHORS

TITLE

JOURNAL

Strausberg, R.

Direct Submission

Submitted (23-APR-2002)

National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadan@systemsbio.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha

Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 46 Row: i Column: 20

This clone was selected for full length sequencing because it

passed the following selection criteria: Hexamer frequency ORF

analysis

This clone has the following problem: frame shifted.

Location/Qualifiers

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FEATURES

source

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ORIGIN
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Score: 716.90 Matches: 171
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Query Match: 27.57% Indels: 48
DB: 11 Gaps: 8

US-09-451-739H-16 (1-512) x BC028407 (1-3443)

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Db 1598 CAAGTGTGTATACCTGAGTCTATGATCATCAAGAAAGTAATGGAGATAAATAGAGAAGTAGAA 1657

QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1658 GAGCTTCCTGAGAGCACTCTCCCTCAAGCTCGCGTTGAATGCATAAAGACTGTTCCA 1717

QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer 60
Db 1718 AATAAGCCTTTGAATTGAAGATGAACAACATTGAGAGCAGCTCAGATGTTCCCATCA 1777

QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuLysGluThr 80
Db 1778 GATCCAAACAAGAGCAATGAAGAAATTTCTGGATTCTGAGAGTCCCTGTGAGAGC 1837

QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysle 100
Db 1838 GTTTCACAGAAGATGTGATTATCCCAAGCTACACATCAAAAGAATTCGATACCTTA 1897

QY 101 AsnGlyLysLeuGlu----- 105
Db 1898 AGTGGAAATTAAGACCTTACCTGTGGAAGAAAGTTCTCTTCCAAATAAAGCCCTTAGA 1957

QY 106 -----GluSerProAspAsnAspGlyPheLeuLysAl 116
Db 1958 ATTAAAGGACAGAGAAACATTCAAAGCAGAGTCTCTGATAAAGATGGTCTTCTCAAGCC 2017

QY 116 aProCysArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnTh 136
Db 2018 TACCTGTGGAAGAAAGTTCTCTTCCAAATAAAGCCTTAGAATTAAGGACAGAGAAC 2077

QY 136 rPheLysAlaGluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLys 156
Db 2078 ACTCAAAGCAGAGTCTCTGATAATGATGGTCTCTGAGCCTACCTGTGGAAGGAAGT 2137

QY 156 sSerValProAsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMe 176
Db 2138 TTCTCTTCCAAATAAAGCTTTAGATTGAAGCAGAGAGAAACATTCAAGCAGCTCAGAT 2197

QY 176 tPheProSerGluSerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLe 196
Db 2198 GTTCCCATCAGATCCAAACAAGAGATGATGAGAAATTTCTGGATTGTGAGAGTT 2257

QY 196 uArgGluThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMe 216
Db 2258 CCTTGAGGCTCTCTTACAGAAATGATGGGTGTTTACCACAGGCTACACATCAAAAGAAATT 2317

QY 216 tAspLysIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrVa 236
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QY 236 lHisSerCysGluArg-----AlaArgGluLeuGlnLysAspHi 249
Db 2376 ----ACCTGTGAAGGAAAGTTTCTCTTCCAAATAAAGCCTTAGAATTAAG- 2423

QY 249 sCysGluGlnArgThrGlyLysMetGluGln-----MetLysLysLysPhe 264

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Db 2424 ----GACAGAGAAACACTCAAGCAGAGTCTCTGTATAAAGATGGTCTTCTGAAGCCTAC 2479
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Db 2480 CTGTGTAAAGGAAAGTTCTCTTCCAAATAAAGCCTTAGAATTAAG-----GACAG 2530
QY 283 nGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsnGlnGlu 303
Db 2531 AGAAACATTAAAGCAGCTCAGATGTTCCCATCAGAAATCAAAACAAGAGATGATGAAGA 2590
QY 303 uGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeuGlyArg 323
Db 2591 AAATCTCTGGGATTTTGAGAGTTTCTCTGAGACTCTCTTACAGAAATGATGTGTGTTACC 2650
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Db 2651 CAAGGCTACACATCAAAAGAAATTCGAT 2678

RESULT 6
BC036210 Homo sapiens, clone IMAGE:5265638, mRNA. linear HTC 20-SEP-2002
DEFINITION Homo sapiens, clone IMAGE:5265638, mRNA.
ACCESSION BC036210
VERSION BC036210.1 GI:23242519
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3794)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.sngc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 63 Row: e Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis
This clone has the following problem: frame shifted.
FEATURES
Location/Qualifiers
1..3794
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:5265638"
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ORIGIN
Alignment Scores: 1,54e-50 Length: 3794
Pred. No.: 646.00 Matches: 191
Score:

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Percent Similarity:	44.48%	Conservative:	95
Best Local Similarity:	29.70%	Mismatches:	177
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DB:	11	Gaps:	16

US-09-451-739H-16 (1-512) x BC036210 (1-3794)

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Qy	50	Gln	50
Db	559	CRAGCATGCACATCAGCTTTTCAGCTTTGGAATTTAATAGTTTGACCTTTAGTAAATGAG	618
Qy	51	-----ThrLeuArgAlaAspGluLeuPro-----	59
Db	619	CTTCATGAAAGATCTGAAATTTGAAAGTTGGTGATCTATGTCCTATGTTGATCTCCACCA	678
Qy	60	-----SerGluSerLysGlnLys-----AspTyrGlu	68
Db	679	ATGACCAACACTGTGTGGGATCCACAGACTTGGGCGAGAAGAACTTAATAGATCAAGAA	738
Qy	69	GluSerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCys---	87
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Qy	88	-----LeuPro-----LysAlaThrHisGln	94
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Qy	95	LysGluIleAspLysIleAsnGlyLysLeuGluSerProAspAsnAspGlyPheLeu	114
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Db	979	GACCGTATTGATATGGTTHAATTCACAGGAGAGAGAAATGGAAAACTGATGTGCAGAA	1038
Qy	136	ThrPheLysAlaGluProProGluLysProSerAlaPheGluProAlaIleGluMetGln	155
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Qy	156	LysSerValProAsnLys-----AlaLeuGlu	164
Db	1093	AAAGTAAAGAAAATAGACATCAAGATGGACCACACAGAAATCTGTGACTTCACTAGTA	1152
Qy	165	LeuLysAsnGluGlnThrLeuArgAlaAspGlnMet---PheProSerGluSerLysGln	183
Db	1153	TTTAAAGAGGCTGATTTAATAACTCTTGATCTGTGCAAGTCACTGATGAGAGCAGTTTA	1212
Qy	184	LysLysValGluGluAsn-----	189
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Qy	190	-----SerTrpAspSerGluSer	195
Db	1273	GTCCAGAAACCAATCCATTCTGTGGATGGCTTTGATGACTTACTTGGTCATCTGAATA	1332
Qy	196	LeuArgGluThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLys---	214
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Qy	215	-----GluMetAspLysIleSerClyLysLeuGluAspSerThrSerLeuSerLysAla	232
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Qy	233	LeuAspThrValHisSerCysGluArgAlaLeuGluGlnLysAspHisCysGluGln	252

Db	1438	CAGATCCAGTTCATTTCATCGGGGAAGATCAATAGAGAGTTGAAAAAATCACTGTGTGAACATA	1497
Qy	253	ArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSer	272
Db	1498	CTTACAGTAAAAATGAAAAATGAAAAATGAGGTCCATGTACTACAAAAGGAGTATCT	1557
Qy	273	GluAlaLysGluLeuLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeu	292
Db	1558	GAAACAACAGAAATAAAATTTACAGTTTGAACATCAAAAGTGAATGGCAACGAGATTTC	1617
Qy	293	CysSerValArgLeuThrLeuAsnGlnGluGluLysArgArgAsnAlaAspIleLeu	312
Db	1618	TACAGTTTGAGTCTACCTTCAGACAAGAAGAGAGAGAGAAAAATCCAGTGCATTG	1677
Qy	313	AsnGluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGlu	332
Db	1678	TATGAAAAAATCAGGGGACACTTAAAGAAAAAGAGAGCAGTACAGGAAAGAAGTTGAA	1737
Qy	333	ValLysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGlu	352
Db	1738	GCAACAAACAACCTTCAGCTGAGCAGTACGAGAACGAGATACGGAATTTGAGGACAGTAAGA	1797
Qy	353	SerAsnLeuAsnGlnVal	358
Db	1798	AATCATTTGAACCAAGTTGTACAAGAGCTAAATGACACCCAGAGGCAACTTTTCTCGGAA	1857
Qy	358	-----	358
Db	1858	CAGAACCCAGATATTACAAGATGAATTTCTGACCAATCACTTTGCCAAACAAAAGGAG	1917
Qy	359	-----SerHisThrHisGluAsnGluAsn	366
Db	1918	ATAGCACTGGCTCGAAGGAAAAAGAAATTTCTCAGATCTCTCAGACCCATGACAAGTACAA	1977
Qy	367	TyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIle	386
Db	1978	GATCTGTTGATGAAATCCCATGTTCCAGACGAAATTCGCCACCTCAGACTGGAAATA	2037
Qy	387	AlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspIleLysIle	406
Db	2038	GACACAATAGAAAAACAGACAGGAAAAATAAAAAAGAACTATTTTGAGGACATT	2091
Qy	407	LeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeuLysGluGluSerLeuThr	426
Db	2092	-----GGTGACCTCCAAAAGACATAAACAAGGATGGGAAATATTAAACA	2136
Qy	427	LysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeu	446
Db	2137	ACAATGATATCCGAGTATCTGCACAGCTTGGTCTCTGACAGCTGAGAAATACCATGCTC	2196
Qy	447	ThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGluAlaGluIleGluSer	465
Db	2197	CATTCTTCTACCTGGAGGGGAAAAACAAGAAAGAACCTGGAGACAGAAAGTTGAATCA	2256
Qy	466	HisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLys	485
Db	2257	CACCGTTGCAGACTGGCTGCTGTTAGACAGTGATTTGTGAACAAAGTGGAGATCCAAAAGA	2316
Qy	486	SerGlnGluProAlaPheHisIleAlaGlyAspAlaCys	503
Db	2317	GACGTGGAACTGTTTCCGGGAGCAAGATGAATGGTTTCATTATCCGAGAAAAATG	2376
Qy	504	AsnValAsp	506
Db	2377	AATTTTGAT	2385
RESULT 7			
BQ429618			
LOCUS			
DEFINITION			
AGENCOURT_7905608 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6105756			
5', mRNA sequence.			
ACCESSION			
BQ429618.1 GI:21168694			
VERSION			
EST 24-MAY-2002			
linear			
mRNA			
596 bp			

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 596)
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LCM2345 row: 1 column: 13
 High quality sequence stop: 477.

FEATURES
 Location/Qualifiers
 1..596
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6105756"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 82"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site: 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTAGAGCGCGCGCGCATG-DT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN
 Alignment Scores:
 Pred. No.: 1,648-41 Length: 596
 Score: 540.50 Matches: 121
 Percent Similarity: 54.76% Conservative: 17
 Best Local Similarity: 48.02% Mismatches: 29
 Query Match: 20.80% Indels: 85
 DB: 13 Gaps: 2

US-09-451-739H-16 (1-512) x BQ429618 (1-596)

QY	60	SerGluSerLysGlnLysAspTyrGluGluSerTrpAspSerGluSerLeuCysGlu	79
Db	57	TCAGAAATTAGGAGAAAGAGATACAAATCACTTCAGATTCTGAGATTATCTCTGTG	116
QY	80	ThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLys	99
Db	117	ACTGATACACAGAAATTATGAGTGTTCCTGAGGCTACATATCAAAAGAAATAAGACA	176
QY	100	IleAsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArg	119
Db	177	ACAAATGCGCAAAATAGAGAGTCT	200
QY	120	MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla	139
Db	200		200
QY	140	GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro	159
Db	201	-----CCTGAAGCCCTTCTCATTGAGCTGCACTGAATCAAAATCTGTGTCCA	254
QY	160	AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSer	179
Db	255	ATAAAGGCTTAGATGGAGAGATAAACAACATTGAGAGCA-----	296

QY	180	GluSerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThr	199
Db	296	-----	296
QY	200	ValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIle	219
Db	296	-----	296
QY	220	SerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCys	239
Db	297	-----GATTCACCTACCTATCAAAATCTTGGATGCACTTCCTTCITGT	341
QY	240	GluArgAlaArgGluLeuGluLysAspHisCysGluGlnArgThrGlyLysMetGluGln	259
Db	342	GAAAGAGGAGGAACTTAAAGAAAGATACGTGACAAATACAGCAAAATGGAACA	401
QY	260	MetLysLysLysPheCysValLeuLysLysLeuSerGluAlaLysGluLysSer	279
Db	402	ACAAAATAAGTTTGTGTACTACAAAGGAAGTGTGAGAGCGAAAGAAATAAATCA	461
QY	280	GlnLeuGluAsnGlnLysValLysTrpGluGlnGluCysSerValArgLeuThrLeu	299
Db	462	CAGTTAGAGACCAAAAGCTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTGACTTTA	521
QY	300	AsnGlnGluGluLysArgArgAsnAlaAspIle	311
Db	522	AATCAAGAGAGAGAGAGAGAGAAATGTCGATATA	557

RESULT 8
 BF746270
LOCUS BF746270
DEFINITION RC1-BT0254-071100-119-a03 BT0254 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF746270
VERSION BF746270.1 GI:12072946
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 443)
AUTHORS Dias Neto, R., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brustein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.G.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BT0254-071100-119-a03&t3=2000-11-07&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 9
 High quality sequence stop: 439.
 Location/Qualifiers
 1..443
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"

/clone lib="BT0254"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 1.01e-39 Length: 443
Score: 520.00 Matches: 100
Percent Similarity: 99.04% Conservative: 3
Best Local Similarity: 96.15% Mismatches: 1
Query Match: 20.01% Indels: 0
DB: 10 Gaps: 0

US-09-451-739H-16 (1-512) x BF746270 (1-443)

Qy 19 LysAlaGluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSer 38
Db 130 CAATCAGAGCTCCGAGAGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCT 189
Qy 39 ValProHnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLeu 58
Db 190 GTTCCAAATGAAGCTTGGAAATGAAGATGAACAAATGAGAGCAGATGACTC 249
Qy 59 ProSerGluSerLysGlnLysAspTyrGluLysSerTrpAspSerGluSerLeuCys 78
Db 250 CCATCAGAAATCCAAACAAAGGACTATGAAGAAAGTCTCGGATCTCGAGAGTCTCTGT 309
Qy 79 GluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAsp 98
Db 310 GAGACTGTTTCACAGAGGATGTGTTCACCAAGTCTACATCAAAAGAAATAGAT 369
Qy 99 LysIleAsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCys 118
Db 370 AAATAATGAAATATAGAGAGTCTCCTGATAATGATGCTTTCTGAGAGGCTCCCTGC 429
Qy 119 ArgMetLysVal 122
Db 430 AGAATGAAAGTT 441

RESULT 9
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LOCUS RCI-BT0254-081100-119-a03 BT0254 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF746340
ACCESSION BF746340
VERSION BF746340.1 GI:12073016
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 443)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

TITLE
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.J.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922

Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCI&t2=RCI-BT0254-081100-119-a03&t3=2000-11-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 439.
Location/Qualifiers

FEATURES

Source
1..443
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BT0254"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 1.01e-39 Length: 443
Score: 520.00 Matches: 100
Percent Similarity: 99.04% Conservative: 3
Best Local Similarity: 96.15% Mismatches: 1
Query Match: 20.01% Indels: 0
DB: 10 Gaps: 0

US-09-451-739H-16 (1-512) x BF746340 (1-443)

Qy 19 LysAlaGluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSer 38
Db 130 CAATCAGAGCTCCGAGAGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCT 189
Qy 39 ValProHnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLeu 58
Db 190 GTTCCAAATGAAGCTTGGAAATGAAGATGAACAAATGAGAGCAGATGACTC 249
Qy 59 ProSerGluSerLysGlnLysAspTyrGluLysSerTrpAspSerGluSerLeuCys 78
Db 250 CCATCAGAAATCCAAACAAAGGACTATGAAGAAAGTCTCGGATCTCGAGAGTCTCTGT 309
Qy 79 GluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAsp 98
Db 310 GAGACTGTTTCACAGAGGATGTGTTCACCAAGTCTACATCAAAAGAAATAGAT 369
Qy 99 LysIleAsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCys 118
Db 370 AAATAATGAAATATAGAGAGTCTCCTGATAATGATGCTTTCTGAGAGGCTCCCTGC 429
Qy 119 ArgMetLysVal 122
Db 430 AGAATGAAAGTT 441

RESULT 10

LOCUS BG539426
DEFINITION 602568046r1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4692635 5', mRNA sequence.
ACCESSION BG539426
VERSION BG539426.1 GI:13531659
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 904)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

[illegible]

Location/Qualifiers

[illegible]

SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
NATIONAL
JOURNAL
COMMENT

1. (Bases 1 to 862)
NH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph. D.
Email: cgabbs@email.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.

```

DNA Sequencing by: Incyte Genomics, Inc.
C-clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LfCM1360 row: d column: 11
High quality sequence stop: 730.
Location/Qualifiers
1. 862
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4612186"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgctctggcc); Site 2: SfiI (ggccattatggc); 5' adaptor
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCATTATGGCC-3' and 3' adaptor sequence
5'-ATTCTAGAGCCGAGCGGCACATG-3' (where B = A,
C, G and N = A, C, G, or T). Average insert size 1.6
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

```

ORIGIN

```

Length:      862
Matches:     108
Conservative: 39

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Best Local Similarity: 48.21% Mismatches: 62
Query Match: 16.83% Indels: 15
DB: 12 Gaps: 5

US-09-451-739H-16 (1-512) x BG431116 (1-862)

QY 291 GluLeuCySerValArgLeuThrLeuAenGlnGluGluLysArgAsnAlaasp 310
DB 2 GAATTCAGGACTGTAAGAAAGTAATTTGAATCAGGTCGTTCAAGAGCGAATGAGCT--- 58
QY 311 IleLeuAsnGluLysIleArgGluLeuGluGlyArgIleGluGluGlnHisArgLysGlu 330
DB 59 -----CAGAGGCAACTTTCTCGA-----GAACAGAAATGCCAGATG 94
QY 331 LeuGluValLysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLysSer 350
DB 95 TTCAAGATGGAATTCGACCAATCACCTTCCAAACAAAGAGGATTTGAATGGCTCAA 154
QY 351 ValGluSerAsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyLeuLeuHis 370
DB 155 AAGAAATGAAT---TCTCAGAAATTCCTATGATCATGAAGAAGAAAGAAAGACTATCGCAT 211
QY 371 GluAsnCyMetLeuLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLys 390
DB 212 AAAATAGCATGTTCAGGAGAAATTCGTATGCTAAGACTAGAAATAGACACATATAA 271
QY 391 HisGlnTyThrGlnGluLysGluAsnLysTyPheGluAspIleLysIleLeuLysGluLys 410
DB 272 ATCAAAACAGGAAAGAAAGAAATGTTCTGAGGACCTTAAATTTGTAAGAAAGAAAG 331
QY 411 AsnAlaGluLeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSer 430
DB 332 AATGAAGACCTTCAGAGACTATAAAACAGAAATGAGGAAACATTAACACAAACATATCC 391
QY 431 GlnTySerGlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeu 450
DB 392 CAGTAAATGAGCGGTGATGTTCTGACGCTGAGATGCAATGCTAAATTCCTAAACTG 451
QY 451 Lys---GluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArg 469
DB 452 GAGAAATGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 511
QY 470 LeuAlaSerAlaValGlnAspHisSerGlnIleValThrSerArgLysSerGln---GluP 489
DB 512 TGGGCTGCTGCTATCATGATCGTATCATGATGAGATCATCAAAAGAAAGAAAGCAAGCAAG 571
QY 489 rolapheHisIleAlaGlyAspAlaCys-----LeuGlnArgLysMetAsnValAspV 507
DB 572 TTGCTTTCCAGAGAGCAAGAGATGAATGTTCTCGTTTACAGACAAATGAATTTTGTATG 631
QY 507 alSerSer 509
DB 632 TGCTAAC 639.

RESULT 12
BG622779
LOCUS 602647567F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4768912 5',
DEFINITION mRNA sequence.

ACCESSION BG622779
VERSION BG622779.1 GI:13674150
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 821)
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1633 row: f column: 17
High quality sequence stop: 818.
Location/Qualifiers
1..821
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4768912"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_79"
/note="Orxan: placenta; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggcgctcgcc); Site_2: Sfil
as follows: 5' and 3' adaptors were used in cloning
(ggcgctcgcc); 5' and 3' adaptor sequence: 5'-CAGGCCATTATGGCC-3',
and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCGGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.3
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 4,31e-31 Length: 821
Score: 433.50 Matches: 117
Percent Similarity: 65.56% Conservative: 60
Best Local Similarity: 43.33% Mismatches: 84
Query Match: 12.68% Indels: 12
DB: 5 Gaps: 5
US-09-451-739H-16 (1-512) x BG622779 (1-821)
QY 216 MetAspLysIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThr 235
DB 20 ATTGATCAACATGAATCAAGTGAAGATTGTTCCACTATTGAAATTAAGAGACA 79
QY 236 ValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGly 255
DB 80 TTGTGTTATGTTAAAGATTAAACAGAACTTAAAGATAATCATCTGTGAGCACTTACAGTA 138
QY 256 LysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLys 275
DB 139 AAAATTCGAAACTGAAATAATAGCTAGTGTACTACAAAGAGACTATCTGAAAGAA 198
QY 276 GluIleLysSerGlnLeuGluAsnGlnLysValLysValLysTrpGluGlnLeuCysSerVal 295
DB 199 GAAATTAATTCGAGTTAAAGCATGAACACTTGAATGGGAAAGAAAGACTCTGTAGTTTG 258
QY 296 ArgLeuThrLeuAsnGlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLys 315
DB 259 AGATTGTCATACAGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 318
QY 316 IleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuValLysGln 335
DB 319 GTTAGGAAAGATTGAAGATTCACAGAGAGCAATATAGGATAGAGCTGATGTGACAAA 378
QY 336 GlnLeuGluGlnAlaLeuArgIleGlnAspIleGlnLeuLysSerValGluSerAsnLeu 355
DB 379 CCAATTAACC-GGCTCTCAATCAGCAGAGGTGGAATTTGAAGACAGAGGAAATATTC 437
QY 356 AsnGlnValSerHisThrHisGluAsnGluAsnTyLeuLeuHisGluAsnCysMetLeu 375
DB 438 AATCAGGTTTCTGAAACTGATGAAGAAAGAAAGAC---CTGCTGATGAAACCG-TTGAATG 493
QY 376 LysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyGlnGlu 395

Db 494 CAAGATGAATTCAGCGCTCAGCTGGAAGACACACATAAATAACCAACCAACCTGGAA 553

Qy 396 LysGluAsnLysTyrPheGluAspIleLysLeuLysGluLysAsnAlaGluLeuGln 415

Db 554 AAG-----AAATACCTTAAAGAGCTTTGAAATTGTGAAAGAAAGCATGAAGACCTTCAA 607

Qy 416 MetThrLeuLysLeuLysGluLysLeuThrLysArgAlaSerGlnTyrSer-GlyG1 435

Db 608 AAGCGCTCTAAACCGAATGAGAAACATTAGCAGAAACGATAGCTCTTATAGTGGACA 667

Qy 435 nLeuLysValLeuLeuAlaGluAsnThrMetLeuThrSerLys-LeuLysGlu---LysG 454

Db 668 AGTTGCTGCTGACGCGATGAAACACA-----ACCTCCGCTTCTTAAACCGGGAGAGC 721

Qy 454 lnaSPysGluLeuLeuGluAlaGluLeuGluSerHisHisProArgLeuAlaSer---A 473

Db 722 AAAGAGAGCGCGGCGAAGACTGGAACAGAAATGATCATACCGTGTGACTGAATGTG 781

Qy 473 lavalGlnAspHisAspGlnIleVal 481

Db 782 CTCATGTGATCCTGATCAAGTCCTC 807

RESULT 13

CA394381

LOCUS

DEFINITION

cs50h08.Y1 Human Retinal pigment epithelium/choroid cDNA

(Un-normalized, unamplified): cs Homo sapiens cDNA clone cs50h08

5', mRNA sequence.

ACCESSION

CA394381

VERSION

CA394381.1 GI:24728876

SOURCE

EST.

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 684)

Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of human RPE/choroid for the

NEIBank Project: Over 6000 non-redundant transcripts, novel genes and splice variants

Mol. Vis. 8 (4), 205-220 (2002)

22103450

12107410

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 50 row: h column: 08

Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers

1. .684

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="cs50h08"

/tissue_type="RPE/choroid"

/dev_stage="Adult"

/lab_host="EMDH108"

/clone_lib="Human Retinal pigment epithelium/choroid cDNA

(Un-normalized, unamplified): cs"

/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp), essentially following the protocols of the SuperScript plasmid System (Invitrogen Corp.

<http://www.invitrogen.com/>). The library code

designation was cs. For this library, cDNA inserts were cloned into the NotI/MluI sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:

Pred. No.: 5,26e-31 Length: 684

Score: 431.50 Matches: 95

Percent Similarity: 68.04% Conservative: 54

Best Local Similarity: 43.38% Mismatches: 67

Query Match: 16.60% Indels: 3

DB: 14 Gaps: 2

US-09-451-739H-16 (1-512) x CA394381 (1-684)

Qy 216 MetAspLysIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThr 235

Db 36 ATGTATCAACATGAATGAAGTGTAAAGATTGTGTTCACCTATTGAAAAATTAATAACA 95

Qy 236 ValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGly 255

Db 96 TTTTGTATTATGGAAGAAGATTATAAACTTAAAGTAACCACTGTGACCAACTTAGATA 155

Qy 256 LysMetGluGlnMetLysLysPheCysValLeuLysLysLeuSerGluAlaLys 275

Db 156 AAAATTGGAAGAACTGAAAAATAAGCTAGTGTACTACAAAAGAGAAATATCTGAAAAAGAA 215

Qy 276 GluIleLysSerGlnLeuGlnLysValLysTrpGluGlnGluLysCysSerVal 295

Db 216 GAAATAAAATCGAGTTAAAGCATGAAATCTGTAATTGGAAAAAGAACTCTGTAGTTTG 275

Qy 296 ArgLeuThrLeuAsnGlnGluGluLysArgAsnAlaAspIleLeuAsnGluLys 315

Db 276 AGATTTCCTATACAGCAAGAAAAAGAAAGAAAGAAATGTTGAAGAGTTGCCACCAAAA 335

Qy 316 IleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGln 335

Db 336 GTTAGGAAAAAGTTAAGAATAACAGAAAGACAAATATAGGATAGAACTGTGTGACAAAA 395

Qy 336 GlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeu 355

Db 396 CCAATTAAACCGGCTCTCAATCAGCAGAGGTGGAAATTGACACAGAGGAATAATTCA 455

Qy 356 AsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeu 375

Db 456 AATCAGGTTTCTGAAACTGATGAAAAAGAAAGAC---CTGCTGATGAAACCGCTTGATG 512

Qy 376 LysLysGluLeuAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGlu 395

Db 513 CAAGATGAAATTCGCCAGGCTCAGGCTGGAAAAAGACACAAATAAAACCAAAACCTGGAA 572

Qy 396 LysGluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGln 415

Db 573 AAG-----AAATACITAAAGACTTTGAAATTGTGAAAAAGAAAGCATGAAGACCTTCAA 626

Qy 416 MetThrLeuLysLeuLysGluLysLeuThrLysArgAlaSerGlnTyrSerGly 434

Db 627 AAGGCTCTAAACCGAATGCGGAACATTAAGCAAAACGATAGCCTGTTATATAGTGA 683

RESULT 14

CF181571

LOCUS

DEFINITION

818415 MARC 3P1G Sus scrofa cDNA 5', mRNA sequence.

ACCESSION

CF181571

VERSION

CF181571.1 GI:33293347

KEYWORDS

EST.

SOURCE

Sus scrofa (pig)

ORGANISM

Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 683)

REFERENCE

Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Fox,J.,

AUTHORS

Wise, T.A., Nonnenan, D.J., Wray, J.E. and Keele, J.W.
A second set of porcine ESTs from a pooled-tissue normalized
library
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: SRG8012 row: M column: 3
Seq primer: GTAATACGACTCATTATAGG.
Location/Qualifiers

FEATURES

source

1..683
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3P1G"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
library made with RNA pooled from multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."

ORIGIN

Alignment Scores:
Pred. No.: 1,278-30 Length: 683
Score: 427.50 Matches: 104
Percent Similarity: 58.47% Conservative: 41
Best Local Similarity: 41.94% Mismatches: 78
Query Match: 16.45% Indels: 25
DB: 14 Gaps: 2

US-09-451-739H-16 (1-512) x CF181571 (1-683)

163 LeuGluLeuLysAsnGluInThrLeuArgAlaAspGlnMetPheProSerGluSerLys 182
Db 1 CTTAAGTGAAGAGACAGATGATGCAGCGCTATAAGAGACACCTAATGAGAGAAC 60
183 GlnLysLysValGluLysSerTrpAspSer-----GluSerLeuArgGlu 198
Db 61 AAGGTCAAGAGACAAATTAATTTCTGTGGATGACTTTGAGACTTAACCTAGTTACCTGAA 120
199 ThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLys 218
Db 121 ACAGCTTCCAAG-----132
219 IleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSer 238
Db 133 -----GATCATTTCTGTAGCGTATTGAAAGACGAGATTCAGTTCTTTCA 177
239 CysGluArgAlaArgGluLysAspHisCysGluGlnArgThrGlyLysMetGlu 258
Db 178 GATGACAGTTTACTAGAGATTAATAAAGCCACTATGAACCTACTACAGGAAATAATAA 237
259 GlnMetLysLysPheCysValLysLysLysLysSerGluAlaLysGluLys 278
Db 238 AAATGAAGAGTAAAGATCATTGGTTACGACCGAGCTATCAGAGCAAAAGAGTGA 297
279 SerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThr 298
Db 298 TCACAGTTAGAACACCAATAATCGGGTGGCAACAGAGTTCTACAGTTTCAGATGCACC 357
299 LeuAsnGluGluGluLysArgArgAlaAspIleLeuAsnGluLysIleArgGlu 318
Db 358 TTAACACAGAGAGAGAGAGAAATGTTTAAAGTTATATGAAAAAATCAGGAG 417
319 GluLeuGlyArgIleGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGlu 338

Db 418 GAGTTAAGAGAGAGAGAGAGATATGATAAGAGCTGAAATGAAACAGCACTTGAA 477
Qy 339 GlnAlaLeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuGlnVal 358
Db 478 CTGACTGTCCAAGCAGCTGGACATGGAATGAGCGGTGAGAAATATCTGACCGGT 537
Qy 359 SerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysGlu 378
Db 538 GATGAGAGTCACGAAAGCAAAAGAACTGTTGCTTAAACACACATGTCCAGAAATGAA 597
Qy 379 IleAlaMetLeuLysGluGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsn 398
Db 598 ATTCCCATGTTTAAACACAGAAATAGAGCGAGTGGAAATCATACCCAGGAATGAGAG 657
Qy 399 LysTyrPheGluAspIleLysIle 406
Db 658 AATATTTTATGGACATGAAAT 681

RESULT 15
BU678550/c
LOCUS
DEFINITION
UI-CF-DUI-aar-o-16-o-UI.s1 UI-CF-DUI Homo sapiens cDNA clone
UI-CF-DUI-aar-o-16-o-UI 3', mRNA sequence.
ACCESSION
BU678550
VERSION
BU678550.1 GI:23525612
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 638)
AUTHORS
Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
PUBMED
889548
COMMENT
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA-res.

FEATURES

source

Location/Qualifiers
1..638
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="UI-CF-DUI-aar-o-16-o-UI"
/tissue_type="Primary Lung Epithelial Cells"
/dev_stage="adult"
/lab_hosts="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-DUI"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-DUI is a normalized cDNA library containing the
following tissue(s): Primary Lung Epithelial Cells. The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT73-Pac vector. The oligonucleotide

used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dr)18 tail. The sequence tag for this library is GGCTGTAGGC.
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-DUI
TAG_SEQ=GGCTGTAGGC"

ORIGIN

Alignment Scores:

Pred. No.:	1.31e-29	Length:	638
Score:	416.50	Matches:	91
Percent Similarity:	74.68%	Conservative:	24
Best Local Similarity:	59.09%	Mismatches:	35
Query Match:	16.03%	Indels:	4
DB:	13	Gaps:	2

US-09-451-739H-16 (1-512) x BUG78550 (1-638)

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Db	636	C	N	A	G	T	C	A	T	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	577				
Qy	380	A	l	a	M	e	t	L	e	u	L	y	s	L	e	u	G	l	u	i	e	A	l	a	T	h	r	L	e	u	-	L	y	s	H	i	s	399	
Db	576	G	C	T	A	T	G	T	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	517				
Qy	399	S	T	R	P	H	e	G	l	u	a	s	p	l	e	L	e	u	L	y	s	G	l	u	L	y	s	A	s	n	A	l	a	G	l	u	419		
Db	516	A	T	G	T	T	T	T	G	A	G	A	C	T	T	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	457			
Qy	419	S	L	e	u	L	y	s	G	l	u	L	y	s	A	r	g	A	l	a	S	e	r	G	l	n	T	y	r	S	e	r	G	l	n	L	e	u	439
Db	456	A	C	A	A	T	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	397				
Qy	439	U	L	E	A	L	A	G	l	u	a	s	n	T	h	r	L	e	u	L	y	s	-	-	G	l	u	L	y	s	G	l	u	i	1	458			
Db	396	G	A	C	A	T	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	337				
Qy	458	E	L	e	u	G	l	u	A	l	a	G	l	u	S	e	r	H	i	s	P	r	o	A	r	g	L	e	u	A	s	e	r	A	l	a	V	478	
Db	336	A	C	T	G	A	G	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	277				
Qy	478	P	G	L	I	E	V	A	L	T	h	r	S	e	r	G	l	n	G	l	u	P	r	o	A	l	a	P	h	e	I	s	I	e	A	l	498		
Db	276	T	C	A	A	A	G	T	G	A	C	A	T	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	217			
Qy	498	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	509					
Db	216	T	T	C	T	G	T	T	T	A	C	A	G	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	177			

Search completed: May 6, 2004, 17:01:19
Job time : 3866 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 07:44:53 ; Search time 81.0178 Seconds

(without alignments)
5870.227 Million cell updates/sec

Title: US-09-451-739H-4

Perfect score: 857
Sequence: 1 cctccgagacgggtccat.....tcataaacccaagggaagt 857

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	605.4	70.8	873	US-09-006-783A-4	Sequence 4, Appli
2	605.6	70.7	1902	US-09-258-257-1	Sequence 1, Appli
3	605.6	70.7	1902	US-09-258-371-1	Sequence 1, Appli
4	605.6	70.7	1902	US-08-569-721A-1	Sequence 1, Appli
5	605.6	70.7	1902	US-08-751-230-1	Sequence 1, Appli
6	605.6	70.7	1902	US-09-499-082-1	Sequence 1, Appli
7	605.6	70.7	1902	US-09-258-372-1	Sequence 1, Appli
8	605.6	70.7	2061	US-09-258-371-9	Sequence 9, Appli
9	605.6	70.7	2061	US-08-751-230-9	Sequence 9, Appli
10	605.6	70.7	2061	US-09-499-082-9	Sequence 9, Appli
11	605.6	70.7	2061	US-09-258-372-9	Sequence 9, Appli
12	604	70.5	2061	US-09-006-783A-2	Sequence 2, Appli
13	604.4	70.3	2061	US-09-159-871-1	Sequence 1, Appli
14	534.4	62.4	633	US-09-006-783A-6	Sequence 6, Appli
15	355	41.4	451	US-09-370-838-146	Sequence 146, App
16	142.6	16.6	840	US-09-601-478-6	Sequence 6, Appli
17	142.6	16.6	1078	US-09-601-478-7	Sequence 7, Appli
18	142	16.6	1154	US-09-484-970B-81	Sequence 81, Appli
19	96.4	11.2	678	US-09-195-286-3	Sequence 3, Appli
20	96.4	11.2	699	US-09-195-286-2	Sequence 2, Appli
21	73.4	8.6	7218	US-08-232-463-14	Sequence 14, Appli
22	65.6	7.8	1864	US-09-620-312D-435	Sequence 435, App
23	61.4	7.2	1926	US-09-249-585A-4	Sequence 4, Appli
24	61.4	7.2	1931	US-09-130-114-2	Sequence 2, Appli
25	59.6	7.0	1926	US-09-249-585A-2	Sequence 2, Appli
26	59.6	7.0	1926	US-09-410-399-3	Sequence 3, Appli
27	59.6	7.0	2580	US-09-050-863-2	Sequence 2, Appli

Query Match 70.8%; Score 606.4; DB 3; Length 873;
Best Local Similarity 99.0%; Pred. No. 1.2e-124;
Matches 610; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ALIGNMENTS

RESULT 1

US-09-006-783A-4

; Sequence 4, Application US/09006783A

; Patent No. 6297366

; GENERAL INFORMATION:

; APPLICANT: Gudkov, Andrey V

; APPLICANT: Garkavstev, Igor

; APPLICANT: Riabowol, Karl

; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling

; TITLE OF INVENTION: Pathway

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

; STREET: 300 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/006,783A

; FILING DATE: 15-JAN-1998

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 6297366nan, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 97,837

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-913-0001

; TELEFAX: 312-913-0002

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 873 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 7..813

; US-09-006-783A-4

; GENERAL INFORMATION:
 ; APPLICANT: Garkavtsev, Igor
 ; APPLICANT: Rabinowol, Karl
 ; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
 ; TITLE OF INVENTION: SUPPRESSOR GENE INGI
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/258,371
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/751,230
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mood, Leslie A.
 ; REGISTRATION NUMBER: 37,047
 ; REFERENCE/DOCKET NUMBER: 028722-144
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-854-7400
 ; TELEFAX: 415-854-8275
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1902 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 109..741
 ; US-09-258-371-1

Query Match	70.74%	Score 605.6	DB 2	Length 1902
Best Local Similarity	95.6%	Pred. No. 2.1e-124		
Matches 623	Conservative 0	Mismatches 29	Indels 0	Gaps 0
QY	206	CTAGGCTCTCGGAGTGGTGTGCTCGGCGCGGAGATGAGATCTCTGAAGAGCTGACGAG	265	
Db	1	CTGACCCGAGGCTGGGGCCGCGCTGGCCCTGGAAACAGATCTCTGAAGAGCTGACGAG	60	
QY	266	TGCTACGAGCGCTTCAGTCCGCGACACAGACGGGGCGCGAGAAGCGGCGGATGCTGCACCTGT	325	
Db	61	TGCTACGAGCGCTTCAGTCCGCGACACAGACGGGGCGCGAGAAGCGGCGGATGCTGCACCTGT	120	
QY	326	GTGCGAGCGCGCTGTATCCGCGAGCCAGGAGCTGGGCGACGAGAGATCCAGATCTGTGAGC	385	
Db	121	GTGCGAGCGCGCTGTATCCGCGAGCCAGGAGCTGGGCGACGAGAGATCCAGATCTGTGAGC	180	
QY	386	CAGATGTGTGAGCTGGTGTGAGAACCGCACGCGGCAGGTGGACACAGCCACTGTGAGCTGTTC	445	
Db	181	CAGATGTGTGAGCTGGTGTGAGAACCGCACGCGGCAGGTGGACACAGCCACTGTGAGCTGTTC	240	
QY	446	GAGGCGCAGCAGGAGCTGTGGGCGACACAGCGGGCAACAGCGGCGAAGGCTCGCGCGACAGG	505	
Db	241	GAGGCGCAGCAGGAGCTGTGGGCGACACAGTGGGCAACAGCGGCAAGGTTGGCGCGACAGG	300	
QY	506	CCCAAGCGCAGGCGGACGCGAGCTGTGACAGCCCAACAGCAAGCGCTCAGCGCGGGCAG	565	
Db	301	CCCAATGTGGCATGTGGTAGCCAGCTGTGACAGCCCAACAGCAAGCGCTCAGCGCGGGCAG	360	
QY	566	CGCAACACGAGAACCGGTGAGAACCGCTCCAGCAACCCACGACGACGAGCGCGCCTCG	625	

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361 CGCAACAAGAGAACCGTGAGAAACGCTCCAGCAACCAAGCAACGACGCGGCGCTCG 420
626 GGCAACACCAAGAGGAAGAGGCCCAAGACCTCCAAGAGAAGAGCGCTCCAAGGGCCAAG 685
421 GGCAACACCAAGAGGAAGAGGCCCAAGACCTCCAAGAGAAGAGCGCTCCAAGGGCCAAG 480
686 GGGAGAGCGAGAGCGTGCCCTGCGAGACTCCGACCTCGACCCCAACGAAACCCACGTACTGT 745
481 GCGGAGCGAGAGGGGTGCCCCCTGCGGACCTCCCCATGACCCCAACGAAACCCACGTACTGT 540
746 CTGTGCAACACAGGTCTCTCTATGCGGAGATGATCGGTGCGACCAACACAGTGCCTCCATC 805
541 CTGTGCAACACAGGTCTCTCTATGCGGAGATGATCGGTGCGACCAACACAGTGCCTCCATC 805
806 GAGTGTGTTCCACTTCTCTGCTGGGGCTCAATCATATAACCCAAAGGGCAAGT 857
601 GAGTGTGTTCCACTTCTCTGCTGGGGCTCAATCATATAACCCAAAGGGCAAGT 652

RESULT 4
US-08-569-721A-1
; Sequence 1, Application US/08569721A
; Patent No. 6037121
; GENERAL INFORMATION:
; APPLICANT: GARKAVTSEV, Igor
; APPLICANT: RIABOKOL, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,721A
; FILING DATE: 08-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 854-7400
; TELEFAX: (650) 854-8275
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1902 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..738
; US-08-569-721A-1

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	Query Match	70.7%	Score 605.6	DB 3	Length 1902
	Best Local Similarity	95.6%	Pred. No. 2.1e-124		
	Matches 623	Conservative	0	Mismatches 29	Indels 0
				Gaps 0	
Qy	206	CTAGGCTGCTGGGAGTGCTGTGTCGGCCGGCGGAATGGAGATCTCTGAAGGAGCTAGACGAG	265		
Db	1	CTGACCCGAGGTGGGCGCGCGGTGCGCTGGGAAACAGATCCTCTGAAGGAGCTAGACGAG	60		

266 TGCTACGAGGCTTCTAGTCGCGAGACAGACGAGGCGGCGCAGAGCGGCGGATGCTGCACTGT 325
Db TGCTACGAGGCTTCTAGTCGCGAGACAGACGAGGCGGCGCAGAGCGGCGGATGCTGCACTGT 120
Qy GTCCAGCGGCGCTGTATCCGACACGAGGAGCTGGGCGGAGAGAGATCCAGATCTGTGAGC 385
Db GTCCAGCGGCGCTGTATCCGACACGAGGAGCTGGGCGGAGAGATCCAGATCTGTGAGC 180
Qy CAGATGTTGAGTGTGTGAGAAACCGACGCGGAGGTGGAAGCAGCCAGTGTGAGTGTTC 445
Db CAGATGTTGAGTGTGTGAGAAACCGACGCGGAGGTGGAAGCAGCCAGTGTGAGTGTTC 240
Qy GAGGCGCAGCAGGAGCTGGGCGGACACAGCGGCGCAACAGCGGCAAGGCTGGCGGACAGG 505
Db GAGGCGCAGCAGGAGCTGGGCGGACACAGTGGGCAACAGCGGCAAGGTTGGCGGACAGG 300
Qy CCAAGAGCGAGGCGGAGCGGAGGTGACAGCCCAACAGCAAGCGCTCAAGCGGCGAG 565
Db CCAAGAGCGGAGCGGAGGTGACAGCCCAACAGCAAGCGCTCAAGCGGCGAG 360
Qy CGCAACCAACGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAAC 625
Db CGCAACCAACGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAAC 420
Qy GGCAACCAACGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAAC 685
Db GGCAACCAACGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAAC 480
Qy GCGGAGCGGAGGCGGCTCCCTGCGGAGCTCCCGACCTCCCGACCTCCCGACCTCCCGACCT 745
Db GCGGAGCGGAGGCGGCTCCCTGCGGAGCTCCCGACCTCCCGACCTCCCGACCTCCCGACCT 540
Qy CTGTGCAACCAAGTCTCTATGGGAGATGATCGGCTGCGACCAACGAGTGTGCGGCTTC 805
Db CTGTGCAACCAAGTCTCTATGGGAGATGATCGGCTGCGACCAACGAGTGTGCGGCTTC 540
Qy GAGTGTGCTTCACTTCTGCTGGGCTCAATCATATAACCAAGGCAAGT 857
Db GAGTGTGCTTCACTTCTGCTGGGCTCAATCATATAACCAAGGCAAGT 652

RESULT 5
US-08-751-230-1
; Sequence 1, Application US/08751230
; Patent No. 6117633
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,230
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A.
; REGISTRATION NUMBER: 37,047

REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 109..741
US-08-751-230-1

Query Match 70.7%; Score 605.6; DB 3; Length 1902;
Best Local Similarity 95.6%; Pred. No. 2.1e-124;
Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
Qy 206 CTAGGCTGCTGGGAGTGGTGGTCCGGCGGCGGAAATGGAGATCTCTGAAGAGCTAGACGAG 265
Db 1 CTGACCCGAGGGTGGGCGCGCGTGGCCGTGAAACAGATCTCTGAAGAGCTAGACGAG 60
Qy 266 TGCTACGAGCGCTTCTAGTTCGCGAGACAGACGCGGCGGCGAGAGCGGCGGATGCTGCACTGT 325
Db 61 TGCTACGAGCGCTTCTAGTTCGCGAGACAGACGCGGCGGCGAGAGCGGCGGATGCTGCACTGT 120
Qy 326 GTGCGAGCGCGCTGTATCCGACACGAGGAGCTGGGCGGAGAGATCCAGATCTGTGAGC 385
Db 121 GTGCGAGCGCGCTGTATCCGACACGAGGAGCTGGGCGGAGAGATCCAGATCTGTGAGC 180
Qy 386 CAGATGTTGAGTGTGTGAGAAACCGACGCGGCAACAGCGGCAAGGCTGGACCGCTGAGTGTTC 445
Db 181 CAGATGTTGAGTGTGTGAGAAACCGACGCGGCAACAGCGGCAAGGCTGGACCGCTGAGTGTTC 240
Qy 446 GAGGCGCAGCAGGAGCTGGGCGGACACAGCGGCGCAACAGCGGCAAGGCTGGCGGACAGG 505
Db 241 GAGGCGCAGCAGGAGCTGGGCGGACACAGTGGGCGCAACAGCGGCAAGGTTGGCGGACAGG 300
Qy 506 CCCAAAGCGGAGCGGCGGAGGCTGCAAGCCCAACAGCAAGCGCTCACCGCGGCGAG 565
Db 301 CCCAAAGCGGAGCTGGTGTGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAAC 360
Qy 566 CGCAACCAACGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAAC 625
Db 361 CGCAACCAACGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAACCGTGTGAGAAC 420
Qy 626 GGCACACCCAGGAGAGAGGCGGCAAGCCTCCAAAGAGAGAGGCGCTCCAAAGGCGCAAG 685
Db 421 GGCACACCCAGGAGAGAGGCGGCAAGCCTCCAAAGAGAGAGGCGCTCCAAAGGCGCAAG 480
Qy 686 GCGGAGCGGAGGCGCTCCCTGCGGAGCTCCCGACCTCCCGACCTCCCGACCTCCCGACCT 745
Db 481 GCGGAGCGGAGGCGCTCCCTGCGGAGCTCCCGACCTCCCGACCTCCCGACCTCCCGACCT 540
Qy 746 CTGTGCAACCAAGTCTCTATGGGAGATGATCGGCTGCGACCAACAGGAGTGTGCGGCTTC 805
Db 541 CTGTGCAACCAAGTCTCTATGGGAGATGATCGGCTGCGACCAACAGGAGTGTGCGGCTTC 600
Qy 806 GAGTGTGCTTCACTTCTGCTGGGCTCAATCATATAACCAAGGCAAGT 857
Db 601 GAGTGTGCTTCACTTCTGCTGGGCTCAATCATATAACCAAGGCAAGT 652

RESULT 6
US-09-499-082-1
; Sequence 1, Application US/09499082
; Patent No. 6143522
; GENERAL INFORMATION:
; APPLICANT: Helbing, Caren C.
; APPLICANT: Riabowol, Karl
; APPLICANT: Johnston, Randall N.

QY 206 CTAGGCTGCTGGAGTGGTGGTCCGCGCCGGAATGGAGATCCCTGAAGGAGCTAGACGAG 265
 Db 1 CTGACCCGAGGGTGGGCGCGCGTGGCGCTGGAACAGATCCTGAGGAGCTAGACGAG 60
 QY 266 TGTCTAGCAGGCTTCTAGTCCGAGACAGACGCGGGCGCAGAGCGGCGGATCTGCATGT 325
 Db 61 TGTCTAGCAGGCTTCTAGTCCGAGACAGACGCGGGCGCAGAGCGGCGGATCTGCATGT 120
 QY 326 GTCCAGCGGCGCTGATCCGCGACGAGGAGCTGGGCGCAGAGATCCAGATCGTGCAGC 385
 Db 121 GTCCAGCGGCGCTGATCCGCGACGAGGAGCTGGGCGCAGAGATCCAGATCGTGCAGC 180
 QY 386 CAGATGCTGAGCTGTGAGAACCGCAGCGGCGAGGTGGACAGCAGCTGGAGCTGTTTC 445
 Db 181 CAGATGCTGAGCTGTGAGAACCGCAGCGGCGAGGTGGACAGCAGCTGGAGCTGTTTC 240
 QY 446 GAGCGCAGCAGAGCTGGGCGCAGACAGCGGCGAACAGCGGCGAACAGGCTGGGCGCAGCAGG 505
 Db 241 GAGCGCAGCAGAGCTGGGCGCAGACAGCTGGGCGAACAGCGGCGAACAGGCTGGGCGCAGCAGG 300
 QY 506 CCCAAGGCGAGCGCGCAGCGAGCTGACAGCCCAACAGAGCGCTACGCGGCGAG 555
 Db 301 CCCAATGGCGAGTGGGTAGCGAGTCTGACAGCCCAACAGAGCGCTACGCGGCGAG 360
 QY 566 CGCAACACAGAACCGTCCGAGAACCGTCCAGCAACCGACCGACCGCGCGCTCG 625
 Db 361 CGCAACACAGAACCGTCCGAGAACCGTCCAGCAACCGACCGACCGCGCGCTCG 420
 QY 626 GGCACACCCAGAGAGAGCGCAGACCTTCAGAGAGAGAGCGCTCCAGGCGCAAG 685
 Db 421 GGCACACCCAGAGAGAGCGCAGACCTTCAGAGAGAGAGCGCTCCAGGCGCAAG 480
 QY 686 GCGAGCGAGAGCGCTCCCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCT 745
 Db 481 GCGAGCGAGAGCGCTCCCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCT 540
 QY 746 CTGTGCAACAGCTCTCTATGGGAGATGATCGGCTCGACAGCAGCTGCCCCATC 805
 Db 541 CTGTGCAACAGCTCTCTATGGGAGATGATCGGCTCGACAGCAGCTGCCCCATC 600
 QY 806 GAGTGTTCACCTTCTGCTGCTGGGCTCAATCAATAAACCAAGGGCAAGT 857
 Db 601 GAGTGTTCACCTTCTGCTGCTGGGCTCAATCAATAAACCAAGGGCAAGT 652

RESULT 8

US-09-258-371-9
 ; Sequence 9, Application US/09258371

; Patent No. 5986078

; GENERAL INFORMATION:

; APPLICANT: Garkavtsev, Igor

; APPLICANT: Riabowol, Karl

; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR

; TITLE OF INVENTION: SUPPRESSOR GENE INGI

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/258,371

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/751,230
 ; FILING DATE: 08/751,230
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mooi, Leslie A.
 ; REGISTRATION NUMBER: 37,047
 ; REFERENCE/DOCKET NUMBER: 028722-144
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-854-7400
 ; TELEFAX: 415-854-8275
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2061 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 16..900
 ; US-09-258-371-9

Query Match 70.7%; Score 605.6; DB 2; Length 2061;
 Best Local Similarity 95.6%; Pred. No. 2.2e-124;
 Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 206 CTAGGCTCTCGGAGTGTGTGTCGCGCGCGGAATGGAGATCCCTGAAGGAGCTAGACGAG 265
 Db 160 CTGACCCGAGGGTGGGCGCGCGTGGCGCTGGAACAGATCCTGAGGAGCTAGACGAG 219
 QY 266 TGTCTAGCAGCGCTTCTAGTCCGAGACAGACGCGGGCGCAGAGCGGCGGATCTGCATGT 325
 Db 220 TGTCTAGCAGCGCTTCTAGTCCGAGACAGACGCGGGCGCAGAGCGGCGGATCTGCATGT 279
 QY 326 GTCCAGCGGCGCTGATCCGCGACGAGGAGCTGGGCGCAGAGATCCAGATCGTGCAGC 385
 Db 280 GTCCAGCGGCGCTGATCCGCGACGAGGAGCTGGGCGCAGAGATCCAGATCGTGCAGC 339
 QY 386 CAGATGCTGAGCTGTGAGAACCGCAGCGGCGAGTGGACAGCAGCTGAGAGCTGTTTC 445
 Db 340 CAGATGCTGAGCTGTGAGAACCGCAGCGCGAGTGGACAGCAGCTGAGAGCTGTTTC 399
 QY 446 GAGGCGCAGCAGGAGCTGGGCGCAGACAGCGGCGCAACAGCGGCAAGCTGGCGGCGCAGG 505
 Db 400 GAGGCGCAGCAGGAGCTGGGCGCAGACAGCTGGGCGCAACAGCGGCAAGCTGGCGGCGCAGG 459
 QY 506 CCCAAGGCGAGCGCGCAGCGAGCTGACAGCCCAACAGAGCGCTACGCGGCGAG 565
 Db 460 CCCAATGGCGAGTGGGTAGCGAGTCTGACAGCCCAACAGAGCGCTACGCGGCGAG 519
 QY 566 CGCAACACAGAACCGTCCGAGAACCGTCCAGCAACCGACCGACCGCGCGCTCG 625
 Db 520 CGCAACACAGAACCGTCCGAGAACCGTCCAGCAACCGACCGACCGCGCGCTCG 579
 QY 626 GGCACACCCAGAGAGAGCGCAGACCTTCAGAGAGAGAGCGCTCCAGGCGCAAG 685
 Db 580 GGCACACCCAGAGAGAGCGCAGACCTTCAGAGAGAGAGCGCTCCAGGCGCAAG 639
 QY 686 GCGAGCGAGAGGCGCTCCCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCT 745
 Db 640 GCGAGCGAGAGGCGCTCCCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCT 699
 QY 746 CTGTGCAACAGCTCTCTATGGGAGATGATCGGCTCGACAGCAGCTGCCCCATC 805
 Db 700 CTGTGCAACAGCTCTCTATGGGAGATGATCGGCTCGACAGCAGCTGCCCCATC 759
 QY 806 GAGTGTTCACCTTCTGCTGCTGGGCTCAATCAATAAACCAAGGGCAAGT 857
 Db 760 GAGTGTTCACCTTCTGCTGCTGGGCTCAATCAATAAACCAAGGGCAAGT 811

RESULT 9

US-08-751-230-9

; Sequence 9, Application US/08751230

Patent No. 6117633
 GENERAL INFORMATION:
 APPLICANT: Garkavtsev, Igor
 APPLICANT: Riabowol, Karl
 TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
 TITLE OF INVENTION: SUPPRESSOR GENE INGI
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Burns, Doane, Swecker & Mathis
 STREET: 699 Prince Street
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/751,230
 FILING DATE: 15-NOV-1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/569721
 FILING DATE: 08-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Mooi, Leslie A.
 REGISTRATION NUMBER: 37,047
 REFERENCE/DOCKET NUMBER: 028722-144
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-7400
 TELEFAX: 415-854-8275
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2061 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 NAME/KEY: CDS
 LOCATION: 16..900
 US-08-751-230-9

Query Match 70.7%; Score 605.6; DB 3; Length 2061;
 Best Local Similarity 95.6%; Pred. No. 2.2e-124;
 Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 QY 206 CTAGGCTCTGGAGTGTGTGTCGGCGCGCGGATGAGATCTCTGAAGGAGCTAGACGAG 265
 Db 160 CTGACCCAGGTTGGGCGCGCGTGGCGGTGGAACAGATCTCTGAAGGAGCTAGACGAG 219
 QY 266 TGCTACGAGCGCTTCAGTCTGGGAGACAGACGCGGCGCGAGAGCGCGGATGCTGCACTGT 325
 Db 220 TGCTACGAGCGCTTCAGTCTGGGAGACAGACGCGGCGCGAGAGCGCGGATGCTGCACTGT 279
 QY 326 GTGCAGCGCGGCTGATCCGCGAGCAGAGCTGGCGGACAGAGATCCAGATCGTGAGC 385
 Db 280 GTGCAGCGCGGCTGATCCGCGAGCAGAGCTGGCGGACAGAGATCCAGATCGTGAGC 339
 QY 386 CAGATGTGGAGCTGGTGGAGAAACGCGACGCGGAGGTTGGGACAGCGCTGGAGCTGTTTC 445
 Db 340 CAGATGTGGAGCTGGTGGAGAAACGCGACGCGGAGGTTGGGACAGCGCTGGAGCTGTTTC 399
 QY 446 GAGGCGGACGAGGAGCTGGGCGACACAGCGGCGGACAGCGGAGGTTGGGCGGACAGG 505
 Db 400 GAGGCGGACGAGGAGCTGGGCGACACAGTGGGCGGACAGCGGAGGTTGGGCGGACAGG 459
 QY 506 CCCAAAGGCGGCGGAGCGGCTGCAAGGCCCAACAGCGCTCACGGCGGAG 565
 Db 460 CCCAATGGGATGCGGTAGGCGAGTCTGCAAGGCCCAACAGCGCTCACGGCGGAG 519

QY 566 CGCAACACGAGAACCGTGAAGACCGGTTCAGCAACACGACACGACGAGCGGCGCTCG 625
 Db 520 CGCAACACGAGAACCGTGAAGACCGGTTCAGCAACACGACACGACGAGCGGCGCTCG 579
 QY 626 GGCACACCCAGGAGAGAGGCGCAAGACCTCCCAAGAGAGAGCGCTCCCAAGGCGCAAG 685
 Db 580 GGCACACCCAGGAGAGAGGCGCAAGACCTCCCAAGAGAGAGCGCTCCCAAGGCGCAAG 639
 QY 686 GCGGAGGAGAGGCGCTCCCTGCGGACCTCCCATCGACCCCAACGACACCGATCTGT 745
 Db 640 GCGGAGGAGAGGCGCTCCCTGCGGACCTCCCATCGACCCCAACGACACCGATCTGT 699
 QY 746 CTGTGCAACACGAGTCTCTATGCGGAGATGATCGGTCGCGACACGAGTGCCTCATC 805
 Db 700 CTGTGCAACACGAGTCTCTATGCGGAGATGATCGGTCGCGACACGAGTGCCTCATC 759
 QY 806 GAGTGGTTCCACTTCTCGTGGTGGGCTCAATCATATAAACCAAGGCAAGT 857
 Db 760 GAGTGGTTCCACTTCTCGTGGTGGGCTCAATCATATAAACCAAGGCAAGT 811
 RESULT 10
 US-09-499-082-9
 Sequence 9, Application US/09499082
 Patent No. 6143522
 GENERAL INFORMATION:
 APPLICANT: Helbing, Caren C.
 APPLICANT: Riabowol, Karl
 APPLICANT: Johnston, Randall N.
 APPLICANT: Garkavtsev, Igor
 TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Burns, Doane, Swecker & Mathis
 STREET: 699 Prince Street
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/499,082
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/828,158
 FILING DATE: 27-MAR-1997
 APPLICATION NUMBER: US 08/751230
 FILING DATE: 15-NOV-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/569721
 FILING DATE: 08-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Mooi, Leslie A.
 REGISTRATION NUMBER: 37,047
 REFERENCE/DOCKET NUMBER: 028722-148
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-854-7400
 TELEFAX: 650-854-8275
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2061 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 NAME/KEY: CDS
 LOCATION: 16..900

US-09-499-082-9

Query Match 70.7%; Score 605.6; DB 3; Length 2061;
Best Local Similarity 95.6%; Pred. No. 2.2e-124; Indels 0; Gaps 0;
Matches 623; Conservative 0; Mismatches 29;

206 CTAGGCTGTGGAGTGTGGTCCGGCCCGGAGATGGAGATCTCTGAAGGAGCTAGACGAG 265
160 CTGACCCGAGGGTGGGGCGCGCTGGCGTGAACACAGATCTCTGAAGGAGCTAGACGAG 219
266 TGTCTAGACGCTTTCAGTCCGAGACAGACGGGGCGAGAGCGCGGATGCTGCACTGT 325
220 TGTCTAGACGCTTTCAGTCCGAGACAGACGGGGCGAGAGCGCGGATGCTGCACTGT 279
326 GTGACGCGCGCTGATCCGACGAGAGCTGGCGACGAGAGATCCAGATCGTAGC 385
280 GTGACGCGCGCTGATCCGACGAGAGCTGGCGACGAGAGATCCAGATCGTAGC 339
386 CAGATGCTGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGACAGCAGCTGGAGCTGTC 445
340 CAGATGCTGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGACAGCAGCTGGAGCTGTC 399
445 GAGGCGCAGCAGAGCTGGCGACACAGCGGGCGACAGCGGCGAGGTGGAGCGGACGAG 505
400 GAGGCGCAGCAGAGCTGGCGACACAGCGGGCGACAGCGGCGAGGTGGAGCGGACGAG 459
506 CCCAAGGCGAGCGCGGACGAGCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAG 565
460 CCCAATGGCGATGGGTAGCGAGTCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAG 519
565 CCCAATGGCGATGGGTAGCGAGTCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAG 625
520 CGCAACCAAGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 579
626 GGCACACCAAGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 685
580 GGCACACCAAGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 639
686 GCGGAGCGAGGCGTCCCTGCGGAGTATCGGCTGCGACACCGCCCAACAGCAAGCGCTCAC 745
640 GCGGAGCGAGGCGTCCCTGCGGAGTATCGGCTGCGACACCGCCCAACAGCAAGCGCTCAC 699
745 CTGTGCAACCAAGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 805
700 CTGTGCAACCAAGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 759
806 GAGTGGTTCACCTTCTGCTGGTGGGCTCAATCATAAACCCCAAGGCGAAGT 857
760 GAGTGGTTCACCTTCTGCTGGTGGGCTCAATCATAAACCCCAAGGCGAAGT 811

RESULT 11

US-09-258-372-9
Sequence 9, Application US/09258372
Patent No. 6238918
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Rabinow, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..900
US-09-258-372-9

Query Match 70.7%; Score 605.6; DB 3; Length 2061;
Best Local Similarity 95.6%; Pred. No. 2.2e-124; Indels 0; Gaps 0;
Matches 623; Conservative 0; Mismatches 29;

206 CTAGGCTGTGGAGTGTGGTCCGGCCCGGAGATGGAGATCTCTGAAGGAGCTAGACGAG 265
160 CTGACCCGAGGGTGGGGCGCGCTGGCGTGAACACAGATCTCTGAAGGAGCTAGACGAG 219
266 TGTCTAGACGCTTTCAGTCCGAGACAGACGGGGCGAGAGCGCGGATGCTGCACTGT 325
220 TGTCTAGACGCTTTCAGTCCGAGACAGACGGGGCGAGAGCGCGGATGCTGCACTGT 279
326 GTGACGCGCGCTGATCCGACGAGAGCTGGCGACGAGAGATCCAGATCGTAGC 385
280 GTGACGCGCGCTGATCCGACGAGAGCTGGCGACGAGAGATCCAGATCGTAGC 339
386 CAGATGCTGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 445
340 CAGATGCTGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 399
445 GAGGCGCAGCAGAGCTGGCGACACAGCGGGCGACAGCGGCGAGGTGGAGCGGACGAG 505
400 GAGGCGCAGCAGAGCTGGCGACACAGCGGGCGACAGCGGCGAGGTGGAGCGGACGAG 459
506 CCCAAGGCGAGCGCGGACGAGCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAG 565
460 CCCAATGGCGATGGGTAGCGAGTCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAG 519
565 CGCAACCAAGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 625
520 CGCAACCAAGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 579
626 GGCACACCAAGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 685
580 GGCACACCAAGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 639
686 GCGGAGCGAGGCGTCCCTGCGGAGTATCGGCTGCGACACCGCCCAACAGCAAGCGCTCAC 745
640 GCGGAGCGAGGCGTCCCTGCGGAGTATCGGCTGCGACACCGCCCAACAGCAAGCGCTCAC 699
745 CTGTGCAACCAAGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 805
700 CTGTGCAACCAAGGAGCTGGTGGAGAACCGCACGCGGCGAGGTGGAGCGGACGAGCTGTC 759
806 GAGTGGTTCACCTTCTGCTGGTGGGCTCAATCATAAACCCCAAGGCGAAGT 857
760 GAGTGGTTCACCTTCTGCTGGTGGGCTCAATCATAAACCCCAAGGCGAAGT 811

RESULT 12

US-09-006-783A-2
; Sequence 2, Application US/09006783A
; Patent No. 6297366
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrey V
; APPLICANT: Garkavstev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: p53/ING1 as a Mediator of p53 Signaling
; TITLE OF INVENTION: Pathway
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,783A
; FILING DATE: 15-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6297366nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 97,837
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16...897
US-09-006-783A-2

Query Match 70.5%; Score 604; DB 3; Length 2061;
Best Local Similarity 95.4%; Pred. No. 4.9e-124;
Matches 622; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 206 CTAGGCTCTGGAGTGGTGTCCGGCGCGGAATGGAGATCCCTGAAGGAGCTAGACGAG 265
DB 160 CTGACCCGAGGTGGGCGCGGTGGCCGTGGAAACAGATCCCTGAAGGCGTAGACGAG 219
QY 266 TGCTACGAGCGCTTCAGTCCGAGACAGACGGGGCGCAGAAAGCGCGGATGCTGCACGT 325
DB 220 TGCTACGAGCGCTTCAGTCCGAGACAGACGGGGCGCAGAAAGCGCGGATGCTGCACGT 279
QY 326 GTGCAGCGCGGCTGATCCGAGCAGGAGCTGGGCGACGAGATCCAGATCGTGAGC 385
DB 280 GTGCAGCGCGGCTGATCCGAGCAGGAGCTGGGCGACGAGATCCAGATCGTGAGC 339
QY 386 CAGATGTTGGAGCTGGTGGAGAACCGACGCGGAGGTGGACAGCAGCTGGAGCTGTTTC 445
DB 340 CAGATGTTGGAGCTGGTGGAGAACCGACGCGGAGGTGGACAGCAGCTGGAGCTGTTTC 399
QY 446 GAGGCGCAGCAGGAGCTGGGCGACACAGCGGGCAACAGCGGCAAGGCTGGCGCGGACAGG 505
DB 400 GAGGCGCAGCAGGAGCTGGGCGACACAGTGGGCAACAGCGGCAAGGTTGGCGCGGACAGG 459
QY 506 CCCAAAGGCGAGCGGCGAGCTGACAAAGCCCAACAGCAAGCGCTCACGCGGCGAG 565

DB 460 CCCAATGGCGATGCGGTAGCGCAGTCTGCAAGACCCCAACAGAGCGCTCACGCGGCGAG 519
QY 566 CGCAACACGAGAACCGTGAAGACCGCTCCAGCAACACCAACACGACGACGCGGCTCG 625
DB 520 CGCAACACGAGAACCGTGAAGACCGCTCCAGCAACACCAACACGACGACGCGGCTCG 579
QY 626 GGCACACCCAAAGGAGAGAGCGGCAAGACTTCCAGAGAGAGAGCGCTCCAGGCGCAAG 685
DB 580 GGCACACCCAAAGGAGAGAGCGGCAAGACTTCCAGAGAGAGAGCGCTCCAGGCGCAAG 639
QY 686 GCGAGCGAGAGGCGTCCCTGCGGAGCTCCCATCGACCCCAACAGCAACCCACTACTGT 745
DB 640 GCGAGCGAGAGGCGTCCCTGCGGAGCTCCCATCGACCCCAACAGCAACCCACTACTGT 699
QY 746 CTGTGCAACACGAGTCTCTATATGGGAGAGATGATCGGCTCGGACAGAGTGCCTCATC 805
DB 700 CTGTGCAACACGAGTCTCTATATGGGAGAGATGATCGGCTCGGACAGAGTGCCTCATC 759
QY 806 GAGTGGTTCACACTTCTGTGCGTGGGCTCAATATAACCCCAAGGCGCAAGT 857
DB 760 GAGTGGTTCACACTTCTGTGCGTGGGCTCAATATAACCCCAAGGCGCAAGT 811

RESULT 13

US-09-159-871-1
; Sequence 1, Application US/09159871A
; Patent No. 6420136
; GENERAL INFORMATION:
; APPLICANT: RIABOWOL, Karl T.
; TITLE OF INVENTION: METHOD OF MODULATING P53 ACTIVITY
; FILE REFERENCE: 028722-181
; CURRENT APPLICATION NUMBER: US/09/159,871A
; CURRENT FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: US 60/060,138
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: US 09/006,783
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)...(897)
US-09-159-871-1

Query Match 70.3%; Score 602.4; DB 4; Length 2061;
Best Local Similarity 95.2%; Pred. No. 1.1e-123;
Matches 621; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 206 CTAGGCTCTGGAGTGGTGTCCGGCGCGGAATGGAGATCCCTGAAGGAGCTAGACGAG 265
DB 160 CTGACCCGAGGTGGGCGCGGTGGCCGTGGAAACAGATCCCTGAAGGAGCTAGACGAG 219
QY 266 TGCTACGAGCGCTTCAGTCCGAGACAGACGGGGCGCAGAAAGCGCGGATGCTGCACGT 325
DB 220 TGCTACGAGCGCTTCAGTCCGAGACAGACGGGGCGCAGAAAGCGCGGATGCTGCACGT 279
QY 326 GTGCAGCGCGGCTGATCCGAGCAGGAGCTGGGCGACGAGATCCAGATCGTGAGC 385
DB 280 GTGCAGCGCGGCTGATCCGAGCAGGAGCTGGGCGACGAGATCCAGATCGTGAGC 339
QY 386 CAGATGTTGGAGCTGGTGGAGAACCGACGCGGAGGTGGACAGCAGCTGGAGCTGTTTC 445
DB 340 CAGATGTTGGAGCTGGTGGAGAACCGACGCGGAGGTGGACAGCAGCTGGAGCTGTTTC 399
QY 446 GAGGCGCAGCAGGAGCTGGGCGACACAGCGGGCAACAGCGGCAAGGCTGGCGCGGACAGG 505
DB 400 GAGGCGCAGCAGGAGCTGGGCGACACAGTGGGCAACAGCGGCAAGGTTGGCGCGGACAGG 459

Db	86	GAGATCCTGAGGAGTACGAGTGTCTACGAGCGCTTCAGTCGGGAGACAGACGGGGCG	145
QY	302	CAGAGCGGGGATGTGCACTGTGTGTGAGCGCGCTGTATCCGAGCCAGGAGCTGGGC	361
Db	146	CAGAGCGGGGATGTGCACTGTGTGTGAGCGCGCTGTATCCGCA-CCAGGAGCTGGGC	204
QY	362	GACGAGAGATCCAGATCGTGAGCCAGATGTGTGAGCTGTGTGAGAAACCGCACCGGCGAG	421
Db	205	GACGAGAGATCCAGATCGTGAGCCAGATGTGTGAGCTGTGTGAGAAACCGCACCGGCGAG	264
QY	422	GTGGACAGCCACGTGAGCTGTGTGAGCGCGAGCGAGGAGCTGGGGGACACAGCGGGCAAC	481
Db	265	GTGGACAGCCACGTGAGCTGTGTGAGCGCGAGCGAGGAGCTGGGGGACACAGCGGGCAAC	324
QY	482	AGCGGCAAGGCTGGCGCGGACAGCGCCAAAGCGGAGGGCGGAGCGGAGCTGACAAAGCCC	541
Db	325	AGCGGCAAGGCTGGCGCGGAGAGGCGCCAAAGCGGAGGGCGGAGCGGAGCTGACAAAGCCC	384
QY	542	AACAGCAAGGCTCACGCGGGCGAGCGCCAAACAGAGAACCGTGAGAACGGCTCCAGCAAC	601
Db	385	AACAGCAAGGCTCACGCGGGCGAGCGCCAAACAGAGAACCGTGAGAACGGCTCCAGCAAC	444
QY	602	CACGACC 608	
Db	445	CACGACC 451	

Search completed: May 6, 2004, 11:51:27
 Job time : 84.0178 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 06:20:28 ; Search time 422.45 Seconds
(without alignments)
8618.076 Million cell updates/sec

Title: US-09-451-739H-4
Perfect score: 857
Sequence: 1 cctccgagacggtgccat.....tcataaacccagggcaagt 857

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04.*

- 1: geneseq1980s.*
- 2: geneseq1990s.*
- 3: geneseq2000s.*
- 4: geneseq2001as.*
- 5: geneseq2001bs.*
- 6: geneseq2002s.*
- 7: geneseq2003as.*
- 8: geneseq2003bs.*
- 9: geneseq2003cs.*
- 10: geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	857	100.0	857	4	Aah28481 Nucleotid
2	616.4	71.9	2886	6	Abk86976 Human inh
3	616	71.9	742	4	Aah28480 Nucleotid
4	616	71.9	1533	4	Aah28478 Nucleotid
5	616	71.9	1905	6	Aad46126 Human tum
6	616	71.9	2897	6	Abk86977 Human inh
7	616	71.9	8487	4	Aal37089 Human mus
8	616	71.9	8487	7	Abx60077 cDNA enco
9	616	71.9	163350	6	Aad46127 Human tum
10	606.4	70.8	911	3	Aas53792 Human p37
11	605.6	70.7	1143	4	Aah28479 Nucleotid
12	605.6	70.7	1502	2	Aat69651 Tumour su
13	605.6	70.7	1902	2	Aav62285 Partial I
14	605.6	70.7	2061	2	Aat69652 Tumour su
15	605.6	70.7	2061	2	Aav62292 Human ING
16	602.4	70.3	2061	2	Aax28688 Nucleotid
17	446.4	52.1	2817	3	Aas33790 Murine p3
18	445.4	52.0	1835	3	Aas33789 Murine in
19	414.8	48.4	693	6	Abq50058 Oligonucl
20	414.8	48.4	693	6	Abq50059 Oligonucl
21	377.2	44.0	683	6	Abq47312 Oligonucl
22	377.2	44.0	683	6	Abq47313 Oligonucl
23	375	43.8	693	6	Abq50060 Oligonucl

24	375	43.8	693	6	Abq50061 Oligonucl
25	355	41.4	451	2	Aaz07188 Human lun
26	355	41.4	451	3	Aac79140 Human lun
27	355	41.4	451	4	Aad23215 Human lun
28	355	41.4	451	9	AAD266454 Human lun
29	355	41.4	451	9	ADe87708 Human lun
30	331	38.6	683	6	Abq47310 Oligonucl
31	331	38.6	683	6	Abq47311 Oligonucl
32	262	30.6	303	6	Abk92991 cDNA enco
33	203.4	23.7	313	3	AAC23407 Human sec
34	175.4	20.5	772	4	AAH28482 Nucleotid
35	156.8	18.3	8370	4	AAH28482 Nucleotid
36	142.6	16.6	840	2	Aaz08595 Human ING
37	142.6	16.6	1078	2	Aaz08596 Human ING
38	142.6	16.6	1080	4	ADL12783 Tumour su
39	142	16.6	1153	3	Aaz47473 Human tum
40	140.4	16.4	1154	6	ABs70424 Human bon
41	140.2	16.4	222	6	ABn26558 Human ORF
42	131.4	15.3	8370	4	ADb51204 Primary r
43	131.4	15.3	8370	4	AAH28482 Nucleotid
44	110.2	12.9	421	8	ACH49821 Human leu
45	99.8	11.6	540	5	AAH74005 DNA enco

ALIGNMENTS

RESULT 1
AAH28481
ID AAH28481 standard; DNA; 857 BP.
XX
AC AAH28481;
XX
DT 17-SEP-2001. (first entry)
XX
DE Nucleotide sequence of a human cancer associated antigen.
XX
KW Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200147959-A2.
XX
PD 05-JUL-2001.
XX
PF 29-NOV-2000; 2000WO-US042334.
XX
PR 30-NOV-1999; 99US-00451739.
XX
PR 24-OCT-2000; 2000US-00602362.
XX
PA (LUDW.) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX (CORR) CORNELL RES FOUND INC.
XX
XX Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;
XX WPI; 2001-441706/47.
XX
XX Isolated cancer associated nucleic acid molecule identified by SEREX
XX (serological identification of antigens by recombinant expression
XX cloning) technique, useful in nucleic acid based therapies to treat
XX cancer.
XX
XX Claim 1; Page 45; 62pp; English.
XX
XX The present sequence encodes a human cancer associated antigen. The
XX sequence is a variant of the INGI gene, which is a tumour suppressor gene
XX candidate. The cancer associated antigen polynucleotides and polypeptides
XX are useful for screening for the possible presence of a pathological
XX condition in a subject such as cancer. The cancer associated antigen
XX polypeptides are useful for producing vaccines
XX
XX Sequence 857 BP; 200 A; 256 C; 297 G; 104 T; 0 U; 0 Other;

Query Match		100.0%; Score 857; DB 4; Length 857;
Best Local Similarity		100.0%; Pred. No. 3.9e-157;
Matches		857; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	CCTCGGAGCGGTGTCATGCGACAGCGCGGGAAGATAGAGCGCTTAGGAGAGCGGCC 60
Db	1	CCTCGGAGCGGTGTCATGCGACAGCGCGGGAAGATAGAGCGCTTAGGAGAGCGGCC 60
Qy	61	CTCGGGCTATCCACCTCTTCCTGGGCTCGGCACTAGGAAGCACTTCCTCTCAGGCC 120
Db	61	CTCGGGCTATCCACCTCTTCCTGGGCTCGGCACTAGGAAGCACTTCCTCTCAGGCC 120
Qy	121	CTTTGTCTCAGCGGTTCGAACTGAGTACCGGGAGCAGACACAAAGGAGGCGCGTGA 180
Db	121	CTTTGTCTCAGCGGTTCGAACTGAGTACCGGGAGCAGACACAAAGGAGGCGCGTGA 180
Qy	181	CGGATGCGCGAGCGCGGAGCCCTAGGCTGCTGGAGTGTGTGTCGCGCCCGCGAAT 240
Db	181	CGGATGCGCGAGCGCGGAGCCCTAGGCTGCTGGAGTGTGTGTCGCGCCCGCGAAT 240
Qy	241	CGGATGCTGAGGAGCTAGAGAGTGTGTCAGAGCGGTTAGTGCAGAGCAGACGCGGC 300
Db	241	CGGATGCTGAGGAGCTAGAGAGTGTGTCAGAGCGGTTAGTGCAGAGCAGACGCGGC 300
Qy	301	CGAGAGCGCGGATGCTGCACTGTGTGCGCGCGCTGATCCGCGAGCAGAGCTGGG 360
Db	301	CGAGAGCGCGGATGCTGCACTGTGTGCGCGCGCTGATCCGCGAGCAGAGCTGGG 360
Qy	361	CGAGAGAGATCCAGATCGTGTGAGCGAGTGTGTGAGAGACCGCGCGCA 420
Db	361	CGAGAGAGATCCAGATCGTGTGAGCGAGTGTGTGAGAGACCGCGCGCA 420
Qy	421	GTTGAGACAGCGCTGAGAGCTGTTGAGCGCGAGCGAGTGTGTGAGAGCGCGCA 480
Db	421	GTTGAGACAGCGCTGAGAGCTGTTGAGCGCGAGCGAGTGTGTGAGAGCGCGCA 480
Qy	481	CAGCGCGAGGCTGCGCGGAGCGCCCAAGGCGAGCGCGAGCGCGAGCTGCAAGCC 540
Db	481	CAGCGCGAGGCTGCGCGGAGCGCCCAAGGCGAGCGCGAGCGCGAGCTGCAAGCC 540
Qy	541	CAACAGCAGCGCTCAGCGCGGAGCGCAACAGAGAACCGTGAGAGCGGTCCAGCA 600
Db	541	CAACAGCAGCGCTCAGCGCGGAGCGCAACAGAGAACCGTGAGAGCGGTCCAGCA 600
Qy	601	CCACGACACGACGAGCGCGCTCGGCGACACCCCAAGAGAGAGGCAAGAGCTCCAA 660
Db	601	CCACGACACGACGAGCGCGCTCGGCGACACCCCAAGAGAGAGGCAAGAGCTCCAA 660
Qy	661	GAGAGAGCGCTCAGAGCGGAGCGGAGCGGAGCGGCTCCCTCGCGACCTCCCAT 720
Db	661	GAGAGAGCGCTCAGAGCGGAGCGGAGCGGAGCGGCTCCCTCGCGACCTCCCAT 720
Qy	721	CGACCCCAACGAGCGGAGCTGCTGTGCAACAGGCTCTCTATGGGAGATGATCGG 780
Db	721	CGACCCCAACGAGCGGAGCTGCTGTGCAACAGGCTCTCTATGGGAGATGATCGG 780
Qy	781	CTGCGACAGCGAGTGCCTCAGGCTGAGTGTGTCACCTTCGTCGTCGTCGTCATCA 840
Db	781	CTGCGACAGCGAGTGCCTCAGGCTGAGTGTGTCACCTTCGTCGTCGTCGTCATCA 840
Qy	841	TAAACCCCAAGGCGAAGT 857
Db	841	TAAACCCCAAGGCGAAGT 857

RESULT 2
ABX86976
ID ABX86976 standard; cDNA; 2886 BP.
XX
AC ABX86976;
XX
DT 24-SEP-2002 (first entry)

XX DE Human inhibitor of growth 1 (ING1) isoform, p47ING1a, cDNA.
XX KW Human; gene; ss; monoclonal antibody; epitope; inhibitor of growth 1;
KW ING1; tumour suppressor; cell cycle; breast tumour; lymphoid malignancy;
KW cell growth; anti-ING1; CAB; isoform; diagnosis; tumour; antigen;
KW p47ING1a.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 433..1701
FT /*tag= a
FT /product= "p47ING1a"
XX PN US2002039735-A1.
XX PD 04-APR-2002.
XX PP 04-JUN-2001; 2001US-00874347.
XX PR 08-DEC-1995; 95US-00569721.
PR 15-NOV-1996; 96US-00751230.
PR 26-FEB-1999; 99US-00258372.
PR 22-MAR-2000; 2000US-00532868.
PR 02-JUN-2000; 2000US-0208829P.
XX PA (RIAB/) RIABOWOL K T.
PA (BOLA/) BOLAND D.
XX PI Riabowol KT, Boland D;
XX DR MPI; 2002-526652/56.
XX DR P-PSDB; AAU79586.
XX PT Novel monoclonal antibody which specifically recognizes epitope of ING1,
PT inhibitor of growth 1 protein, and designated CAB1-10, useful for
PT detecting two different isoforms of ING1 and diagnosing a medical
PT condition.
XX PS Disclosure; Page 7-9; 15pp; English.
XX CC The invention discloses monoclonal antibodies which can be used, in
CC combination, to specifically recognise epitopes of ING1 (inhibitor of
CC growth 1) protein isoforms. ING1 is a tumour suppressor gene and its
CC expression is regulated through the cell cycle, peaking in the S phase.
CC Expression of ING1 is down regulated in breast tumours and lymphoid
CC malignancies. Overexpression of a construct containing the ING1 gene is
CC able to inhibit cell growth by reducing the fraction of cells which enter
CC into the S phase. The monoclonal antibodies are useful for detecting an
CC ING1 protein in a cell, which involves selecting a cell that ectopically
CC or endogenously expresses ING1 protein. The anti-ING1 monoclonal antibody
CC combination consists of two or more antibodies of CAB1-CAB10 (not
CC defined), preferably a mixture of CAB1-CAB4, which can detect at least
CC two different isoforms of ING1. The antibodies are also useful for
CC diagnosing a disease e.g. tumour or medical condition in an animal
CC (preferably, human) associated with aberrant levels of an ING1 protein.
CC The sequence presented is the human inhibitor of growth 1 (ING1) isoform,
CC p47ING1a, cDNA, isolated from a human cDNA library, which encodes a
CC protein used to raise antibodies
XX SQ Sequence 2886 BP; 741 A; 649 C; 789 G; 707 T; 0 U; 0 Other;

Query Match 71.9%; Score 616.4; DB 6; Length 2886;
Best Local Similarity 85.5%; Pred. No. 1.9e-110;
Matches 686; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
Qy 56 CGCCCTCGGCTATCCACCTCTTCCTGGGCTCGGCACTAGGAGCAGCTTCCCTCTCA 115
Db 811 CTCTCCCGCTCAGCCCGGCACTTTCGGGCGCGGATTTATAGCATGATGATCCCG 870
Qy 116 GGCCCTTTCTCTCCAGCGGTTCCTCAAACTAGTACCGGAGACGACACAAAGGGAGGC 175
|||||

Db 871 GGCTGTGGGCTCGGGCGGGGCTGCAGTTCGGACCGCTCCCGGACCCCGGGGGCG 930
Qy 176 GTGACGGATGGCGAGCGGGAGCGGCTAGGCTGTGGAGTGGTGGTCCGGCGC 235
Db 931 GCTCGGAGACAGTTTCAGGCGCGCATTTTCTGACCCGAGGGTGGGGCGCGTGGCG 990
Qy 236 GGAATGAGATCTTGAAGGAGCTAGACGAGTGTACGAGCGCTTCAGTCCGAGACAGAC 295
Db 991 TGGAAACAGATCTGAAGGAGCTAGACGAGTGTACGAGCGCTTCAGTCCGAGACAGAC 1050
Qy 296 GGGCGGAGAGCGGGGATGCTGCACTGTGTGACGGCGCGTGTATCCGACGACGAG 355
Db 1051 GGGCGGAGAGCGGGGATGCTGCACTGTGTGACGGCGCGTGTATCCGACGACGAG 1110
Qy 356 CTGGCGACAGAGATCCAGATCGTGGACGAGTGTGAGCTGTGGAGAACCCGACG 415
Db 1111 CTGGCGACAGAGATCCAGATCGTGGACGAGTGTGAGCTGTGGAGAACCCGACG 1170
Qy 416 CGGAGTGTGACAGCGCTGTGAGCTGTTCGAGCGCGAGCAGAGTGTGGCGACAGCG 475
Db 1171 CGGAGTGTGACAGCGCTGTGAGCTGTTCGAGCGCGAGCAGAGTGTGGCGACAGCG 1230
Qy 476 GGCAACAGCGGCAAGGCTGGCGGAGCAGCGCCCAAGGGCGAGCGCGCAGCGAGTGTGAC 535
Db 1231 GGCAACAGCGGCAAGGCTGGCGGAGCAGCGCCCAAGGGCGAGCGCGCAGCGAGTGTGAC 1290
Qy 536 AAGCCCAACAGAGCGCTCAAGCGCGAGCGCAACAGAGAACCGTGTGAGAACCGGTCC 595
Db 1291 AAGCCCAACAGAGCGCTCAAGCGCGAGCGCAACAGAGAACCGTGTGAGAACCGGTCC 1350
Qy 596 AGCAACCAACAGAGCGCTCAAGCGCGAGCGCAACAGAGAACCGTGTGAGAACCGGTCC 655
Db 1351 AGCAACCAACAGAGCGCTCAAGCGCGAGCGCAACAGAGAACCGTGTGAGAACCGGTCC 1410
Qy 656 TCCAAGAGAGAGAGCGCTCAAGCGCGAGCGCAACAGAGAACCGTGTGAGAACCGGTCC 715
Db 1411 TCCAAGAGAGAGAGCGCTCAAGCGCGAGCGCAACAGAGAACCGTGTGAGAACCGGTCC 1470
Qy 716 CCATGACCCACAGAGCGCTCAAGCGCGAGCGCAACAGAGAACCGTGTGAGAACCGGTCC 775
Db 1471 CCATGACCCACAGAGCGCTCAAGCGCGAGCGCAACAGAGAACCGTGTGAGAACCGGTCC 1530
Qy 776 ATCGGCTGCGACAGAGCGCTCAAGCGCGAGCGCAACAGAGAACCGTGTGAGAACCGGTCC 835
Db 1531 ATCGGCTGCGACAGAGCGCTCAAGCGCGAGCGCAACAGAGAACCGTGTGAGAACCGGTCC 1590
Qy 836 AATCATTAACCAAGGCGAGT 857
Db 1591 AATCATTAACCAAGGCGAGT 1612

RESULT 3
AAH28480
ID AAH28480 standard; DNA; 742 BP.
XX
AC
XX
XX
DT 17-SEP-2001 (first entry)
XX
DE Nucleotide sequence of a human cancer associated antigen.
XX
KW Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200147959-A2.
XX
PD 05-JUL-2001.
XX
PF 29-NOV-2000; 2000WO-US042334.
XX
PR 30-NOV-1999; 99US-00451739.
PR 24-OCT-2000; 2000US-00602362.

XX (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;
PI WPI; 2001-441706/47.
XX
DR Isolated cancer associated nucleic acid molecule identified by SEREX
PT (serological identification of antigens by recombinant expression
PT cloning; technique, useful in nucleic acid based therapies to treat
PT cancer.
XX
PS Claim 1; Page 44-45; 62pp; English.
XX
CC The present sequence encodes a human cancer associated antigen. The
CC sequence is a variant of the INGI gene, which is a tumour suppressor gene
CC candidate. The cancer associated antigen polynucleotides and polypeptides
CC are useful for screening for the possible presence of a pathological
CC condition in a subject such as cancer. The cancer associated antigen
CC polypeptides are useful for producing vaccines
XX
SQ Sequence 742 BP; 174 A; 243 C; 247 G; 78 T; 0 U; 0 Other;
Query Match 71.9%; Score 616; DB 4; Length 742;
Best Local Similarity 100.0%; Pred. No. 2.1e-110; Indels 0; Gaps 0;
Matches 616; Conservative 0; Mismatches 0;
Qy 242 GAGATCCTGAAGGAGCTAGACGAGTGTACGAGCGCTTCAGTCCGAGACAGACGGGCG 301
Db 127 GAGATCCTGAAGGAGCTAGACGAGTGTACGAGCGCTTCAGTCCGAGACAGACGGGCG 186
Qy 302 CAGAACGGCGGATGCTCAGTGTGACGCGCGCTGATCCGACGACGAGCTGGGCG 361
Db 187 CAGAACGGCGGATGCTCAGTGTGACGCGCGCTGATCCGACGACGAGCTGGGCG 246
Qy 362 GACGAGAGATCCAGATCGTGCAGCAGATGTGTGAGCTGTGTGAGAACCGCACGGCGAG 421
Db 247 GACGAGAGATCCAGATCGTGCAGCAGATGTGTGAGCTGTGTGAGAACCGCACGGCGAG 306
Qy 422 GTGGAACAGCAGTGTGAGCTGTGAGCGCGACGAGAGCTGGGCGACACAGCGGCAAC 481
Db 307 GTGGAACAGCAGTGTGAGCTGTGAGCGCGACGAGAGCTGGGCGACACAGCGGCAAC 366
Qy 482 AGCGCAAGGCTGGCGCGGACAGCGCCCAAGCGCGAGCGCGAGCTGTGACAAAGCCC 541
Db 367 AGCGCAAGGCTGGCGCGGACAGCGCCCAAGCGCGAGCGCGAGCTGTGACAAAGCCC 426
Qy 542 AACAGCAAGCGCTACGCGCGGAGCGCAACAAAGAGAACCGTGTGAGAACCGTTCAGGCAAC 601
Db 427 AACAGCAAGCGCTACGCGCGGAGCGCAACAAAGAGAACCGTGTGAGAACCGTTCAGGCAAC 486
Qy 602 CACGACCAAGCGCTCCAAAGCCCAAGCGCGGAGCGGCTCCCTGTGCGAGCTCCCTCCATC 721
Db 547 AAGAGAGAGCGCTCCAAAGCCCAAGCGCGGAGCGGCTCCCTGTGCGAGCTCCCTCCATC 606
Qy 722 GACCCCAAGCAACCGTACTGTGTGCAACAGGCTCTCTATGGGAGATGATCGGC 781
Db 607 GACCCCAAGCAACCGTACTGTGTGCAACAGGCTCTCTATGGGAGATGATCGGC 666
Qy 782 TCGCAACAGCAGAGTGGCCCATCGAGTGGTTCCACTTCTCGTGGGCTCAATCAT 841
Db 667 TCGCAACAGCAGAGTGGCCCATCGAGTGGTTCCACTTCTCGTGGGCTCAATCAT 726
Qy 842 AAACCCCAAGGCGAAGT 857
Db 727 AAACCCCAAGGCGAAGT 742

RESULT 4	
AAH28478	
ID	AAH28478 standard; DNA; 1533 BP.
XX	
AC	AAH28478;
XX	
DT	17-SEP-2001 (first entry)
XX	
DE	Nucleotide sequence of a human cancer associated antigen.
XX	
KW	Cancer associated antigen; INGI1; tumour suppressor; cancer; vaccine; ss.
XX	
CS	Homo sapiens.
XX	
Key	Location/Qualifiers
FD	451..1290
FT	/*tag= a
FT	/transl_except= (pos: 817..819, aa: Val)
FT	/transl_except= (pos: 835..837, aa: Val)
FT	/transl_except= (pos: 853..855, aa: Asn)
FT	/transl_except= (pos: 859..861, aa: Asp)
FT	/transl_except= (pos: 865..867, aa: Val)
FT	/transl_except= (pos: 874..876, aa: Ser)
FT	/product= cancer associated antigen
XX	
FN	WO200147959-A2.
XX	
PD	05-JUL-2001.
XX	
PF	29-NOV-2000; 200WO-US042334.
XX	
PR	30-NOV-1999; 99US-00451739.
PR	24-OCT-2000; 2000US-00602362.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
PA	(SLOK) SLOAN KETTERING INST CANCER RES.
PA	(CORR) CORNELL RES FOUND INC.
XX	
PI	Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;
XX	
DR	WPI; 2001-441706/47.
DR	P-PSDB; AAB84698.
XX	
PT	Isolated cancer associated nucleic acid molecule identified by SEREX
PT	(serological identification of antigens by recombinant expression
PT	cloning) technique, useful in nucleic acid based therapies to treat
PT	cancer.
XX	
PS	Claim 1; Page 43-44; 62pp; English.
XX	
CC	The present sequence encodes a human cancer associated antigen. The
CC	sequence is a variant of the INGI gene, which is a tumour suppressor gene
CC	candidate. The cancer associated antigen polynucleotides and polypeptides
CC	are useful for screening for the possible presence of a pathological
CC	condition in a subject such as cancer. The cancer associated antigen
CC	polypeptides are useful for producing vaccines
XX	
SQ	Sequence 1533 BP; 336 A; 431 C; 521 G; 244 T; 0 U; 1 Other;
	Query Match 71.9%; Score 616; DB 4; Length 1533;
	Best Local Similarity 100.0%; Pred. No. 2.2e-110;
	Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	242 GAGATCCTGAAGAGCTACGACGAGTCTACGAGCGCTTCAGTCGGGAGACACACGGGGCG 301
Db	586 GAGATCCTGAAGAGAGCTACGAGAGTCTACGAGCGCTTCAGTCGGGAGACACACGGGGCG 645
Oy	302 CAGAACGGCGGATGTGTCACTGTGTGACGCGCGCTGATCCGACGACGAGCTGGGC 361
Db	646 CAGAACGGCGGATGTGTCACTGTGTGACGCGCGCTGATCCGACGACGAGCTGGGC 705
Oy	362 GAGCAGAAGATCCAGATCGTGACCGCAGATGTTGTGGAGAACCGCACGCGGCAG 421

[illegible]

XX WPI; 2002-698658/75.
DR P-PSDB; AAE28633.
XX
PT New human tumor suppressor proteins, useful for developing human
PT therapeutic agents, or preventing or treating inflammation, or disorders
PT associated with cell proliferation, e.g. bone cancer, brain cancer,
PT leukemia or lymphoma.
XX
PS Claim 4; Fig 1; 200pp; English.
XX
CC The invention relates to human tumor suppressor polypeptides and
CC polynucleotides. Sequences of the invention are useful for diagnosing,
CC preventing or treating inflammation, or disorders associated with cell
CC proliferation and apoptosis e.g. bone cancer, brain cancer, cervix
CC cancer, adenocarcinoma, leukemia, lymphoma or melanoma. They are
CC particularly useful as models for developing human therapeutic targets,
CC identifying therapeutic proteins, or serving as targets for the
CC development of human therapeutic agents that modulate tumor suppressor
CC protein activity in cells and tissues that express the tumor suppressor
CC protein. Polypeptides of the invention are used for identifying agents
CC that modulate their activity. They are useful for raising antibodies or
CC eliciting an immune response; as a reagent in assays designed to
CC quantitatively determine levels of the protein (or its binding partner or
CC ligand) in biological fluids; or as markers for tissues in which the
CC corresponding protein is preferentially expressed. The invention is also
CC used as vaccines. The present sequence is human tumor suppressor protein
CC encoding cDNA. The tumor suppressor gene is located on chromosome 13
XX
SQ Sequence 1905 BP; 532 A; 428 C; 528 G; 417 T; 0 U; 0 Other;

Query Match 71.9%; Score 616; DB 6; Length 1905;
Best Local Similarity 100.0%; Pred. No. 2.3e-110;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 GAGATCTGAGGAGTACGAGTGTGACGCGCTTACGCGGACGAGCAGCGGGCG 301
Db 332 GAGATCTGAGGAGTACGAGTGTGACGCGCTTACGCGGACGAGCAGCGGGCG 391
Qy 302 CAGAGCGGGCGGATGCTGACATGTGTGACGCGCGCTGTATCGCAGCCAGGAGCTGGGC 361
Db 392 CAGAGCGGGCGGATGCTGACATGTGTGACGCGCGCTGTATCGCAGCCAGGAGCTGGGC 451
Qy 362 GACGAGAGATCCAGATCGTGAGCAGATGTGTGAGCTGTGGAGACCGCAGCGCGCAG 421
Db 452 GACGAGAGATCCAGATCGTGAGCAGATGTGTGAGCTGTGGAGACCGCAGCGCGCAG 511
Qy 422 GTGGACACGCCACGTGGAGCTGTTCGAGCGCAGCAGGAGTGGCGGACACAGCGGGCAAC 481
Db 512 GTGGACACGCCACGTGGAGCTGTTCGAGCGCAGCAGGAGTGGCGGACACAGCGGGCAAC 571
Qy 482 AGCGGCAAGGTGGCGGACAGCGCCCAAGCGCAGCGCGCAGCGAGGCTGACAGCCC 541
Db 572 AGCGGCAAGGTGGCGGACAGCGCCCAAGCGCAGCGCGCAGCGAGGCTGACAGCCC 631
Qy 542 AACGACAGCGCTCAGCGCGCGCAGCGCAACCAACGAGAACCGTGAGAGCGGCTCCAGCAAC 601
Db 632 AACGACAGCGCTCAGCGCGCGCAGCGCAACCAACGAGAACCGTGAGAGCGGCTCCAGCAAC 691
Qy 602 CACGACACGAGCAGCGCGCTCGGGCACACCCAGGAGAGAGAGGCGCAGACCTCCAG 661
Db 692 CACGACACGAGCAGCGCGCTCGGGCACACCCAGGAGAGAGAGGCGCAGACCTCCAG 751
Qy 662 AAGAGAGCGCTCCAGGCGCAAGCGGAGGAGGCGTCCCTGCGGACCTCCCGATC 721
Db 752 AAGAGAGCGCTCCAGGCGCAAGCGGAGGAGGCGTCCCTGCGGACCTCCCGATC 811
Qy 722 GACCCCAACGACCCCACTATGTGTGTGCAACAGAGTCTCTATGGGGAGATGATCGGC 781
Db 812 GACCCCAACGACCCCACTATGTGTGTGCAACAGAGTCTCTATGGGGAGATGATCGGC 871
Qy 782 TCGGACACGAGGAGTGGCCCATCGATGAGTGTTCACATCTCTGCGTGGGGCTCAATCAT 841

Db 872 TCGGACACGAGGAGTGGCCCATCGATGAGTGTTCACATCTCTGCGTGGGGCTCAATCAT 931
Qy 842 AAACCCCAAGGCAAGT 857
Db 932 AAACCCCAAGGCAAGT 947
RESULT 6
ABK86977 standard; cDNA; 2897 BP.
XX
AC ABK86977;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human inhibitor of growth 1 (ING1) isoform, p33ING1b, cDNA.
XX
KW Human; gene; ss; monoclonal antibody; epitope; inhibitor of growth 1;
KW ING1; tumor suppressor; cell cycle; breast tumour; lymphoid malignancy;
KW cell growth; anti-ING1; CAB; isoform; diagnosis; tumour; antigen;
KW p33ING1b.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 873..1712
FT /*tag= a
FT /product= "p33ING1b"
XX
PN US2002039735-A1.
XX
PD 04-APR-2002.
XX
PF 04-JUN-2001; 2001US-00874347.
PR 08-DEC-1995; 95US-00569721.
PR 15-NOV-1995; 94US-00751230.
PR 26-FEB-1995; 93US-00258372.
PR 22-MAR-2000; 2000US-00532868.
PR 02-JUN-2000; 2000US-02088299.
XX
PA (RIAB/) RIABOWOL K T.
PA (BOLA/) BOLAND D.
XX
PI Riabowol KT, Boland D;
XX
XX WPI; 2002-526652/56.
DR P-PSDB; AAU79587.
XX
PT Novel monoclonal antibody which specifically recognizes epitope of ING1,
PT inhibitor of growth 1 protein, and designated Cabi-10, useful for
PT detecting two different isoforms of ING1 and diagnosing a medical
PT condition.
XX
PS Disclosure; Page 10-12; 15pp; English.
XX
CC The invention discloses monoclonal antibodies which can be used, in
CC combination, to specifically recognise epitopes of ING1 (inhibitor of
CC growth 1) protein isoforms. ING1 is a tumour suppressor gene and its
CC expression is regulated through the cell cycle, peaking in the S phase.
CC Expression of ING1 is down regulated in breast tumours and lymphoid
CC malignancies. Overexpression of a construct containing the ING1 gene is
CC able to inhibit cell growth by reducing the fraction of cells which enter
CC into the S phase. The monoclonal antibodies are useful for detecting an
CC ING1 protein in a cell, which involves selecting a cell that ectopically
CC or endogenously expresses ING1 protein. The anti-ING1 monoclonal antibody
CC combination consists of two or more antibodies of Cabi-CAB10 (not
CC defined), preferably a mixture of Cabi-CAB4, which can detect at least
CC two different isoforms of ING1. The antibodies are also useful for
CC diagnosing a disease e.g. tumour or medical condition in an animal
CC (preferably, human) associated with aberrant levels of an ING1 protein.
CC The sequence presented is the human inhibitor of growth 1 (ING1) isoform,
CC p33ING1b, cDNA, isolated from a human cDNA library, which encodes a

Fri May 7 09:17:27 2004

us-09-451-739h-4.rng

CC protein used to raise antibodies

XX Sequence 2897 BP; 733 A; 710 C; 819 G; 635 T; 0 U; 0 Other;

Query Match 71.9%; Score 616; DB 6; Length 2897;
Best Local Similarity 100.0%; Pred. No. 2.3e-110; Indels 0; Gaps 0;
Matches 616; Conservative 0; Mismatches 0;

QY	242	GAGATCCTGAAGAGCTAGACGAGTCTACGAGCGTTTACGTCGCGAGACACGCGGCGG	301
DB	1008	GAGATCCTGAAGAGCTAGACGAGTCTACGAGCGTTTACGTCGCGAGACACGCGGCGG	1067
QY	302	CAGAGCGCGGAGTCTGCTACTGTGTCAGCGCGGCTGATCCGACGAGAGTGGGC	361
DB	1068	CAGAGCGCGGAGTCTGCTACTGTGTCAGCGCGGCTGATCCGACGAGAGTGGGC	1127
QY	362	GAGGAGAAGATCCAGATCTGTGACGAGTGTGAGTGTGAGAACCGCAGCGGCGAG	421
DB	1128	GAGGAGAAGATCCAGATCTGTGAGCGTGTGAGAACCGCAGCGGCGAG	1187
QY	422	GTGACAGCCAGCTGGAGCTGTTTCGAGCGCAGCAGAGTGGCGACACAGCGGCGAAC	481
DB	1188	GTGACAGCCAGCTGGAGCTGTTTCGAGCGCAGCAGAGTGGCGACACAGCGGCGAAC	1247
QY	482	AGCGGCAAGGCTGGCGCGGACAGCGCCCAAGGCGAGCGCGCAGCGTGTGACAGCCG	541
DB	1248	AGCGGCAAGGCTGGCGCGGACAGCGCCCAAGGCGAGCGCGCAGCGTGTGACAGCCG	1307
QY	542	AACAGCAAGCGCTCAGCGCGGCGACGCAACACAGAACCGTGTGACGCGTCCAGCAAC	601
DB	1308	AACAGCAAGCGCTCAGCGCGGCGACGCAACACAGAACCGTGTGACGCGTCCAGCAAC	1367
QY	602	CACGACCAAGCGCTCAGCGCGGCGCTCGGCGACACCCCAAGGAGAGGCGCAAGACTCCAAG	661
DB	1368	CACGACCAAGCGCTCAGCGCGGCGCTCGGCGACACCCCAAGGAGAGGCGCAAGACTCCAAG	1427
QY	662	AAGAAAGCGCTCAGAGCCCAAGCGGAGCGGAGCGGCTCCCTCGGACCTCCCATC	721
DB	1428	AAGAAAGCGCTCAGAGCCCAAGCGGAGCGGAGCGGCTCCCTCGGACCTCCCATC	1487
QY	722	GACCCCAAGCAACCCAGTCTGTGTCGCAACCCAGGTCCTATGGGAGAGATCGGC	781
DB	1488	GACCCCAAGCAACCCAGTCTGTGTCGCAACCCAGGTCCTATGGGAGAGATCGGC	1547
QY	782	TGCGAACAAGCAGTGTGCCCCCATCGAGTGTTCATCTCTGTCGTCGGGCTCAATCAT	841
DB	1548	TGCGAACAAGCAGTGTGCCCCCATCGAGTGTTCATCTCTGTCGTCGGGCTCAATCAT	1607
QY	842	AAACCCAGGCGAAGT 857	
DB	1608	AAACCCAGGCGAAGT 1623	

RESULT 7

AAL37089

ID AAL37089 standard; DNA; 8487 BP.

XX AC AAL37089;

XX AC AAL37089;

XX AC AAL37089;

XX AC AAL37089;

XX AC AAL37089;

DE Human musculoskeletal system related polynucleotide SEQ ID NO 3454.

Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;
antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
neurological disease; infection; human; secreted protein;
musculoskeletal system; ds.

OS Homo sapiens.

XX WO200155367-A1.

PN WO200155367-A1.

XX	02-AUG-2001.	
PD		
XX	17-JAN-2001; 2001WO-US001338.	
XX		
XX	31-JAN-2000; 2000US-0179065P.	
PR	04-FEB-2000; 2000US-0180628P.	
PR	24-FEB-2000; 2000US-0184664P.	
PR	02-MAR-2000; 2000US-0186350P.	
PR	16-MAR-2000; 2000US-0189874P.	
PR	17-MAR-2000; 2000US-0190076P.	
PR	18-APR-2000; 2000US-0198123P.	
PR	09-MAY-2000; 2000US-0209467P.	
PR	28-JUN-2000; 2000US-0214886P.	
PR	30-JUN-2000; 2000US-0215135P.	
PR	07-JUL-2000; 2000US-0216647P.	
PR	07-JUL-2000; 2000US-0216880P.	
PR	11-JUL-2000; 2000US-0217487P.	
PR	11-JUL-2000; 2000US-0217496P.	
PR	14-JUL-2000; 2000US-0218290P.	
PR	26-JUL-2000; 2000US-0220963P.	
PR	26-JUL-2000; 2000US-0220964P.	
PR	14-AUG-2000; 2000US-0224518P.	
PR	14-AUG-2000; 2000US-0224519P.	
PR	14-AUG-2000; 2000US-0225213P.	
PR	14-AUG-2000; 2000US-0225214P.	
PR	14-AUG-2000; 2000US-0225266P.	
PR	14-AUG-2000; 2000US-0225267P.	
PR	14-AUG-2000; 2000US-0225268P.	
PR	14-AUG-2000; 2000US-0225270P.	
PR	14-AUG-2000; 2000US-0225447P.	
PR	14-AUG-2000; 2000US-0225757P.	
PR	14-AUG-2000; 2000US-0225758P.	
PR	14-AUG-2000; 2000US-0225759P.	
PR	18-AUG-2000; 2000US-0226279P.	
PR	22-AUG-2000; 2000US-0226681P.	
PR	22-AUG-2000; 2000US-0226682P.	
PR	22-AUG-2000; 2000US-0227182P.	
PR	23-AUG-2000; 2000US-0227009P.	
PR	30-AUG-2000; 2000US-0228924P.	
PR	01-SEP-2000; 2000US-0229287P.	
PR	01-SEP-2000; 2000US-0229343P.	
PR	01-SEP-2000; 2000US-0229344P.	
PR	01-SEP-2000; 2000US-0229345P.	
PR	05-SEP-2000; 2000US-0229509P.	
PR	05-SEP-2000; 2000US-0229513P.	
PR	06-SEP-2000; 2000US-0230437P.	
PR	08-SEP-2000; 2000US-0230438P.	
PR	08-SEP-2000; 2000US-0231242P.	
PR	08-SEP-2000; 2000US-0231243P.	
PR	08-SEP-2000; 2000US-0231244P.	
PR	08-SEP-2000; 2000US-0231413P.	
PR	08-SEP-2000; 2000US-0231414P.	
PR	08-SEP-2000; 2000US-0232080P.	
PR	08-SEP-2000; 2000US-0232081P.	
PR	12-SEP-2000; 2000US-0231968P.	
PR	14-SEP-2000; 2000US-0232397P.	
PR	14-SEP-2000; 2000US-0232398P.	
PR	14-SEP-2000; 2000US-0232399P.	
PR	14-SEP-2000; 2000US-0232400P.	
PR	14-SEP-2000; 2000US-0232401P.	
PR	14-SEP-2000; 2000US-0233063P.	
PR	14-SEP-2000; 2000US-0233064P.	
PR	14-SEP-2000; 2000US-0233065P.	
PR	21-SEP-2000; 2000US-0234223P.	
PR	21-SEP-2000; 2000US-0234274P.	
PR	25-SEP-2000; 2000US-0234997P.	
PR	25-SEP-2000; 2000US-0234998P.	
PR	26-SEP-2000; 2000US-0235484P.	
PR	27-SEP-2000; 2000US-0235834P.	
PR	27-SEP-2000; 2000US-0235836P.	
PR	29-SEP-2000; 2000US-0236327P.	

PR	29-SEP-2000;	2000US-0236367P.	DR	WPI; 2001-451937/48.
PR	29-SEP-2000;	2000US-0236368P.	XX	
PR	29-SEP-2000;	2000US-0236369P.	PT	Isolated polypeptide for treating, preventing and/or prognosing
PR	29-SEP-2000;	2000US-0236370P.	PT	disorders related to the musculoskeletal system including musculoskeletal
PR	02-OCT-2000;	2000US-0236802P.	PT	cancers and also for testing and detection e.g. diagnosis.
PR	02-OCT-2000;	2000US-0237037P.	XX	
PR	02-OCT-2000;	2000US-0237038P.	PS	Example 2; SEQ ID NO 3454; 781pp + Sequence Listing; English.
PR	02-OCT-2000;	2000US-0237039P.	XX	
PR	02-OCT-2000;	2000US-0237040P.	XX	
PR	13-OCT-2000;	2000US-0239935P.	CC	The invention relates to novel genes (AAL34669-AAL37666) and proteins
PR	13-OCT-2000;	2000US-0239937P.	CC	(AB03087-AB04109) associated with the musculoskeletal system useful for
PR	20-OCT-2000;	2000US-0240960P.	CC	preventing, treating or ameliorating medical conditions e.g. by protein
PR	20-OCT-2000;	2000US-0241221P.	CC	or gene therapy. The genes are isolated from a range of human tissues
PR	20-OCT-2000;	2000US-0241785P.	CC	disclosed in the specification. The nucleic acids, proteins, antibodies
PR	20-OCT-2000;	2000US-0241787P.	CC	of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
PR	20-OCT-2000;	2000US-0241808P.	CC	adrenal gland, bone marrow, breast, gastrointestinal tract, liver,
PR	20-OCT-2000;	2000US-0241809P.	CC	lung, or urogenital; (b) immune disorders e.g. Addison's disease,
PR	20-OCT-2000;	2000US-0241846P.	CC	allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
PR	01-NOV-2000;	2000US-0244617P.	CC	diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
PR	08-NOV-2000;	2000US-0246474P.	CC	arthritis and ulcerative colitis; (c) cardiovascular disorders such as
PR	08-NOV-2000;	2000US-0246475P.	CC	myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g.
PR	08-NOV-2000;	2000US-0246476P.	CC	cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
PR	08-NOV-2000;	2000US-0246477P.	CC	bacterial, fungal and parasitic infections. Note: The sequence data for
PR	08-NOV-2000;	2000US-0246478P.	CC	this patent did not form part of the printed specification, but was
PR	08-NOV-2000;	2000US-0246523P.	CC	obtained in electronic format directly from WIPO at
PR	08-NOV-2000;	2000US-0246524P.	CC	ftp.wipo.int/pub/published_pct_sequences
PR	08-NOV-2000;	2000US-0246525P.	XX	
PR	08-NOV-2000;	2000US-0246526P.	XX	Sequence 8487 BP; 1948 A; 1987 C; 2408 G; 2144 T; 0 U; 0 Other;
PR	08-NOV-2000;	2000US-0246527P.	SQ	
PR	08-NOV-2000;	2000US-0246528P.		
PR	08-NOV-2000;	2000US-0246532P.		
PR	08-NOV-2000;	2000US-0246609P.		
PR	08-NOV-2000;	2000US-0246610P.		
PR	08-NOV-2000;	2000US-0246611P.		
PR	08-NOV-2000;	2000US-0246613P.		
PR	17-NOV-2000;	2000US-0249207P.		
PR	17-NOV-2000;	2000US-0249208P.		
PR	17-NOV-2000;	2000US-0249209P.		
PR	17-NOV-2000;	2000US-0249210P.		
PR	17-NOV-2000;	2000US-0249211P.		
PR	17-NOV-2000;	2000US-0249212P.		
PR	17-NOV-2000;	2000US-0249213P.		
PR	17-NOV-2000;	2000US-0249214P.		
PR	17-NOV-2000;	2000US-0249215P.		
PR	17-NOV-2000;	2000US-0249216P.		
PR	17-NOV-2000;	2000US-0249217P.		
PR	17-NOV-2000;	2000US-0249218P.		
PR	17-NOV-2000;	2000US-0249244P.		
PR	17-NOV-2000;	2000US-0249245P.		
PR	17-NOV-2000;	2000US-0249264P.		
PR	17-NOV-2000;	2000US-0249265P.		
PR	17-NOV-2000;	2000US-0249297P.		
PR	17-NOV-2000;	2000US-0249299P.		
PR	17-NOV-2000;	2000US-0249300P.		
PR	01-DEC-2000;	2000US-0250160P.		
PR	01-DEC-2000;	2000US-0250391P.		
PR	05-DEC-2000;	2000US-0251030P.		
PR	05-DEC-2000;	2000US-0251988P.		
PR	05-DEC-2000;	2000US-0256719P.		
PR	06-DEC-2000;	2000US-0251473P.		
PR	08-DEC-2000;	2000US-0251856P.		
PR	08-DEC-2000;	2000US-0251868P.		
PR	08-DEC-2000;	2000US-0251869P.		
PR	08-DEC-2000;	2000US-0251989P.		
PR	08-DEC-2000;	2000US-0251990P.		
PR	11-DEC-2000;	2000US-0254097P.		
PR	05-JAN-2001;	2001US-0259678P.		
XX	(HUMA-)	HUMAN GENOME SCI INC.		
PA				
XX	Rosen CA,	Barash SC, Ruben SM;		
XX				
XX				

[illegible]

06-SEP-2002.

05-FEB-2002; 2002WO-US003235.

27-FEB-2001; 2001US-00793706.

(PEKE) PE CORP NY.

Gong F, Yan C;
WPI; 2002-698658/75.
P-PSDB; AAE28633.

New human tumour suppressor proteins, useful for developing human therapeutic agents, or preventing or treating inflammation, or disorders associated with cell proliferation, e.g. bone cancer, brain cancer, leukemia or lymphoma.

Claim 4; Fig 3; 200pp; English.

The invention relates to human tumour suppressor polypeptides and polynucleotides. Sequences of the invention are useful for diagnosing, preventing or treating inflammation, or disorders associated with cell proliferation and apoptosis e.g. bone cancer, brain cancer, cervix cancer, adenocarcinoma, leukaemia, lymphoma or melanoma. They are particularly useful as models for developing human therapeutic targets, identifying therapeutic proteins, or serving as targets for the development of human therapeutic agents that modulate tumour suppressor protein activity in cells and tissues that express the tumour suppressor protein. Polypeptides of the invention are used for identifying agents that modulate their activity. They are useful for raising antibodies or eliciting an immune response; as a reagent in assays designed to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids; or as markers for tissues in which the corresponding protein is preferentially expressed. The invention is also used as vaccines. The present sequence is human tumour suppressor gene located on chromosome 13

Sequence 163350 BP; 40430 A; 36356 C; 37002 G; 39020 T; 0 U; 10542 Other;

Identity Match 71.9%; Score 616; DB 6; Length 163350;

Identity Local Similarity 100.0%; Pred. No. 2.9e-110;

Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

242 GAGATCCTCAAGGAGCTAGACGAGTGTCTAGACGGCTTCAGTCCGAGACACAGCGGGCG 301

159807 GAGATCCTCAAGGAGCTAGACGAGTGTCTAGACGGCTTCAGTCCGAGACACAGCGGGCG 159866

302 CAGAGCGCGGATCTGCTGATGTGTGAGCGCGCTGATCCGACGAGCTGGCG 361

159867 CAGAGCGCGGATCTGCTGATGTGTGAGCGCGCTGATCCGACGAGCTGGCG 159926

362 GACGAGAGATCCAGATCGTTCAGCCAGATGGTGGAGTGGTGGAGAACCGCACGCGGCGAG 421

159927 GACGAGAGATCCAGATCGTTCAGCCAGATGGTGGAGTGGTGGAGAACCGCACGCGGCGAG 159986

422 GTGGACAGCCAGCTGGAGCTGTTGAGCGCGACGAGAGCTGGCGACACAGCGGGCGAAC 481

159987 GTGGACAGCCAGCTGGAGCTGTTGAGCGCGACGAGAGCTGGCGACACAGCGGGCGAAC 160046

482 AGCGGCAAGGCTGGGCGGACAGCCACAGCCGAGCGCGACGCGAGCTGACAGGCC 541

160047 AGCGGCAAGGCTGGGCGGACAGCCACAGCCGAGCGCGACGCGAGCTGACAGGCC 160106

542 AACGACAGCGCTACAGCGCGGACGCGACACAGAGAACCGGTGAGAACCGGTCCAGCGAAC 601

160107 AACGACAGCGCTACAGCGCGGACGCGACACAGAGAACCGGTGAGAACCGGTCCAGCGAAC 160166

602 CACGACACGACGAGCGGCGCTCGGGGACACCCAAAGGAGAAAGGCCAAGACCTCCAG 661

160167 CACGACACGACGAGCGGCGCTCGGGGACACCCAAAGGAGAAAGGCCAAGACCTCCAG 160226

QY 662 AAGAAGACGCTCCCAAGCCAGGCGGAGCGAGCGCTCCCTCCGACCTCCCATC 721
AAAS3792
Db 160227 AAGAAGACGCTCCCAAGCCAGGCGGAGCGAGCGCTCCCTCCGACCTCCCATC 160286
QY 722 GACCCCAACGAACCCACGCTCTCTGTGCAACACGAGTCTCTATGGGAGATGATCGGC 781
Db 160287 GACCCCAACGAACCCACGCTCTCTGTGCAACACGAGTCTCTATGGGAGATGATCGGC 160346
QY 782 TGGGACACGACGAGTCCCATCGATGCTTCCACTTCTCTGCTGGGCTCAATCAT 841
Db 160347 TGGGACACGACGAGTCCCATCGATGCTTCCACTTCTCTGCTGGGCTCAATCAT 160406
QY 842 AAACCCCAAGGGCAAGT 857
Db 160407 AAACCCCAAGGGCAAGT 160422

RESULT 10
ID AAAS3792 standard; cDNA; 911 BP.
AC AAAS3792;
XX 19-DEC-2000 (first entry)
XX Human P37ING1 coding sequence.
DE P53; tumour; cancer; detection; antibody; hybridisation; exon 1b; INGI;
XX ing1; p33ING1; p37ING1; oncogene; gene therapy; diagnosis;
KW proliferation disorder; transformation; transformed cell; human; ds.
XX Homo sapiens.
OS
FN WO2000046370-A1.
XX
XX 10-AUG-2000.
XX
XX 04-FEB-2000; 2000WO-US002959.
XX
XX 04-FEB-1999; 99US-0118941P.
XX
XX (UNII) UNIV ILLINOIS FOUND.
XX
XX Gudkov A, Zeremski M, Gurova KV, Grigorian IA;
PI
XX WPI; 2000-491278/43.
DR P-PSDB; AAY97244.
XX
XX Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing
PT and treating cancer, comprises contacting sample with isolated nucleic
PT acid comprising sequence of exon 1b and detecting hybridized products.
XX
XX Disclosure; Page 122-123; 134pp; English.

Mutations in or loss of the p53 gene occur in more than 50% of human
tumours and tumour cell lines, but functional inactivation of the p53
pathway occurs in a much larger proportion of tumours. In many cases the
mechanism of functional inactivation of the p53 gene remains unknown but
p53 has been found to act in cooperation with INGI. Functional
cooperation between INGI and p53 suggested that INGI encoded a tumour
suppressor protein that functioned within the p53 pathway. This data
suggested a possible role for INGI in head and neck cancers and
chromosomal location of the INGI placed it within a region that is
frequently rearranged in head and neck cancers. Large scale analysis of
tumours involving INGI has not revealed mutations in INGI nor significant
variations in its expression suggesting that INGI was not a useful gene
to study in cancer etiology. However, alternative initiation exons of the
ING1 gene, each having their own promoter have been discovered.
Expression of one promoter (1a) produces a protein identical to INGI.
Expression of a second promoter (1b) produces a protein having an
identical C-terminal fragment to INGI but an additional 104 N-terminal
amino acids. The newly discovered protein has been designated p37ING1
(Wild type: p33ING1). p37ING1 has the characteristics of an oncogene.

CC When overexpressed in cells (even those expressing wild type p53) p37ING1
CC is able to cause proliferation or transformation of those cells. Thus
CC detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with
CC an isolated nucleic acid having the sequence of exon 1b of ing1 or its
CC antisense sequence can identify individuals expressing the oncogenic form
CC of ing1. Novel peptide sequences taken from the 104 N-terminal peptide of
CC p37ING1 can also be used to raise antibodies that can also be used in
CC detection methods for the p37ING1 variant. The polypeptides may be useful
CC in gene therapy for treatment of cell proliferation disorders, especially
CC cancers and for diagnosing and studying cancers
XX
SQ Sequence 911 BP; 228 A; 255 C; 305 G; 123 T; 0 U; 0 Other;

Query Match 70.8%; Score 606.4; DB 3; Length 911;
Best Local Similarity 99.0%; Pred. No. 1.6e-108;
Matches 610; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 242 GAGATCCTGAGGAGCTAGACGAGTCTACGAGCGTTTCAGTCCGAGACAGACGGGGCG 301
Db 180 GAGATCCTGAGGAGCTAGACGAGTCTACGAGCGTTTCAGTCCGAGACAGACGGGGCG 239
QY 302 CAGAAGCGGGGATGCTGCACTGTGTGCAGCGCGCGCTGATCCGACGCCAGGAGTGGGC 361
Db 240 CAGAAGCGGGGATGCTGCACTGTGTGCAGCGCGCGCTGATCCGACGCCAGGAGTGGGC 299
QY 362 GACGAGAGATCCAGATCGTGAGCCAGATGGTGAGAGTGGTGAGAACCCGACGCGCAG 421
Db 300 GACGAGAGATCCAGATCGTGAGCCAGATGGTGAGAGTGGTGAGAACCCGACGCGCAG 359
QY 422 GTGACACGCCACGCTGGAGCTGTTTCGAGCGCGCAGCAGAGTGGCGGCACACAGCGGGCAAC 481
Db 360 GTGACACGCCACGCTGGAGCTGTTTCGAGCGCGCAGCAGAGTGGCGGCACACAGTGGGCAAC 419
QY 482 AGCGCAAGGCTGGCGGGACAGCGCCCAAGGCGAGCGCGCGCAGCGAGGTGACAAAGCCC 541
Db 420 AGCGCAAGGCTGGCGGGACAGCGCCCAAGGCGAGCGCGCGCAGCGAGGTGACAAAGCCC 479
QY 542 AACAGCAAGCGCTCACGCGCGCAGCGCAACAAACAGAGAACCGTGAGAACCGGTCCAGCAAC 601
Db 480 AACAGCAAGCGCTCACGCGCGCAGCGCAACAAACAGAGAACCGTGAGAACCGGTCCAGCAAC 539
QY 602 CACGACCAAGCAGCAGCGCGCTCGGGCACCACCAAGGAGAGAGAGGCGCAGACCTCCAAG 661
Db 540 CACGACCAAGCAGCAGCGCGCTCGGGCACCACCAAGGAGAGAGAGGCGCAGACCTCCAAG 599
QY 662 AAGAAGAGCGCTCCCAAGGCCAAGCGGAGGAGCGGTCCCTCGCGAGCTCCCTCCCATC 721
Db 600 AAGAAGAGCGCTCCCAAGGCCAAGCGGAGGAGCGGTCCCTCGCGAGCTCCCTCCCATC 659
QY 722 GACCCCAACGAACCCACGCTACTGTGTGCAACACGAGTCTCTATGGGAGATGATCGGC 781
Db 660 GACCCCAACGAACCCACGCTACTGTGTGCAACACGAGTCTCTATGGGAGATGATCGGC 719
QY 782 TCGGACACGACGAGTGGCCCATCGAGTGGTTCCACTTCTCTGCTGGGCGTCAATCAT 841
Db 720 TCGGACACGACGAGTGGCCCATCGAGTGGTTCCACTTCTCTGCTGGGCGTCAATCAT 779
QY 842 AAACCCCAAGGGCAAGT 857
Db 780 AAACCCCAAGGGCAAGT 795

RESULT 11
ID AAH28479 standard; DNA; 1143 BP.
XX
XX AC AAH28479;
XX
XX DT 17-SEP-2001 (first entry)
XX
XX Nucleotide sequence of a human cancer associated antigen.
XX
XX Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine; ss.

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 16..900
XX FT /*tag= a
XX FT /transl_except= (pos: 25..30, aa: Cys)
XX FT /transl_except= (pos: 124..126, aa: Pro, Ala)
XX FT /product= cancer associated antigen
XX PN WO200147959-A2.
XX PD 05-JUL-2001.
XX PF 29-NOV-2000; 2000WO-US042334.
XX PR 30-NOV-1999; 99US-00451739.
XX PR 24-OCT-2000; 2000US-00602362.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX PA (CORR) CORNELL RES FOUND INC.
XX PI Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;
XX PI WPI; 2001-441706/47.
XX DR P-PSDB; AAB84697.
XX PT Isolated cancer associated nucleic acid molecule identified by SEREX
XX PT (serological identification of antigens by recombinant expression
XX PT cloning) technique, useful in nucleic acid based therapies to treat
XX PT cancer.
XX PS Example 4; Page 44; 62pp; English.
XX CC The present sequence encodes a human cancer associated antigen. The
XX CC sequence is the wildtype of the INGI gene, which is a tumour suppressor
XX CC gene candidate. The cancer associated antigen polynucleotides and
XX CC polypeptides are useful for screening for the possible presence of a
XX CC pathological condition in a subject such as cancer. The cancer associated
XX CC antigen polypeptides are useful for producing vaccines
XX SQ Sequence 1143 BP; 289 A; 291 C; 366 G; 197 T; 0 U; 0 Other;
Query Match 70.7%; Score 605.6; DB 4; Length 1143;
Best Local Similarity 95.6%; Pred. No. 2.3e-108;
Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 206 CTAGGCTGTGGAGTGTGTGTCGCGCCGCGGAATGGAGATCTCTGAAGAGCTAGACGAG 265
DB 160 CTGACCCGAGGTGGGGCGCGCGTGGCGGTGGAACACAGATCTCTGAAGAGCTAGACGAG 219
QY 266 TGCTACGAGCGTTTCAGTTCGCGAGACAGAGCGGGCGCAGAGCGGGATGCTGCACTGT 325
DB 220 TGCTACGAGCGTTTCAGTTCGCGAGACAGAGCGGGCGCAGAGCGGGATGCTGCACTGT 279
QY 326 GTGACGCGCGCTGTATGCGACGCCAGAGAGCTGGCGCAGAGAGATCCAGATCGTGAGC 385
DB 280 GTGACGCGCGCTGTATGCGACGCCAGAGAGCTGGCGCAGAGATCCAGATCGTGAGC 339
QY 386 CAGATGGTGAGCTGTGGAGACCCGACGCGCAGTGGACAGCCACGTGGAGCTGTTC 445
DB 340 CAGATGGTGAGCTGTGGAGAACCCGACGCGCAGTGGACAGCCACGTGGAGCTGTTC 399
QY 446 GAGCGCAGCAGGAGCTGGCGCAGACAGCGGGCAACAGCGGCAAGCTGGCGGACAGG 505
DB 400 GAGCGCAGCAGGAGCTGGCGCAGACAGTGGGCAACAGCGGCAAGCTGGCGGACAGG 459
QY 506 CCCAAGGCGAGCGGCGAGCGAGGTGACAGCCCAACAGCAAGCGCTCACGGGGCAG 565
DB 460 CCCAATGGCGATCGGTAGCGCAGTCTGACAGCCCAACAGCAAGCGCTCACGGGGCAG 519
QY 566 CGCAACAAAGAGAACCGTGAGAACCGGTCTCAGCAACACAGCAACGACGCGCGCTCG 625

DB 520 CGCAACAAAGAGAACCGTGAGAACCGTCCAGAACACCGACCCAGCAGCGCGCCCTCG 579
QY 626 GGCACACCCCAAGGAGAAGAGCCCAAGACCTCCAAAGAAAGAGAGCGCTCCAAAGCCCAAG 685
DB 580 GGCACACCCCAAGGAGAAGAGCCCAAGACCTCCAAAGAAAGAGAGCGCTCCAAAGCCCAAG 639
QY 686 GCGGAGCGAGAGCGCTCCCTCCGACACCTCCGACCTCCGACCCCAAGCAAGCCGACTGT 745
DB 640 GCGGAGCGAGAGCGCTCCCTCCGACACCTCCGACCTCCGACCCCAAGCAAGCCGACTGT 699
QY 746 CTGTGCAACCAAGTCTCTCTATGGGAGATGATCGGCTCGCAACAGCAGAGTGCCTCATC 805
DB 700 CTGTGCAACCAAGTCTCTCTATGGGAGATGATCGGCTCGCAACAGCAGAGTGCCTCATC 759
QY 806 GAGTGTTCACCTCTCTCTGCTGGGCTCAATCATTAACCCCAAGGCAAGT 857
DB 760 GAGTGTTCACCTCTCTCTGCTGGGCTCAATCATTAACCCCAAGGCAAGT 811
RESULT 12
AAT69651
ID AAT69651 standard; cDNA; 1902 BP.
XX AC AAT69651;
XX XX 27-AUG-1997 (first entry)
XX DE Tumour suppressor gene INGI partial cDNA.
XX KW Tumour suppressor gene; INGI; p33ING1; breast cancer; brain cancer;
XX KW diagnosis; gene therapy; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 109..741
XX FT /*tag= a
XX PN WO9721809-A1.
XX XX 19-JUN-1997.
XX PF 06-DEC-1996; 96WO-CA000819.
XX PR 08-DEC-1995; 95US-00569721.
XX PR 15-NOV-1996; 96US-00751230.
XX PA (UYTE-) UNIV TECHNOLOGIES INT INC.
XX PI Garkavstev I, Riabowol K;
XX PI WPI; 1997-332781/30.
XX DR P-PSDB; AAW19118.
XX PT Isolated tumour suppressor gene, INGI - useful to develop products for
XX PT inhibiting or increasing cell proliferation, in particular for treatment
XX PT or diagnosis of cancer.
XX PS Claim 1; Fig 2; 63pp; English.
XX CC A partial cDNA clone (AAT69651), designated INGI, codes for a novel
XX CC tumour suppressor protein p33ING1 (AAW19118) that is a potent inhibitor
XX CC of cell growth. It was isolated by subtractive hybridization between
XX CC normal mammary and transformed epithelial cDNAs, isolation of an
XX CC antisense INGI cDNA insert that caused increased cell proliferation, and
XX CC use of the insert to screen normal human fibroblast and HeLa cDNA
XX CC libraries. A complete INGI sequence (AAT69652) was obt'd. by 5'RACE. INGI
XX CC is localised to the 13q33-34 chromosome region, to which a number of
XX CC human cancers have been mapped. INGI nucleic acids can be used in the
XX CC diagnosis of breast cancer; a decreased level of INGI mRNA indicates
XX CC cancerous cells. They can also be used in gene therapy methods to block
XX CC the proliferation of cancer cells


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Db 301 CCATGCGATGCGGTAGCGAGTCTGACAGCCCAACAGAGCGCTCACGGCGCAG 360
Qy 566 CGCAACACAGAGAACCGTGAAGCGCTCAGCAACACACAGACGAGCGGCTCG 625
Db 361 CGCAACACAGAGAACCGTGAAGCGCTCAGCAACACACAGACGAGCGGCTCG 420
Qy 626 GGCACACCCAGGAGAGAGCGGCTCAGCAACCGCTCAGCAACCGCTCAGGCGCAAG 685
Db 421 GGCACACCCAGGAGAGAGCGGCTCAGCAACCGCTCAGCAACCGCTCAGGCGCAAG 480
Qy 686 GCGAGCGAGAGCGGCTCAGCAACCGCTCAGCAACCGCTCAGCAACCGCTCAGGCTACTGT 745
Db 481 GCGAGCGAGAGCGGCTCAGCAACCGCTCAGCAACCGCTCAGCAACCGCTCAGGCTACTGT 540
Qy 746 CTGTGCAACACAGGCTCCTATGGGAGATGATCGCTGCGACACGACGAGTGCCCATC 805
Db 541 CTGTGCAACACAGGCTCCTATGGGAGATGATCGCTGCGACACGACGAGTGCCCATC 600
Qy 806 GAGTGGTTCCACTTCTCGTGGGCGCTCAATCATATAACCCAGGCGCAAGT 857
Db 601 GAGTGGTTCCACTTCTCGTGGGCGCTCAATCATATAACCCAGGCGCAAGT 652

RESULT 14
ID AAT69652
XX AAT69652 standard; cDNA; 2061 BP.
AC AAT69652;
XX
XX 27-AUG-1997 (first entry)
XX Tumour suppressor gene ING1 full-length cDNA.
XX Tumour suppressor gene; ING1; p33ING1; breast cancer; brain cancer;
XX diagnosis; gene therapy; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 16..900
XX primer_bind /tag= a
XX primer_bind complement(474..494)
XX primer_bind /tag= b
XX primer_bind /note= "direct primer 1"
XX primer_bind complement(763..782)
XX primer_bind /tag= c
XX primer_bind /note= "direct primer 2"
XX primer_bind /tag= d
XX primer_bind /note= "reverse primer 3"
XX primer_bind 890..900
XX primer_bind /tag= e
XX primer_bind /note= "reverse primer 4"
XX
XX WO9721809-A1.
XX
XX 19-JUN-1997.
XX
XX 06-DEC-1996; 96WO-CA000819.
XX
XX 08-DEC-1995; 95US-00569721.
XX
XX 15-NOV-1996; 96US-00751230.
XX
XX (UYTE-) UNIV TECHNOLOGIES INT INC.
XX
XX Garkavstev I, Riabowol K;
XX
XX WPI; 1997-332781/30.
XX
XX P-PSDB; AAW18119.
XX
XX Isolated tumour suppressor gene, ING1 - useful to develop products for
XX inhibiting or increasing cell proliferation, in particular for treatment
XX or diagnosis of cancer.

```

```

XX Claim 11; Fig 3; 63pp; English.
XX
XX A full-length cDNA clone (AAT69652), designated ING1, codes for a novel
XX 33 kDa tumour suppressor protein p33ING1 (AAW19119), formerly p33ING1,
XX that is a potent inhibitor of cell growth. A partial clone (AAT69651) was
XX isolated by subtractive hybridisation between normal mammary and
XX transformed epithelial cDNAs, isolation of an antisense ING1 cDNA insert
XX that caused increased cell proliferation, and use of the insert to screen
XX normal human fibroblast and HeLa cDNA libraries. The complete ING1
XX sequence was then obt'd. by 5'RACE. ING1 is localised to the 13q33-34
XX chromosome region, to which a number of human cancers have been mapped.
XX ING1 nucleic acids can be used in the diagnosis of breast cancer; a
XX decreased level of ING1 mRNA indicates cancerous cells. They can also be
XX used in gene therapy methods to block the proliferation of cancer cells
XX
XX Sequence 2061 BP; 602 A; 439 C; 515 G; 505 T; 0 U; 0 Other;
XX
XX Query Match 70.7%; Score 605.6; DB 2; Length 2061;
XX Best Local Similarity 95.6%; Pred. No. 2.4e-108;
XX Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
XX
XX Qy 206 CTAGGCTGCTGGAGTGTGTGTCGCGCGCGGAGATGAGATCTCTGAGGAGCTAGACGAG 265
XX Db 160 CTGACCCGAGGTGGGGCGCGCGTGGCGGTGGAAACAGATCTCTGAGGAGCTAGACGAG 219
XX Qy 266 TGCTACGAGCGCTTCAGTCCGCGAGACAGACGCGGCGGAGAGCGCGGATGCTGACTGT 325
XX Db 220 TGCTACGAGCGCTTCAGTCCGCGAGACAGACGCGGCGGAGAGCGCGGATGCTGACTGT 279
XX Qy 326 GTGCGCGCGCGCTGATCCGCGAGCCAGGAGCTGGCGGAGAGAGATCCAGATCTGTGAGC 385
XX Db 280 GTGCGCGCGCGCTGATCCGCGAGCCAGGAGCTGGCGGAGAGATCCAGATCTGTGAGC 339
XX Qy 386 CAGATGTTGGAGCTGTTGGAGAACCGCACGCGCGAGTGGACAGCAGCGTGTGAGCTGTTTC 445
XX Db 340 CAGATGTTGGAGCTGTTGGAGAACCGCACGCGCGAGTGGACAGCAGCGTGTGAGCTGTTTC 399
XX Qy 446 GAGGCGCAGCGAGCTGGCGGACAGCGGCGCAACAGCGGAGCTGGCGCGGACAGG 505
XX Db 400 GAGGCGCAGCGAGCTGGCGGACAGCGGCGCAACAGCGGAGCTGGCGCGGACAGG 459
XX Qy 506 CCCAAGGCGGAGCGGCGGAGCGGAGTGAACAGCCCAACAGCAAGCGGTTCACGGCGGCGAG 565
XX Db 460 CCCAATGGCGATGCGGTAGCGAGTCTGACAAAGCCCAACAGCAAGCGGTTCACGGCGGCGAG 519
XX Qy 566 CGCAACACAGAGAACCGTGAAGCGGTCAGCAACCGGAGCGGAGCGGAGCGGCGGCTCG 625
XX Db 520 CGCAACACAGAGAACCGTGAAGCGGTCAGCAACCGGAGCGGAGCGGAGCGGCGGCTCG 579
XX Qy 626 GGCACACCCCAAGGAGAGAGCGGAGCGGAGCTTCAAGAGAGAGAGCGGTCTCAAGGCGCAAG 685
XX Db 580 GGCACACCCCAAGGAGAGAGAGCGGAGCGGAGCTTCAAGAGAGAGAGCGGTCTCAAGGCGCAAG 639
XX Qy 686 GCGGAGCGAGAGCGGCTCCCTGCGGAGCTCCCGATCGACCCCAACAGCAAGCGGAGCTACTGT 745
XX Db 640 GCGGAGCGAGAGCGGCTCCCTGCGGAGCTCCCGATCGACCCCAACAGCAAGCGGAGCTACTGT 699
XX Qy 746 CTGTGCAACCGAGTCTCTATGGGAGATGATCGGCTGCGACACAGCGAGTGGCGGCGGCTACT 805
XX Db 700 CTGTGCAACCGAGTCTCTATGGGAGATGATCGGCTGCGACACAGCGAGTGGCGGCGGCTACT 759
XX Qy 806 GAGTGGTTCCACTTCTCGTGGGCGCTCAATCATATAACCCAGGCGCAAGT 857
XX Db 760 GAGTGGTTCCACTTCTCGTGGGCGCTCAATCATATAACCCAGGCGCAAGT 811

RESULT 15
AAV62292
ID AAV62292 standard; cDNA; 2061 BP.
XX
XX AAV62292;
XX
XX

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18-JAN-1999 (first entry)
Human INGI1 full-length cDNA sequence.
INGI1 gene; p33INGI1; human; apoptosis; cell death; breast cancer;
brain tumour; gene therapy; tumour suppressor; ss.
Homo sapiens.

Key Location/Qualifiers
CDS 16..900
/*tag= a

W09844102-A2.

08-OCT-1998.

26-MAR-1998; 98WO-CA000277.

27-MAR-1997; 97US-00828158.

(UYTE-) UNIV TECHNOLOGIES INT INC.

Helbing CC, Riabowol K, Johnston RN, Garkavtsev I;

WPI; 1998-542700/46.

P-PSDB; AAW9675.

Modulating eukaryotic apoptosis by increasing p33INGI activity - using
p33INGI derivatives, to induce apoptosis in cancer cells, and in the
investigation of apoptotic pathways.

Claim 7; Fig 3; 66pp; English.

This is the nucleotide sequence of a human INGI1 (Inhibitor of Growth)
that codes for a p33INGI polypeptide (see AAW9675), a novel inhibitor
of cell growth and a candidate tumour suppressor. INGI1 is a new gene that
is expressed in normal mammary epithelial cells, but which is expressed
only at lower levels in several cancerous mammary epithelial cell lines
and is not expressed in many primary brain tumours. To isolate INGI1, a
subtractive hybridisation of breast cancer cell line cDNAs was performed
with cDNA from normal mammary epithelial cells, and subtracted cDNAs were
cloned into retrovirus vector pLNCX. Following passage through a
packaging line, normal mouse mammary epithelial cells were infected, and
infected cells were injected into nude mice. Putative transforming
fragments from tumours were isolated by PCR (see AAW62230-91) and
subcloned into LNCX. An INGI1 fragment was obtained and used to screen
normal human fibroblast and HeLa cell cDNA libraries. 2 Clones were
sequenced to obtain a partial INGI1 sequence (see AAW62285). The complete
cDNA sequence was then obtained by RACE. A claimed method to potentiate
apoptosis in a eukaryotic cell involves administering an active p33INGI
peptide or an oligonucleotide encoding such as a peptide. A claimed
method for inhibiting apoptosis in a eukaryotic cell involves
administering an antisense oligonucleotide. Also claimed are a method for
determining the apoptotic characteristics of a eukaryotic cell, an assay
for determining the level of p33INGI activity in a eukaryotic cell, and
an isolated eukaryotic cell substantially free of p33INGI biological
activity. The invention discloses INGI1 derivatives or variants that may
be used to induce apoptosis in eukaryotic cancer cells

Sequence 2061 BP; 602 A; 439 C; 515 G; 505 T; 0 U; 0 Other;

Query Match 70.7%; Score 605.6; DB 2; Length 2061;
Best Local Similarity 95.6%; Pred. No. 2.4e-105;
Matches 623; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 206 CTAGGCTGCTGGAGTGGTGGTCCGGCCGCGAATGGAGATCCTGAAGAGCTAGACGAG 265
DB 160 CTGACCCGAGGTGGGGCGCGCGTGGTGAACACAGATCCTCAAGAGCTAGACGAG 219
QY 266 TCGTAGGCGCTTACGTCCGAGACAGACGGGGCGAGAGCGCGGATGCTGCACTGT 325
DB 220 TCGTAGGCGCTTACGTCCGAGACAGACGGGGCGAGAGCGCGGATGCTGCACTGT 279

QY 326 GTGCAGCGCGCGCTGATCCGACGACGAGAGCTGGCGGACGAGAGATCCAGATCGTGAGC 385
DB 280 GTGCAGCGCGCGCTGATCCGACGACGAGAGCTGGCGGACGAGAGATCCAGATCGTGAGC 339
QY 386 CAGATGTTGAGTGGTGGAGAACCCGACGCGGCGAGTGGACAGCCACGTCGGAGCTGTTC 445
DB 340 CAGATGTTGAGTGGTGGAGAACCCGACGCGGCGAGTGGACAGCCACGTCGGAGCTGTTC 399
QY 446 GAGCGCAGCAGAGCTGGCGGACGACGCGGGCAAACAGCGGCAAGGTCGCGCGGACAGG 505
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DB 520 CGCAACACGAGAACCGTGGAGAACCGTCCAGCAACCCAGCAGCAGCAGCGCGCTCG 579
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DB 580 GGCACACCCAGAGAGAGAGGCGCAAGCCTCCAAAGAGAGAGCGCTCCAAAGGCCAAG 639
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DB 640 GCGGAGCGAGAGGCGTCCCTGCGGACCTCCCAATCCGACCCCAACGACCACTACTGT 699
QY 746 CTGTGCAACCAAGGCTCTCTATGGGAGATGATCGGCTGGCAGACGACGAGTGCCTCATC 805
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Search completed: May 6, 2004, 08:19:34
Job time : 426.45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM'nucleic - nucleic search, using sw model

Run on: May 6, 2004, 06:25:29 ; Search time 3731.55 Seconds
(without alignments)
9954.293 Million cell updates/sec

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Perfect score: 857
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank

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- 37: em_hg_vit.*
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- 39: em_hgo_hum.*
- 40: em_hgo_mus.*
- 41: em_hgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	857	100.0	857	6	AX367045 Sequence
2	847.4	98.9	1189	9	AF149723 Homo sapi
3	618	72.1	2296	9	BC018348 Homo sapi
4	617.6	72.1	888	9	AB037594 Homo sapi
5	616.4	71.9	2886	9	AF181849 Homo sapi
6	616	71.9	742	6	AX367044 Sequence
7	616	71.9	840	9	AF078835 Homo sapi
8	616	71.9	845	9	AF078835 Homo sapi
9	616	71.9	1533	6	AX367042 Homo sapi
10	616	71.9	1905	6	AX839842 Sequence
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12	616	71.9	2552	9	AF167551 Homo sapi
13	616	71.9	2897	9	AF181850 Homo sapi
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21	606.4	70.8	911	9	AF044076 Homo sapi
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24	606.4	70.8	1980	9	AB024404 Homo sapi
25	606.4	70.8	2444	9	AB024401 Homo sapi
26	606.4	70.8	2891	9	AB024402 Homo sapi
27	605.6	70.7	1143	6	AX367043 Sequence
28	605.6	70.7	1902	6	AR079046 Sequence
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33	605.6	70.7	2061	6	AR110653 Sequence
34	605.6	70.7	2061	6	AR154570 Sequence
35	605.6	70.7	2061	9	AF001954 Homo sapi
36	604	70.5	2061	6	AF171883 Sequence
37	602.4	70.3	2061	6	AR219160 Sequence
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42	446.4	52.1	184918	2	AC114608 Mus muscu
43	446.4	52.1	235079	2	AC124475 Mus muscu
44	444.8	51.9	840	10	AF149820 Mus muscu
45	444.8	51.9	1584	10	BC016573 Mus muscu

ALIGNMENTS

RESULT 1	AX367045	Sequence 4 from Patent WO0147959.	857 bp	DNA	linear	PAT 16-FEB-2002
LOCUS	AX367045	Sequence 4 from Patent WO0147959.				
DEFINITION	AX367045	Sequence 4 from Patent WO0147959.				
ACCESSION	AX367045.1	GI:18855270				
VERSION	AX367045.1	GI:18855270				
KEYWORDS						
SOURCE						
ORGANISM						
	Homo sapiens (human)					
REFERENCE						
AUTHORS						
	Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and Chen,Y.T.					
TITLE						
	Isolated nucleic acid molecules encoding cancer associated					

Pred. No. is the number of results predicted by chance to have a

antigens, the antigens per se, and uses thereof
 Patent: WO 0147959-A 4 05-JUL-2001;
 LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL
 SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation
 (US)

Journal Location/Qualifiers
 i. .857
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FEATURES
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 Best Local Similarity 100.0%; Pred. No. 4.2e-119; Indels 0; Gaps 0;
 Matches 857; Conservative 0; Mismatches 0;

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Db 841 TAAACCCCAAGGAGGAGT 857

RESULT 2
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 LOCUS Homo sapiens ING1 tumor suppressor, variant C (ING1) mRNA, complete cds.
 DEFINITION
 ACCESSION AF149723 GI:7158368
 VERSION AF149723
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (Bases 1 to 1189)
 Jaeger, D., Stockert, E., Scanlan, M.J., Gure, A.O., Jaeger, E., Knuth, A.,
 Old, L.J., and Chen, Y.T.
 Cancer-testis antigens and ING1 tumor suppressor gene product are
 breast cancer antigens: characterization of tissue-specific ING1
 transcripts and a homologue gene
 Cancer Res. 59 (24), 6197-6204 (1999)
 JOURNAL MEDLINE
 PUBMED 10628813
 REFERENCE 2 (Bases 1 to 1189)
 Jaeger, D.
 Direct Submission
 Submitted (11-MAY-1999) Pathology, Cornell University, 1300 York
 Avenue, New York, NY 10021, USA
 JOURNAL Location/Qualifiers
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ORIGIN

Query Match 98.9%; Score 847.4; DB 9; Length 1189;
 Best Local Similarity 99.3%; Pred. No. 1e-116;
 Matches 851; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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 Db 121 CTCTTCCTCAAGCGCTTCCAACTGAGTACCGGAGACGACACAAAGGAGGCGGTGA 180
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Db      1026 AATCATAAACCCAAAGGCGAAGT 1047

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LOCUS   AB037594                888 bp    mRNA    linear    PRI 20-DEC-2002
DEFINITION Homo sapiens mRNA for INGI isoform, complete cds.
ACCESSION AB037594
VERSION   AB037594.2    GI:27263168
KEYWORDS  INGI isoform.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 Gunduz, M., Ouchida, M., Fukushima, K., Hanafusa, H., Etani, T., Nishio, S., Nishizaki, K. and Shimizu, K. Genomic structure of the human INGI gene and tumor-specific mutations detected in head and neck squamous cell carcinomas Cancer Res. 60 (12), 3143-3146 (2000) 20322670
REFERENCE 2 (bases 1 to 888) 10866301
AUTHORS   Ouchida, M. and Hanafusa, H.
TITLE     Direct Submission
JOURNAL   Submitted (25-JAN-2000) Mamoru Ouchida, Okayama University Medical School, Department of Molecular Genetics; Shikata-cho, 2-5-1, Okayama 700-8558, Japan (E-mail:ouchidam@med.okayama-u.ac.jp, Tel:81-86-235-7379, Fax:81-86-235-7383)
COMMENT   On Dec 19, 2002 this sequence version replaced gi:12231169.
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ORIGIN
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Best Local Similarity 97.8%; Pred. No. 1.6e-82;
Matches 626; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY      278 TTCAGTCGAGACAGCGGGCGGAGAGCGCGGATGCTGCTCACTGTGTGACGCGCGC 337
Db      128 TTCAGTCGAGACAGCGGGCGGAGAGCGCGGATGCTGCTCACTGTGTGACGCGCGC 187
QY      338 CTGATCCCGACGAGCTGGGCGGACGAGAGATCCAGATCGTGAGCCAGATGTGGAG 397

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Db      188 CTGATCCGACGACGAGCTGGCGGACGAGATCCAGATCGTGAGCCAGATGTGGAG 247
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QY      638 GAGAAGAGGCCAAGACCTCCAAAGAGAGAGCGCTCCAAAGGCCAAAGCGGAGCGAG 697
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DEFINITION Homo sapiens p47ING1a (ING1) mRNA, complete cds.
ACCESSION AF181849
VERSION   AF181849.1    GI:6409277
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 2886)
AUTHORS   Ma, D., Lawless, D. and Riabowol, K.
TITLE     Sequence conservation of INGI1 splicing isoforms in divergent species
JOURNAL   Nat. Genet. 23, 373 (1999)
REFERENCE 2 (bases 1 to 2886)
AUTHORS   Ma, D., Lawless, D. and Riabowol, K.
TITLE     Direct Submission
JOURNAL   Submitted (30-AUG-1999) Department of Biochemistry and Molecular Biology, University of Calgary, 3330 Hospital Drive N.W., Calgary, Alberta T2N 4N1, Canada
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ORIGIN

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Best Local Similarity 85.5%; Pred. No. 1.8e-82;
Matches 686; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

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Qy 116 GCGCCCTTGTCTCCAGCGCTTCCAACTGAGTACCGGAGACACACAAAGGAGGCG 175
Db 871 GCGCTGTGGGCTCGGCGCGGGGTGCGATTCGACACCGCTCCCGCGCGGGGCGG 930

Qy 176 GGTGACGATGCGCGGAGCGCGCGCTAGCTGTGGAGTGTGGTGTGGGCGCG 235
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Qy 236 GGAATGGAGATCTTGAAGAGCTAGACAGTGTACGAGCGCTTCAGTCGCGAGACAG 295
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RESULT 6
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LOCUS Sequence 3 from Patent WO0147959.
DEFINITION AX367044
ACCESSION AX367044.1 GI:18855269
VERSION AX367044.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Jager, D., Stockert, E., Scanlan, M., Knuth, A., Old, L., Gure, A. and
Chen, Y.T.
Isolated nucleic acid molecules encoding cancer associated
antigens, the antigens per se, and uses thereof
Patent: WO 0147959-A 3 05-JUL-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL
SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation
(US)
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Best Local Similarity 100.0%; Pred. No. 3e-82;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 GAGTCTCTGAAGAGCTAGACGAGTCTACGAGCGCTTCAGTCGCGAGACAGCGGGGCG 301
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Db 187 CAGAACGCGCGGATGTGCACTGTGTGACGCGCGCTGATCCGACGAGAGTGGCG 246

Qy 362 GACGAGAGATCCAGATCGTGAACCGAGTGTGGAGCTGTGGAGAACCGGACGCGGAG 421
Db 247 GACGAGAGATCCAGATCGTGAACCGAGTGTGGAGCTGTGGAGAACCGGACGCGGAG 306

Qy 422 GTGACACAGCCACGTGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACACGCGGCAAC 481
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Qy 482 AGCGCAAGGCTGGCGGACAGGCGCCAAAGCGGAGGCGGAGCTGCAAGGCC 541
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Qy 662 AAGNAGAGCGCTCCAGGCGCAAGGCGGAGGCGGCTGCCCTGCCAGCTCCCATC 721
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Qy 722 GACCCCAACGAAACCGTACTGTGTGTGCAACAGAGTCTCTATGGGAGATGATCGGC 781
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RESULT 7

AF078835

LOCUS

DEFINITION Homo sapiens p33ING1 (ING1) mRNA, complete cds.

ACCESSION AF078835

VERSION AF078835.1 GI:10039544

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 840)

Nagashima, M., Shieski, M., Miura, K., Hagiwara, K., Linke, S.P., Pedoux, R., Wang, X.W., Yokota, J., Riabowol, K. and Harris, C.C. DNA damage-inducible gene p33ING2 negatively regulates cell proliferation through acetylation of p53

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001)

MEDLINE 21396501

PUBMED 11481424

REFERENCE

2 (bases 1 to 840)

Nagashima, M., Hagiwara, K., Hancock, A.R. and Harris, C.C. Direct Submission

AUTHORS Submitted (16-JUL-1998) Laboratory of Human Carcinogenesis, National Cancer Institute, National Institutes of Health, 37 National Cancer Center Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA

JOURNAL

CONVENT Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA

FEATURES

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ORIGIN

Query Match 71.9%; Score 616; DB 9; Length 840;

Best Local Similarity 100.0%; Pred. No. 2.9e-82;

Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 GAGATCTCTAAGAGCTAGACAGTCTACGAGCGCTTCAGTCGCGAGACAGAGCGGCG 301

Db 136 GAGATCTCTAAGAGCTAGACAGTCTACGAGCGCTTCAGTCGCGAGACAGAGCGGCG 195

Qy 302 CAGAGCGCGGATGCTGACCTGTGTGCGAGCGCGGCTGATCCGCGAGCAGGAGCTGGGC 361

Db 196 CAGAGCGCGGATGCTGACCTGTGTGCGAGCGCGGCTGATCCGCGAGCAGGAGCTGGGC 255

Qy 362 GACGAGAGATCAGATCTGAGCCGATGTTGGAGCTGTGGAGAACCGACCGGCGAG 421

Db 256 GACGAGAGATCAGATCTGAGCCGATGTTGGAGCTGTGGAGAACCGACCGGCGAG 315

Qy 422 GTGGACAGCCACTGAGCTGTTTCGAGGCGGCGAGGAGCTGGGCGACACAGCGGCGAAC 481

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Db 556 AAGAAGAGGCTTCAAGGCGAGCGGCAACACAGAGAACCGTGAGAACCGGCTCCAGCAC 615

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Db 616 GACCCCAAGGCTTCAAGGCGAGCGGCAACACAGAGAACCGTGAGAACCGGCTCCAGCAC 675

Qy 782 TGGGACCAAGGCTTCAAGGCGAGCGGCAACACAGAGAACCGTGAGAACCGGCTCCAGCAC 841

Db 676 TGGGACCAAGGCTTCAAGGCGAGCGGCAACACAGAGAACCGTGAGAACCGGCTCCAGCAC 735

Qy 842 AAACCCCAAGGCAAGT 857

Db 736 AAACCCCAAGGCAAGT 751

RESULT 8

HS310392

LOCUS

DEFINITION Homo sapiens mRNA for p33ING1b (ING1b gene).

ACCESSION AJ310392

VERSION AJ310392.1 GI:13992538

KEYWORDS ING1b; p33ING1b.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

Nouman, G.S., Anderson, J.J., Angus, B. and Lunec, J. Supplement: Sequencing of ING1 tumour suppressor gene cDNAs generated from mRNA recovered from normal and neoplastic cell lines J. Pathol. 192, 266-266 (2000)

JOURNAL

REFERENCE

2

Nouman, G.S., Angus, B., Lunec, J., Lodge, A.J. and Anderson, J.J. Comparative Assessment of ING1 Expression in Normal and Neoplastic Tissues Unpublished

REFERENCE

3 (bases 1 to 845)

Nouman, G.S. Direct Submission

AUTHORS Submitted (24-APR-2001) Nouman G.S., Pathology Department, Royal Victoria Infirmary, Faculty of Medicine, University of Newcastle upon Tyne, Department of Pathology, Royal Victoria Infirmary, Newcastle upon Tyne, NE3 4PH, UNITED KINGDOM

JOURNAL

TITLE

Identical sequence found in: Newborn Foreskin Fibroblast Hs-68 Epithelial Lung Carcinoma line: A549 Breast Carcinoma Cell lines: ZR75, T47D, MCF-7 Neuroblastoma lines: SK-N-SH, SKN-BE, SKN-BE-2C Cervical Carcinoma line: HeLa.

LOCATION/Qualifiers

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ORIGIN
Query Match 71.9%; Score 616; DB 9; Length 845;
Best Local Similarity 100.0%; Pred. No. 2.9e-82;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 242 GAGATCCTGAAGGAGCTAGACGAGTGTCTACGAGCGCTTCAGTCCGCGAGACAGACGCGGCG 301
DB 141 GAGATCCTGAAGGAGCTAGACGAGTGTCTACGAGCGCTTCAGTCCGCGAGACAGACGCGGCG 200
QY 302 CAGAAAGCGCGGATGCTGCTGTGTGAGCGCGGCTGATCCGAGCGAGGAGCTGGGC 361
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QY 362 GACGAGAGATCCAGATCGTGAGCGAGATGTGTGAGCTGTGTGAGGAGACCGCAGCGCGAG 421
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QY 422 GTGACAGCAGCAGTGTGTGAGCGCGAGCAGGAGGAGTGTGTGAGGAGACCGCAGCGCGAG 481
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DB 381 ACCGCAAGGCTGGCGGAGCAGGCGCCAAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 440
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DB 501 CACGACCAAGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 560
QY 662 AAGAGCAAGCGCTCAAGCGCGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 721
DB 561 AAGAGCAAGCGCTCAAGCGCGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 620
QY 722 GACCCCAAGCAAGCGGAGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 781
DB 621 GACCCCAAGCAAGCGGAGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 680
QY 782 TGCAGCAAGCGAGGAGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 841
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QY 842 AACCCCAAGGCGAAGT 857
DB 741 AACCCCAAGGCGAAGT 756

LOCUS AX367042 1533 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 1 from Patent WO0147959.
ACCESSION AX367042
VERSION AX367042.1 GI:18855267
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Jager, D., Stockert, E., Scanlan, M., Knuth, A., Old, L., Gure, A. and
AUTHORS Chen, Y.T.
TITLE Isolated nucleic acid molecules encoding cancer associated
antigens, the antigens per se, and uses thereof
JOURNAL Patent: WO 0147959-A 1 05-JUL-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL
SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation
(US)
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Best Local Similarity 100.0%; Pred. No. 2.5e-82;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 10
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LOCUS
DEFINITION
Sequence 1 from Patent WO20068468.
ACCESSION
AX839842
VERSION
AX839842.1 GI:39978381
KEYWORDS
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SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Isolated human tumor suppressor proteins, nucleic acid molecules
encoding these human tumor suppressor proteins, and uses thereof
Patent: WO 02068468-A 1 06-SEP-2002;
JOURNAL
PE Corporation (NY) (US)
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
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ORIGIN
Query Match 71.9%; Score 616; DB 5; Length 1905;
Best Local Similarity 100.0%; Pred. No. 2.3e-82;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 452 GACGAGAGATCCAGATCTGTGAGCCAGATGTTGAGAGCTGTGGAGAACCGCACGCGGCGAG 511
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RESULT 11
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LOCUS
DEFINITION
Homo sapiens p33ING1 (ING1) gene, exon 2 and complete cds.
ACCESSION
AF078837
VERSION
AF078837.1 GI:10039548
KEYWORDS
2 of 2
SEGMENT
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2096)
Nagashima, M., Hagiwara, K. and Harris, C.C.
Direct Submission
Submitted (18-JUL-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, National Institutes of Health, 37
Convent Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA
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Best Local Similarity 100.0%; Pred. No. 2.3e-82;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 242 GAGATCCTGAAGGAGCTAGACAGAGTCTACGAGCGCTTCAGTCCGCGAGACAGACGCGGCG 301
DB 145 GAGATCCTGAAGGAGCTAGACAGAGTCTACGAGCGCTTCAGTCCGCGAGACAGACGCGGCG 204
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DB 265 GACGAGAGATCCAGATCTGTGAGCGCAAGATGTTGAGAGTCTGTGAGAACCCGACCGCGCAG 324
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RESULT 12
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 LOCUS
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 ACCESSION AF167551
 VERSION AF167551.1 GI:9944279
 KEYWORDS
 SEGMENT
 SOURCE 3 of 3
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 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE	1 (cases 1 to 2552)
AUTHORS	Barancova, A.V., Ivanov, D.V., Makeeva, N.V., Corcoran, M., Nikitin, E.A., Poltarauk, A.B., Glinshikova, O., Soudarikov, A.B., Osicir, D., and Yankovsky, N.K.
TITLE	Genomic organization of the INCI tumor suppressor gene
JOURNAL	FEBS Lett. (1999) in press
REFERENCE	2 (cases 1 to 2552)
AUTHORS	Barancova, A.V., Ivanov, D.V., Makeeva, N.V., Corcoran, M., Poltarauk, A.B., Borodina, T.A. and Tyazelova, T.A.

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            General Genetics, Gubkina, 3, Moscow 117809 GSP-1, Russia
            Submitted (12-JUL-1999) Genome Analysis Lab, Vavilov Institute of
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REFERENCE 1 (bases 1 to 2897)
AUTHORS Ma, D., Lawless, D. and Riabowol, K.
TITLE Sequence conservation of ING1 splicing isoforms in divergent
JOURNAL Nat. Genet. 23, 373 (1999)
REFERENCE 2 (bases 1 to 2897)
AUTHORS Ma, D., Lawless, D. and Riabowol, K.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-1999) Department of Biochemistry and Molecular
Biology, University of Calgary, 3330 Hospital Drive N.W., Calgary,
Alberta T2N 4N1, Canada
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QY 302 CAGAACGGCGGATGCTGCACTGTGTGCACGCGCGCTGATCCGACGACGAGAGCTGGGC 361
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gunduz, M., Ouchida, M., Fukushima, K., Hanafusa, H., Etani, T.,
Nishio, S., Nishizaki, K. and Shimizu, K.
TITLE Genomic structure of the human ING1 gene and tumor-specific
mutations detected in head and neck squamous cell carcinomas
JOURNAL Cancer Res. 60 (12), 3143-3146 (2000)
MEDLINE 20322670
PUBMED 10866301
REFERENCE 2 (bases 1 to 2925)
AUTHORS Ouchida, M., Mehmet, G. and Shimizu, K.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2000) Mamoru Ouchida, Okayama University Medical
School, Department of Molecular Genetics, Shikata-cho, 2-5-1,
Okayama 700-8558, Japan (E-mail:ouchidamed@med.okayama-u.ac.jp,
Tel:81-86-235-7379, Fax:81-86-235-7383)
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* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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Fri May 7 09:17:27 2004

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